A transcriptome-wide association study among 97,898 women to identify candidate susceptibility genes for epithelial ovarian cancer risk

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Abstract:

Large-scale genome-wide association studies (GWAS) have identified approximately 35 loci associated with epithelial ovarian cancer (EOC) risk. The majority of GWAS-identified disease susceptibility variants are located in non-coding regions, and causal genes underlying these associations remain largely unknown. Here we performed a transcriptome-wide association study to search for novel genetic loci and plausible causal genes at known GWAS loci. We used RNA sequencing data (68 normal ovarian-tissue samples from 68 individuals and 6,124 cross-tissue samples from 369 individuals) and high-density genotyping data from European descendants of the Genotype-Tissue Expression (GTEx V6) project to build ovarian and cross-tissue models of genetically regulated expression using elastic net methods. We evaluated 17,121 genes for their cis-predicted gene expression in relation to EOC risk using summary statistics data from GWAS of 97,898 women, including 29,396 EOC cases. With a Bonferroni-corrected significance level of P<2.2×10-6, we identified 35 genes including *FZD4* at 11q14.2 (Z=5.08, $P=3.83\times10^{-7}$, the cross-tissue model; 1 Mb away from any GWAS-identified EOC risk variant), a potential novel locus for EOC risk. All other 34 significantly-associated genes were located within 1 Mb of known GWAS-identified loci, including 23 genes at 6 loci not previously linked to EOC risk. Upon conditioning on nearby known EOC GWAS-identified variants, the associations for 31 genes disappeared and 3 genes remained ($P<1.47 \times 10^{-3}$). These data identify one novel locus (*FZD4*) and 34 genes at 13 known EOC risk loci associated with EOC risk, providing new insights into EOC carcinogenesis.

Introduction

Epithelial ovarian cancer (EOC) has a substantial heritable component with a heritability estimated to be 22% (1). Genome-wide association studies (GWAS) have identified approximately 35 loci associated with EOC risk (2-12). Most reported associations are specific to the most common histologic subtype, serous EOC (2-7,9-12). Together, known GWAS-identified variants account for approximately 6.4% of EOC risk in the general population (12), indicating that additional susceptibility variants remain to be identified. In addition, genes that underlie the large majority of GWAS-identified risk loci remain unknown; most GWAS-identified variants are located in noncoding genomic regions that may be involved in regulation of gene expression. Recent mechanistic studies have demonstrated that GWAS-identified variants are more frequently located in active chromatin regions, and highly-enriched with expression quantitative trait loci (eQTL)(13,14). This evidence underscores the importance of transcriptional regulation in influencing human traits and disease susceptibility.

Prior studies on genetically-regulated gene expression were largely limited to easily accessible sources, such as adipose tissue and peripheral blood cells (15). Although the sample size in eQTL studies of peripheral blood cells recently reached the thousands, a relatively small number of genes are expressed in blood cells compared with other tissue types (14). Conclusions from eQTL studies in tumor tissue (*e.g.,* TCGA) should also be interpreted with caution due to the inherent complexity of transcriptional regulation caused by acquired somatic alterations (16). The Genotype-Tissue Expression (GTEx) project provides high-density genotype data and RNA sequencing (RNA-seq) transcriptome data from 53 tissues (14). We used these data to build models of genetically regulated expression for 17,121 genes. We investigated the association between these genetically-predicted gene expressions and EOC risk using data from 97,898 women including 29,396 EOC cases. We identified 35 genes at 14 loci associated with EOC risk, and provide additional evidence of a potential role for dysregulated ovarian function and imbalanced ovarian hormone production in ovarian carcinogenesis.

Materials and Methods

Genomic and transcriptomic data

The GTEx preliminary cleaned genome-wide genotype data and RNA-seq transcriptome data across 53 unique tissues (released on 2015-01-12) were downloaded from dbGaP (accession phs000424.GTEx.v6.p1). It included 183 GTEx donors genotyped on Illumina's Omni 5M and 267 GTEx donors genotyped on Omni 2.5M. Genomic and transcriptomic data were processed according to the GTEx protocol (http://www.gtexportal.org/home/documentationPage). The Omni 2.5M portion of hard-called genotypes from the Omni 2.5M or Omni 5M across all 450 donors were extracted and merged for analysis. We excluded variants with a genotyping call rate < 98%, with differential missingness between Omni 2.5M and Omni 5M arrays, with Hardy-Weinberg equilibrium P-value$<10^{-6}$ (for subjects of European ancestry), or with batch effects. Genotype data were imputed to the Haplotype Reference Consortium reference panel using minimac3 for imputation and SHAPEIT for prephasing (17). Variants with high imputation quality ($R^2 \geq 0.8$), minor allele frequency (MAF) ≥ 0.05, and inclusion in the HapMap Phase 2 project were used to build predicted expression models.

We used gene level expression in Reads Per Kilobase of transcript per Million mapped reads (RPKM) from RNA-SeQC for gene expression data. For ovarian transcriptomic data, genes were required to have expression in ≥10 individuals with >0.1 RPKM and raw counts >6. For our analysis of cross-tissue derived transcriptomic data (below), genes were filtered on mean expression levels with >0.1 RPKM and RPKM >0 required in at least 3 individuals (18). We performed quantile normalization to transform the expression profile of each sample to the same scale, and performed inverse quantile normalization for each gene to map each set of expression values to a normal distribution. Residual expression was calculated by regressing transformed expression data against three top principal components (PCs) derived from common genetic variants (MAF $\geq$0.05), top 15 or 35 probabilistic estimation of expression residuals (PEER) factors respectively for ovarian tissue and cross-tissue derived models (below)(19), sex (for cross-tissue only) to correct for batch effects and other potential experimental confounders.

European ancestry analysis of GTEx subjects

The ancestral analysis was conducted with 2,836 ancestry informative markers for 450 GTEx individuals and 1,092 individuals included in the 1000 Genome project (Phase 1)(20). Of the individuals with both genotype and transcriptome data available, 369 were clustered together with EUR populations (CEU, FIN, GBR, IBS and TSI) on the multidimensional scaling plot of the pairwise Identity-By-State distance and were included in the analysis, 68 of whom had transcriptome data available for ovarian tissue.

Orthogonal tissue decomposition derived cross tissue estimation

Mixed effect models were used to decompose gene expression levels into subject-specific and subject-by-tissue-specific components (18). GTEx data consisted of expression measurements from multiple tissues for each subject. The expression level of a gene at a given tissue for individual *i* was considered to be composed of a cross-tissue component represented as Y_i^{CT} and a tissue-specific component that was estimated as the difference between the expression levels and cross-tissue components given the lack of replicated measurement for a specific tissue/subject pair (18). Z'_i represents a vector of covariates that have effects of β on the expression levels of the gene, such as PEER factors, ancestry information derived from the principal component analysis, and sex. The expression of a gene for individual i in tissue t, $Y_{i,t}$, is modeled as

$$Y_{i,t} = Y_i^{CT} + Z'_i \beta + \epsilon_{i,t}$$

The mixed effect model parameters were estimated using the lme4 package in R. Posterior modes of the subject level random intercepts were used as estimates of the cross-tissue components (18). Cross-tissue model included gene expression from 6,124 GTEx tissue samples from 369 unique European individuals who had genome-wide genotype data available.

Ovarian-specific and cross-tissue genetically regulated expression model building

We built an expression prediction model for each gene using the elastic net method as implemented in the glmnet R package, with a ridge-lasso mixing parameter of $\alpha = 0.5$ and a penalty parameter lambda chosen through 10-fold cross-validation (18,21,22). The elastic net method with $\alpha = 0.5$ is a compromise between the ridge-regression penalty ($\alpha = 0$) for solutions with many parameters (each of small effects) and the lasso penalty ($\alpha = 1$) for solutions with fewer parameters (each of large effects)(18). The genetically regulated expression for each gene was estimated by including SNPs within 1 Mb of the gene start or end, as defined by GENCODE V19 gene annotations. Expression prediction models were built for protein-coding genes, long non-coding RNAs (lncRNAs), microRNAs (miRNAs), processed transcripts, immunoglobulin genes, and T cell receptor genes, according to categories described in the GENCODE V19 gene annotation file. Pseudogenes were not included in the present study because of potential concerns of inaccurate calling (23). Prediction r^2 values (the square of the correlation between predicted and observed expression) were generated to estimate the prediction performance for each gene in our prediction models.

With genome-wide genomic data and RNAseq-based tissue transcriptome data, we built an ovarian tissue *cis* genetically-regulated expression model for 8,580 genes that had predicted performance of $r^2 > 0.01$ and a cross-tissue *cis* genetically-regulated expression model for 14,085 genes that had predicted performance of $r^2 > 0.01$.

Association analysis of predicted gene expression with EOC risk

Associations between predicted gene expression levels and EOC risk were evaluated using MetaXcan (22). Briefly, the formula:

$$Z_g \approx \sum_{l \in \mathrm{Model}_g} w_{lg} \frac{\hat{\sigma}_l}{\hat{\sigma}_g} \frac{\hat{\beta}_l}{\mathrm{se}(\hat{\beta}_l)}$$

was used to estimate the Z-score of the association between predicted gene expression and ovarian cancer risk. Here w_{lg} is the weight of SNP l for predicting the expression of gene g, $\hat{\beta}_l$and $\mathrm{se}(\hat{\beta}_l)$ are the association regression coefficient and its standard error for SNP l in GWAS, and $\hat{\sigma}_l$ and $\hat{\sigma}_g$ are the estimated variances of SNP l and the predicted expression of gene g respectively. The input variables for the MetaXcan analyses include the weights for gene expression predicting SNPs, GWAS summary statistics results, and correlations between predictor SNPs. We integrated prediction models of gene expression levels with summary statistics from GWAS of EOC risk for 97,898 European women with 29,396 EOC cases from the Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of *BRCA1/2* (CIMBA)(12) based on the variance and covariance matrix of genetic variants derived from 1000 Genome phase 3 EUR population (N = 503). The performance of MetaXcan has been shown to be similar to PrediXcan that uses individual level genetic data for the identification of genes with expression that is associated with disease risk (21,22).

Details of individual contributing studies were previously reported (12). Briefly, the OCAC summary statistics were based on analysis of 40,941 controls and 25,509 population-based EOC cases (22,406 invasive cases and 3,103 borderline cases). OCAC cases included 1,954 serous borderline ovarian cancers, 1,149 mucinous borderline ovarian cancers, 1,417 mucinous invasive ovarian cancer, 1,012 low-grade serous ovarian cancers, 13,037 high-grade serous ovarian cancers, 2,810 endometrioid ovarian cancers, 1,366 clear-cell ovarian cancer and 2,764 other EOC cases. The CIMBA summary statistics were based on the analysis of 19,036 *BRCA1* and 12,412 *BRCA2* mutation carriers, of whom 2,933 and 954, respectively, were diagnosed with EOC. Details of the genotyping procedure and QC have been described elsewhere (12). In brief, samples were excluded if they had a genotyping call rate < 95%, excessively low or high heterozygosity, if they were not female or had ambiguous sex, or were duplicates (cryptic or intended)(12). SNPs were excluded for a call rate <95%, deviating from Hardy-Weinberg equilibrium ($P<10^{-7}$ in controls or unrelated samples in CIMBA and $P <10^{-12}$ in cases) and concordance <98% among 5,280 duplicate pairs (12). All participants provided written informed consent and each contributing study was approved by the appropriate local institutional ethical review board. The studies were conducted in accordance with Declaration of Helsinki.

We used a Bonferroni-corrected *P*-value threshold of 2.21×10^{-6} (adjusting for 22,665 gene-tissue pairs) to determine a statistically significant association in our analysis. This threshold was conservative as 5,544 genes appeared in both ovarian and cross-tissue models. We did the primary analysis for high-grade serous EOC, as this had the largest sample size. In our secondary analyses, we also evaluated other histotypes or the combined histotypes, even though power to discover novel gene associations was relatively low for some (*i.e.* clear-cell, endometrioid, or low-grade serous). To determine whether associations identified between genetically-predicted gene expression and EOC risk were influenced by variants previously-identified by GWAS, we conducted conditional analyses adjusting for index SNPs. Briefly, we performed conditional analyses developed by Yang *et al.* (24) (GCTA-COJO) to calculate association betas and standard errors of SNPs with ovarian cancer risk after adjusting for index SNPs of interest. This was followed by re-performing MetaXcan analyses using updated summary statistics.

Results

Gene expression prediction model building

We constructed genetically-regulated expression models based on genome-wide genotype data and RNA-seq transcriptome data from the GTEx project (14) (Supplementary Figure 1). Ovarian transcriptome data were available for 68 European individuals, and 8,580 genes achieved a prediction performance of $r^2 \geq 0.01$ in the ovarian model (**Table S1**). Because a large portion of *cis* expression regulation is shared across multiple tissues (14,18), we also used transcriptome data for 6,124 tissue samples from 369 European individuals to build cross-tissue models for 14,085 genes with a prediction performance of $r^2 \geq 0.01$ (**Table S1**).

Association analyses between predicted gene expression and EOC risk

We evaluated associations between predicted gene expression levels and EOC risk using MetaXcan (22) with summary statistics for individual GWAS SNPs from 97,898 European women including 29,396 EOC cases from OCAC and CIMBA(12) (Supplementary Figure 1). Our primary analysis focused on high-grade serous EOC; secondary analyses included other EOC histotypes (Supplementary Figure 1).

In total, we identified 35 genes with genetically-predicted expression that were associated with EOC risk at a Bonferroni-corrected threshold of $P < 2.21 \times 10^{-6}$ (**Figure 1, Supplementary Figure 2, Supplementary Figure 3, Tables 1, 2 and S2**). One gene at 11q14.2 (*FZD4*), was more than 1 Mb away from any GWAS-identified EOC susceptibility variant (**Figure 1**), suggesting a potential novel risk locus for this disease. High predicted *FZD4* expression was associated with increased risk of high-grade serous EOC ($Z = 5.08$, $P = 3.83 \times 10^{-7}$, **Figure 1**). The remaining 34 genes were located within 1 Mb of previously identified EOC susceptibility variants (**Tables 1, 2, S2 and S3**), including 11 genes (at 8 loci) that were previously implicated in EOC risk using functional annotation, bioinformatic prediction, *in vitro* cellular models or known gene biology. Our study provides additional evidence to support these previous findings (**Tables 2 and S3**). However, 23 genes (at 6 known risk loci) had not been reported to be associated with EOC risk in prior studies (**Tables 1 and S3**). For 31 of these 34 genes, the associations were no longer statistically significant at $P < 1.47 \times 10^{-3}$ (multiple comparisons correction of 0.05/34) after adjustment for the nearest SNP identified by EOC GWAS (**Table**

S4), indicating that the previously identified GWAS SNPs for EOC at these 31 regions might regulate the expression of these associated gene to affect EOC risk. Associations for three genes (Z= 6.84 vs 3.27 for *DNALI1*, Z= 5.16 vs 3.81 for *HOXD3* and Z= -8.60 vs -4.18 for *CCDC171;* Table 1, 2 and S4) remained statistically significant at $P < 1.47 \times 10^{-3}$ after adjusting for the nearest EOC risk SNP, although the strength of the association was attenuated. Four loci (2q31.1, 9p22.3, 17q21.31 and 17q21.32) had multiple nearby genes associated with EOC risk (**Tables 1 and 2**). This may be partially due to co-regulated gene expression in these chromosomal regions (**Table S5** and **Online Supplementary Material**).

Consistent with the etiologic heterogeneity of EOC(25), GWAS-identified risk variants differed across histologic subtypes(12). Therefore, we investigated associations between genes with $P < 2.21 \times 10^{-6}$ across all major histotypes of EOC (**Table S6**). The majority of identified genes were associated with high-grade serous EOC risk, likely due to the large number of cases in our primary analysis. A few additional histotype specific associations were identified from secondary analyses. *HOXD3* at 2q31.1 was associated with borderline mucinous EOC risk (**Tables 2 and S6**: $Z = 5.16$, $P = 2.42 \times 10^{-7}$). *RP11-403A21.1* at 18q11.2 was associated with low-grade or borderline serous EOC risk (**Tables 1 and S6**: $Z = -5.53$, $P = 3.13 \times 10^{-8}$). *ZNF546* at 19q13.2 was associated with mucinous EOC risk (**Tables 1 and S6**: $Z = 7.14$, $P = 9.07 \times 10^{-13}$ for invasive/borderline mucinous EOC combined; $Z = 5.99$ and $P = 2.14 \times 10^{-9}$ for borderline mucinous EOC only). *HOXD1* at 2q31.1 was associated with both invasive serous (**Table S6**: $Z = 4.92$, $P = 8.55 \times 10^{-7}$) and borderline mucinous (**Table S6:** $Z = 5.24$, $P = 1.59 \times 10^{-7}$) EOC risk.

Evidence from previous eQTL analyses of identified EOC susceptibility risk variants supports several currently identified gene associations (**Tables 2 and S3**). Reduced *OBFC1* expression was associated with risk allele of GWAS identified EOC SNP at 10q24.33 (12), and we found that higher predicted *OBFC1* expression was associated with lower EOC risk. Similarly, reduced *RCCD1* expression was associated with risk allele of GWAS identified EOC SNP (11), and we found that higher predicted *RCCD1* expression was associated with reduced EOC risk at 15q26.1. In addition, multiple lines of evidence support our finding between higher predicted *ABHD8* and increased EOC risk at 19p13.11. Increased *ABHD8* expression was associated with risk allele of GWAS identified EOC SNP (26). Copy number variant analysis indicated that forty-six percent of high-grade serous EOC had amplification at 19p13.11 that contains *ABHD8* (3).

Discussion

In this large transcriptome-wide association study (TWAS) among 97,898 women of European ancestry, we identified 35 genes with genetically-predicted expression levels associated with EOC risk. One of these genes (*FZD4*) is located more than 1 Mb away from any previously identified GWAS EOC variant (25 Mb away from the nearest reported EOC risk variant(11)), suggesting it is a potential novel risk locus. All other 34 genes identified were located within 1 Mb of known GWAS loci, including 23 genes at 6 loci that had not previously been associated with EOC risk. After adjustment for nearby known EOC GWAS-identified variants, the associations for 3 of the 34 genes retained.

FZD4 is a member of the frizzled gene family that encodes seven-transmembrane domain proteins (Fzs) as the receptors for the secreted Wnts signaling ligands. Several Wnts and Fzs (including Fzd4 and Wnt4), as well as downstream targets of the canonical WNT signaling pathway, are expressed at different stages of ovarian follicular development, ovulation, and luteinization, suggesting specific functions for these signaling molecules in the mature ovary(27). Recent studies using transgenic mouse models demonstrated that Wnt4, Fzd4 and Ctnnb1 are required for normal folliculogenesis, luteogenesis and steroidogenesis, and that dysregulated WNT signaling leads to granulosa cell tumor development (27,28). *FZD4*-null female mice are infertile and exhibit reduced progesterone production, reduced luteinization-associated gene expression, impaired corpora lutea formation and function, and impaired vascular development (28). Interestingly, *WNT4* (1p36.12) encodes a potential Fzd4 binding ligand, which was also recently identified as a potentially causal gene underlying EOC risk by GWAS (**Table S3**)(7). Aberrant activation of WNT signaling in adult tissues has been implicated in the pathogenesis of several types of cancer, including colorectal cancer (29). The positive association between *FZD4* expression and invasive serous EOC risk suggests that dysregulated corpus luteum function and/or progesterone production may contribute to EOC pathogenesis.

A locus 17q21.31 was previously identified by GWAS as associated with EOC risk (10,30). This region contains a 900-kb inversion in Europeans that has extensive linkage-disequilibrium likely due to restriction from crossovers in individuals who are heterozygous with respect to inversion (31). The H2 haplotype is less frequent (20% in Europeans) and is associated with higher number of children born to women (31). Interestingly, minor alleles of genetic variants in this region were almost universally associated with reduced breast cancer risk but increased EOC risk at genome-wide significance levels (**Table S7** and Online Supplementary Material)(10,30). Permuth-Wey *et al.*(10) investigated several of these genes, including *KIF18B, C1QL1, DCAKD, NMT1*, *PLCD3, ACBD4, HEXIM1*, *HEXIM2, FMNL1*, *C17orf46, MAP3K14*, *ARHGAP27, PLEKHM1*, *CRHR1*, *IMP5* and *MAPT*; extensive functional analysis suggested that *ARHGAP27* and *PLEKHM1* may be EOC susceptibility genes (10). One of the other candidate genes at this region, *CRHR1*, is involved in regulating ovarian function; it is expressed in ovarian thecal cells, granulosa cells and luteal cells (32), and upregulated in EOC (10). High *CRHR1* expression was almost universally associated with minor alleles of multiple genetic variants in this chromosome 17 region (**Table S8** and Online Supplementary Material)(33). Enhanced *CRHR1* activation in the ovary leads to reduced production of testosterone(32) and estrogen(32,34-36), but increased progesterone accumulation and production (32). This may explain the lower breast cancer risk associated with variants in this region from lower estrogen exposure and higher progesterone exposure associated with multiparity (31,37). Similarly, this also suggests that imbalanced estrogen and/or progesterone production contributes to EOC pathogenesis.

Two of the candidate genes at the 17q21.32 locus, *HOXB2* and *HOXB3*, belong to the homeobox gene family, which is important for normal vertebrate limb and organ development. This gene family was also recently shown to be enriched for genes underlying serous EOC risk by GWAS (38). Inconsistent tumorigenic effects of *HOXB2* and *HOXB3* were reported across several types of cancers (breast, pancreatic, lung, cervical cancer and acute myeloid leukemia)(39-43). This may be due to context-dependent effects from specific tumor microenvironments (39,43). With regard to ovarian cancer, increased *HOXB2* and *HOXB3* expression were associated with reduced EOC risk; potential molecular mechanisms underlying *HOXB* suppressive effect on EOC warrant further investigation.

Several additional findings from this study are noteworthy. The precise function of *DNALI1* at 1p34.3 is not known. It is a potential candidate gene for primary cilia syndrome or Kartagener syndrome, in which the action of cilia lining the respiratory tract and Fallopian tube is compromised (44). A marked reduction in fertility was observed in female Kartagener's syndrome patients due to dysfunction of the oviductal cilia (45). The predicted expression of *CCDC171* at 9p22.3 was associated with reduced EOC risk. *CCDC171* was shown to interact with *KRAS* by a stringent screening for Ras-synthetic-lethal genes (46). Several lncRNAs were associated with EOC risk, including *RP11-403A21.1* at 18q11.2 (Table 1). Little is known about their particular function in either tumor initiation or tumor development, but lncRNAs have been increasingly implicated in many classic cancer biology pathways (47). In addition to *HOXD3* and *HOXD1* at 2q31.1 (**Table 2** and **Table S3**)(4,8), *ZNF546* at 19q13.2 was identified as a novel candidate gene for mucinous EOC. Enrichment for expression in gonadal tissues (14) supports a potential role in EOC pathogenesis. Because of the complexity of mucinous EOC, and undetermined cell/tissue of origin, identification of associated genetic variants and/or genes is particularly important (8,25).

The tissue samples used in building gene expression models in GTEx (V6) came most from the people who recently died of traumatic injury (for these young donors) or cardio-cerebrovascular diseases (for the old donors). There were no overlaps between the tissues used in building gene expression models and the samples used in EOC GWAS in OCAC or CIMBA. Our ability to detect genes significantly associated with EOC risk is affected by tissue specificity and the sample size of the data set used to build genetic prediction models for gene expression. Four genes were identified from both ovarian and cross-tissue models; eight genes were only identified based on ovarian models; and twenty-three genes were only identified from cross-tissue models (**Table S2**). The ovarian tissue transcriptome that we used to model gene expression was potentially derived from multiple ovarian cell types, including surface epithelial cells, oocytes, granulosa cells, Theca cells, luteal cells and other interstitial cells. Because of the importance of tissue or cell specific regulators (*i.e.*, transcription factors or epigenomic features) in governing development and function, the ovarian-specific model should best capture transcriptional regulatory mechanisms of the ovary. However, in light of abundant shared *cis* regulation of expression across multiple tissues (14,18), we also pooled constitutive variant-dependent regulatory information across tissues and built cross-tissue gene expression models.

We would expect this model to yield greater power as the number of tissues in which a variant is functional increases. By coupling both tissue specific and cross-tissue models, we aimed to robustly capture genetically regulated genes expression using a large sample size. Due to insufficient samples in the GTEx project, we did not build Fallopian tube-specific models.

In summary, we identified one novel locus (*FZD4*) and 34 genes at 13 known EOC risk loci associated with EOC risk, and these findings may help improve our mechanistic understanding of EOC pathogenesis. In line with tentative observations of increased borderline EOC risk from ovarian hormone dysregulation for women who received fertility drug treatment with *in vitro* fertilization(48-50), the known biology of *FZD4* and *CRHR1* in the ovary implicates the potential of long-term dysregulated ovarian function or imbalanced ovarian hormone production as a possible mechanism underlying EOC pathogenesis.

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Table 1. Association results for genes in known loci not previously reported in association with epithelial ovarian cancer risk

Region	Gene[a]	Z-score	*P value*	*r*^{2b}	Histotype	Model	GWAS Index SNP[e]	Distance to the index SNP (kb)[f]
1p34.3	*DNALI1*	6.84	7.84E-12	0.29	High-grade serous[c]	cross-tissue	rs58722170	64
9p22.3	*CCDC171*	-8.60	8.08E-18	0.02	High-grade serous[c]	ovary	rs10962692	854
9p22.3	*C9orf92*	-5.16	2.45E-07	0.15	High-grade serous[c]	ovary	rs10962692	640
17q21.31	*ADAM11*	-4.86	1.19E-06	0.05	High-grade serous[c]	ovary	rs1879586	708
17q21.31	*AC091132.1*	-7.18	7.02E-13	0.03	High-grade serous[c]	cross-tissue	rs1879586	26
17q21.31	*RP11-798G7.8*	6.58	4.77E-11	0.05	High-grade serous[c]	ovary	rs1879586	42
17q21.31	*CRHR1*	8.61	7.23E-18	0.60	High-grade serous[c]	cross-tissue	rs1879586	132
17q21.31	*RP11-105N13.4*	6.77	1.33E-11	0.05	High-grade serous[c]	ovary	rs1879586	132
17q21.31	*MAPT-AS1*	7.74	9.60E-15	0.10	High-grade serous[c]	cross-tissue	rs1879586	354
17q21.31	*RP11-669E14.6*	-8.35	6.64E-17	0.30	High-grade serous[c]	cross-tissue	rs1879586	545
17q21.31	*KANSL1-AS1*	8.26	1.48E-16	0.85	High-grade serous[c]	cross-tissue	rs1879586	704
17q21.31	*LRRC37A*	8.38	5.08E-17	0.54	High-grade serous[c]	ovary	rs1879586	803
17q21.31	*LRRC37A2*	8.26	1.44E-16	0.55	High-grade serous[c]	ovary	rs1879586	1022
17q21.31	*NSF*	-5.55	2.78E-08	0.02	High-grade serous[c]	ovary	rs1879586	1101
17q21.32	*RP11-138C9.1*	5.54	3.04E-08	0.02	High-grade serous[c]	cross-tissue	rs7207826	741
17q21.32	*RP11-6N17.6*	5.93	3.00E-09	0.19	High-grade serous[c]	cross-tissue	rs7207826	475
17q21.32	*PNPO*	5.34	9.38E-08	0.30	High-grade serous[c]	cross-tissue	rs7207826	475
17q21.32	*PRR15L*	-4.91	9.18E-07	0.04	High-grade serous[c]	cross-tissue	rs7207826	465
17q21.32	*HOXB2*	-5.48	4.28E-08	0.40	High-grade serous[c]	cross-tissue	rs7207826	118
17q21.32	*HOXB-AS1*	-5.15	2.59E-07	0.29	High-grade serous[c]	cross-tissue	rs7207826	120
17q21.32	*HOXB3*	-5.59	2.30E-08	0.12	High-grade serous[c]	cross-tissue	rs7207826	126
18q11.2	*RP11-403A21.1*	-5.53	3.13E-08	0.11	Low grade/borderline serous[d]	cross-tissue	rs8098244	132
19q13.2	*ZNF546*	7.14	9.07E-13	0.01	Invasive/borderline mucinous[d]	ovary	rs688187	757

[a] *ARHGAP27* and *PLEKHM1* were previously considered as potential EOC candidate susceptibility genes by Permuth-Wey *et al.*(10) with an integrated molecular analysis of multiple genes at 17q21.31 locus (See Table 2 and Table S3);

[b] *r*^{2} of tissue model's correlation to gene's measured transcriptome (prediction performance);

[c] the analyses were based on summary statistics for high-grade serous ovarian cancers from Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA);

[d] the analyses were based on summary statistics from OCAC;
[e] See Table S4 for detailed information in selecting the GWAS index SNPs;
[f] If the GWAS index SNP is located upstream of the gene, the gene start position is used; otherwise, the gene end position was used; *LRRC37A2* and *NSF* are within 1M of reported GWAS SNPs considering the association of all variants with EOC risk at $P < 5\times10^{-8}$ at this locus (See text and Table S4 for details).

Table 2. Association results for genes in known loci previously reported in association with ovarian cancer risk

Region	Gene	Z-score	*P value*	r^{2a}	Histotype	Model	GWAS Index SNP[e]	Distance to the index SNP (kb) [f]
2q31.1	*HOXD3*	5.16	2.42E-07	0.04	Borderline mucinous[c]	cross-tissue	rs711830	0
2q31.1	*HOXD1*	6.07	1.31E-09	0.04	High-grade serous[b]	cross-tissue	rs711830	16
3q25.31	*LEKR1*	-5.81	6.24E-09	0.46	High-grade serous[b]	cross-tissue	rs62274041	108
8q21.13	*CHMP4C*	-6.69	2.24E-11	0.47	High-grade serous[c]	cross-tissue	rs11782652	0
9q34.2	*ABO*	5.44	5.37E-08	0.49	High-grade serous[b]	ovary	rs635634	4
10q24.33	*OBFC1*	-5.09	3.66E-07	0.01	Borderline serous[c]	cross-tissue	rs7902587	16
15q26.1	*RCCD1*	-5.46	4.64E-08	0.59	High-grade serous[c]	cross-tissue	rs8037137	0
17q21.31[d]	*PLEKHM1*	4.80	1.59E-06	0.01	High-grade serous[b]	cross-tissue	rs1879586	0
17q21.31[d]	*KANSL1*	4.74	2.15E-06	0.18	High-grade serous[b]	ovary	rs1879586	540
17q21.31[d]	*WNT3*	6.81	9.82E-12	0.40	High-grade serous[b]	cross-tissue	rs1879586	1273
19p13.11	*ABHD8*	4.79	1.69E-06	0.23	High-grade serous[b]	cross-tissue	rs4808075	13

[a] r^2 of tissue model's correlation to gene's measured transcriptome (prediction performance);

[b] the analyses were based on summary statistics for high-grade serous ovarian cancers from Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA);

[c] the analyses were based on summary statistics from OCAC;

[d] Eleven novel genes associated with EOC risk at this locus were presented in Table 1;

[e] See Table S4 for detailed information in selecting the GWAS index SNPs;

[f] If the GWAS index SNP is located upstream of the gene, the gene start position is used; otherwise, the gene end position was used; *WNT3* is within 1M of reported GWAS SNPs considering the association of all variants with EOC risk at $P < 5\times10^{-8}$ at this locus (See text and Table S4 for details).

Figure 1 | Regional plot of OCAC and CIMBA GWAS summary statistics around the *FZD4* gene associated with high-grade serous EOC risk (Z = 5.08, $P = 3.83 \times 10^{-7}$ based on the cross-tissue model of $r^2 = 0.07$, see supplementary Table 2 for details). Each symbol represents the significance (*P* value on a log10 scale) of a SNP with invasive EOC risk as a function of the SNP's genomic position (NCBI Build 37). The most significantly associated SNP is represented in the purple color. The color of all other SNPs indicates LD with this SNP (estimated by EUR r^2 from the 1000 Genome Project data). Recombination rates were also estimated from 1000 Genome Project data, and gene annotations were obtained from the UCSC Genome Browser. The circle shape denotes the SNPs included in the model construction of genetically regulated *FZD4* expression and the square shape denotes the SNPs not included in the model construction. The gene model was constructed including SNPs within 1 Mb of the gene start or end, and one SNP included in the model construction was located outside the 1Mb window size of the locus zoom plot (rs7944482 at chr11:86091532, $P = 0.52$ for association with high-grade serous EOC risk).

Online Supplementary Notes:

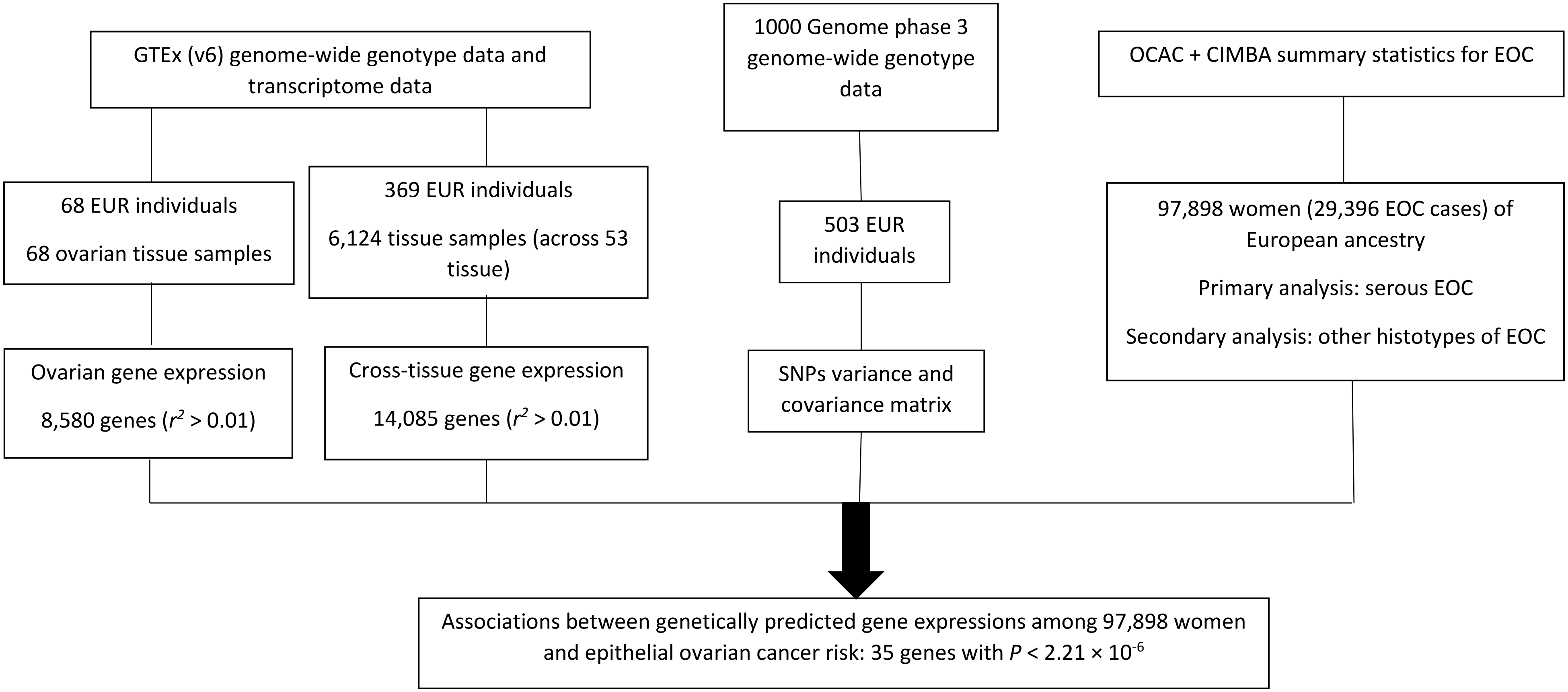
Additional Methods:

At each of four genetic loci (2q31.1, 9p22.3, 17q21.31 and 17q21.32), predicted expression levels of multiple genes were found to be associated with ovarian cancer risk (Tables 1 and 2). For Supplementary Table 5, the respective genetically predicted expression values for genes at these four loci were extracted from the glmnet model with the best lambda based on the expression dataset of Genotype-Tissue Expression project (See methods for details) and were correlated with each other at each locus. The Pearson correlation method was used. Genes with significant correlation (P value < 0.05) in predicted expression were highlighted in bold.

For Table S7, we defined the genomic interval based on the genes associated with epithelial ovarian cancer (EOC) at 17q21.31. The most upstream gene was *ADAM11* (Chromosome 17: 42,836,399-42,859,214; GENODE V19) and the most downstream gene was *WNT3* (Chromosome 17: 44,839,872-44,910,520, GENODE V19). All the variants that showed associations with either breast cancer or ovarian cancer with $P < 5\times10^{-8}$ and were located between 42,836,399 and 44,910,520 were extracted from the OCAC (OCAC overall invasive meta-analysis) and BCAC (OncoArray-iCOGS-GWAS meta-analysis) latest meta-analysis datasets. The effect direction of minor alleles was consistently opposite between breast cancer risk and EOC risk. The minor allele frequency for these variants is around 20%. Generally speaking, these minor alleles were associated with reduced breast cancer risk but increased EOC risk. However, there are five variants (17_43657437_A_G [MAF = 0.50], 17_43784228_T_C [MAF = 0.35], 17_43848495_G_T [MAF = 0.35], 17_44332093_G_A [MAF = 0.44] and 17_44342378_G_A [MAF = 0.44] in red) showed an opposite association pattern. These might be outlier variants based on their frequencies that deviated from the average 20%.

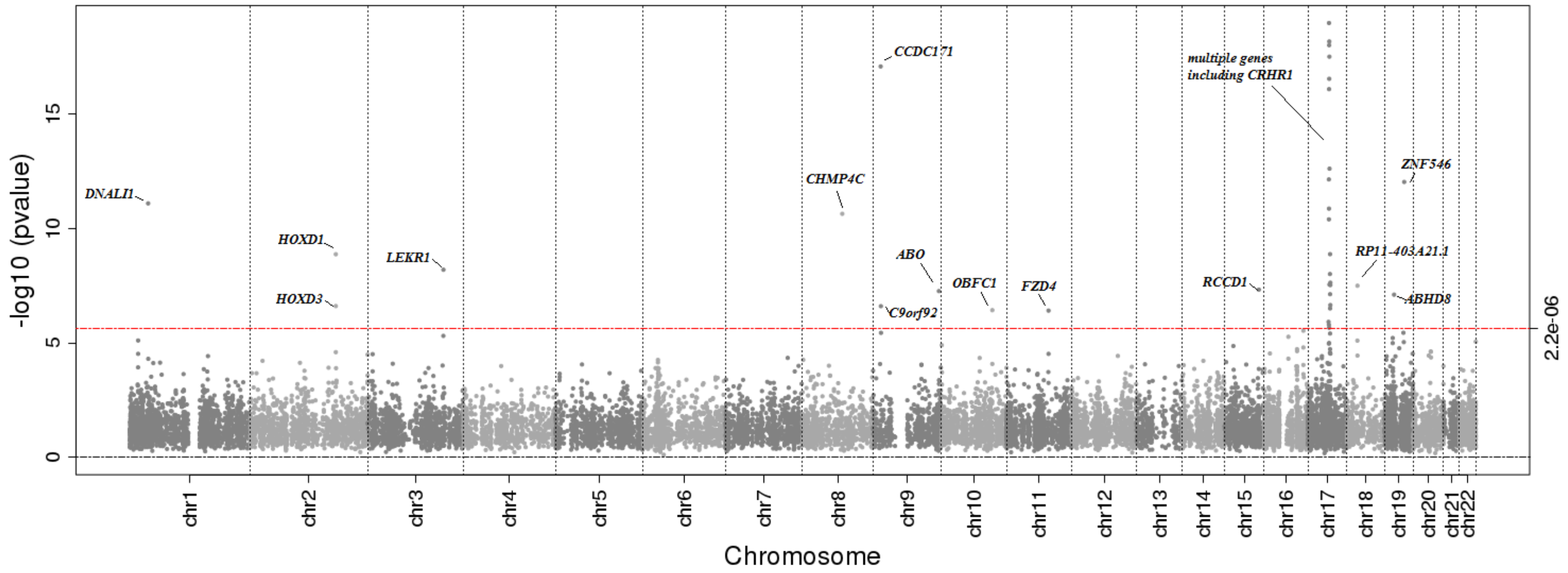
For Table S8, in the *CRHR1* cross-tissue gene expression prediction model, 467 variants were retained in the final model construction, among which 456 variants had significant associations with either breast cancer risk or epithelial ovarian cancer risk with $P < 5\times10^{-8}$ (Tables S7 and S8). The minor alleles of these 456 variants were all associated with increased *CRHR1* expression. For the other 11 variants, the minor alleles of 7 variants were also associated with increased *CRHR1* expression (rs8069296 [MAF = 0.21], rs962888 [MAF = 0.30], rs12449792 [MAF = 0.46], rs7216796 [MAF = 0.48], rs4328483 [MAF = 0.42], rs4792814 [MAF = 0.42], rs17686238 [MAF = 0.10]), and the minor alleles of other 4 variants (rs9911406 [MAF = 0.08], rs9890538 [MAF = 0.08], rs1635299 [MAF = 0.14] and rs16940742 [MAF = 0.06], highlighted in red) were associated with reduced *CRHR1* expression. The association between these four variants and either breast cancer risk or EOC risk were not strong (Table S8). Their minor allele frequencies for these four variants deviated from the overall 22% based on the 369 Europeans that were incorporated in the cross-tissue gene prediction model construction.

Supplementary Figure 1. The analysis flow chart

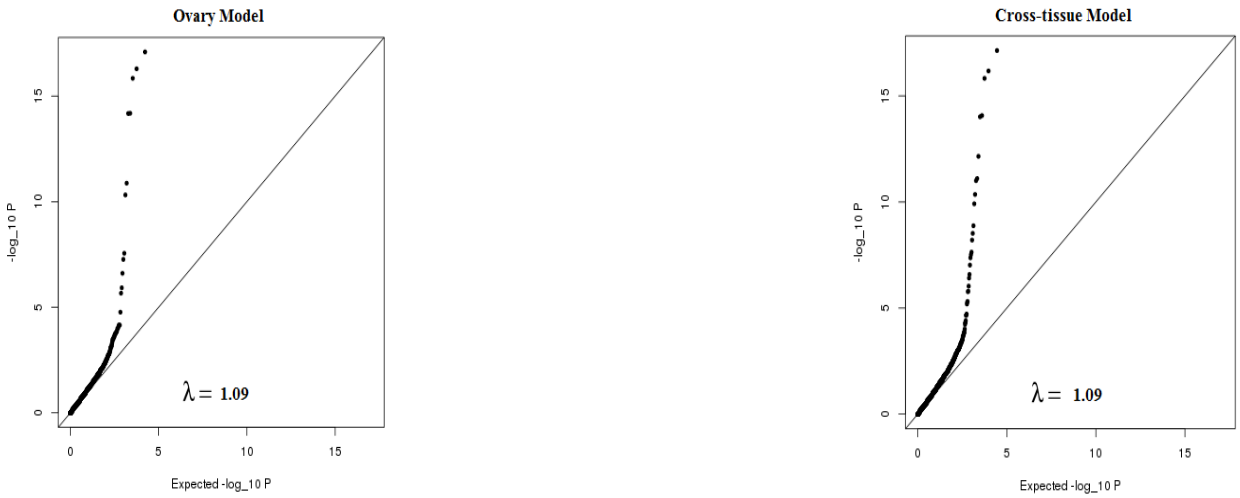


GTEx: Genotype-Tissue Expression project; EUR: individuals of European ancestry; OCAC: Ovarian Cancer Association Consortium; CIMBA: Consortium of Investigators of Modifiers of *BRCA1/2*; EOC: epithelial ovarian cancer. The tissue samples used in building gene expression models in GTEx (V6) came most from the people who recently died of traumatic injury (for these young donors) or cardio-cerebrovascular diseases (for the old donors). There were no overlaps between the tissues used in building gene expression models and the samples used in EOC GWAS in OCAC or CIMBA.

Supplementary Figure 2. The Manhattan plot of gene associations with epithelial ovarian cancer risk



Supplementary Figure 3. The QQ plot of gene associations with epithelial ovarian cancer risk



Supplementary Table S1. Internal performance of ovarian and cross-tissue gene expression prediction models built using GTEx data

Model	r^{2a}	All	Protein	lncRNAs	miRNAs	others[b]
Ovarian	0.01	8,580	5,969	2,331	96	184
	0.04	5,521	3,869	1,492	50	110
	0.09	3,049	2,138	827	20	64
	0.16	1,480	1,035	403	8	34
	N	11,921	8,302	3,226	139	254
Cross-tissue	0.01	14,085	9,951	3,798	60	276
	0.04	9,822	6,830	2,747	35	210
	0.09	6,710	4,543	1,979	27	161
	0.16	4,472	2,974	1,363	22	113
	N	18,896	13,371	5,016	109	400

Protein: Protein coding genes; lncRNAs: long non-coding RNAs; miRNAs: microRNAs

a r^2 of tissue model's correlation to gene's measured transcriptome (prediction performance)

b including processed transcripts, immunoglobulin genes, and T cell receptor genes

Supplementary Table S2. Chromosomal regions with predicted gene expression levels associated with epithelial ovarian cancer risk at $P < 2.21 \times 10^{-6}$ with either ovarian or cross-tissue model

Region	Gene ID	Gencode ID	Z-score	*P value*	r^{2}[a]	N[b]	covariance_N[b]	model_N[b]	Histotype	Model
1p34.3	*DNALI1*	ENSG00000163879.9	6.84	**7.84E-12**	0.29	90	90	90	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
2q31.1	*HOXD3*	ENSG00000128652.7	5.16	**2.42E-07**	0.04	52	52	52	mucinous: borderline[d]	cross-tissue
			-	-	-	-	-	-		ovary
2q31.1	*HOXD1*	ENSG00000128645.11	6.07	**1.31E-09**	0.04	42	42	42	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
3q25.31	*LEKR1*	ENSG00000197980.7	-5.81	**6.24E-09**	0.46	33	33	33	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.69	**2.24E-11**	0.47	39	39	39	Serous: high grade[d]	cross-tissue
			-	-	-	-	-	-		ovary
9p22.3	*CCDC171*	ENSG00000164989.11	-8.60	**8.08E-18**	0.02	8	8	8	High-grade serous[c]	ovary
			1.08	2.81E-01	0.26	92	92	92		cross-tissue
9p22.3	*C9orf92*	ENSG00000205549.4	-5.16	**2.45E-07**	0.15	51	51	51	High-grade serous[c]	ovary
			-	-	-	-	-	-		cross-tissue
9q34.2	*ABO*	ENSG00000175164.9	5.44	**5.37E-08**	0.49	53	53	53	High-grade serous[c]	ovary
			2.76	5.70E-03	0.52	68	69	69		cross-tissue
10q24.33	*OBFC1*	ENSG00000107960.6	-5.09	**3.66E-07**	0.01	28	28	28	Serous: borderline[d]	cross-tissue
			-	-	-	-	-	-		ovary
11q14.2	*FZD4*	ENSG00000174804.3	5.08	**3.83E-07**	0.07	8	8	8	High-grade serous[c]	cross-tissue
			-0.42	6.75E-01	0.13	56	56	56		ovary
15q26.1	*RCCD1*	ENSG00000166965.8	-5.46	**4.64E-08**	0.59	38	38	38	Serous: high grade[d]	cross-tissue
			-3.86	1.14E-04	0.08	22	22	22		ovary
17q21.31	*ADAM11*	ENSG00000073670.9	-4.86	**1.19E-06**	0.05	12	12	12	High-grade serous[c]	ovary
			-0.14	8.91E-01	0.16	12	12	12		cross-tissue
17q21.31	*AC091132.1*	ENSG00000236234.1	-7.18	**7.02E-13**	0.03	28	28	28	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.31	*PLEKHM1*	ENSG00000225190.4	4.80	**1.59E-06**	0.01	11	11	11	High-grade serous[c]	cross-tissue
			2.02	4.34E-02	0.01	29	29	29		ovary
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	6.58	**4.77E-11**	0.05	210	210	210	High-grade serous[c]	ovary
			-	-	-	-	-	-		cross-tissue
17q21.31	*CRHR1*	ENSG00000120088.10	8.61	**7.23E-18**	0.60	467	467	467	High-grade serous[c]	cross-tissue
			7.79	**6.51E-15**	0.49	36	36	36		ovary
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	6.77	**1.33E-11**	0.05	19	19	19	High-grade serous[c]	ovary
			-	-	-	-	-	-		cross-tissue
17q21.31	*MAPT-AS1*	ENSG00000264589.1	7.74	**9.60E-15**	0.10	30	30	30	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.31	*KANSL1*	ENSG00000120071.8	4.74	**2.15E-06**	0.18	75	75	75	High-grade serous[c]	ovary
			-0.07	9.46E-01	0.43	39	39	39		cross-tissue
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-8.35	**6.64E-17**	0.30	370	370	370	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	8.26	**1.48E-16**	0.85	58	58	58	High-grade serous[c]	cross-tissue
			7.79	**6.66E-15**	0.51	172	172	172		ovary
17q21.31	*LRRC37A*	ENSG00000176681.10	8.38	**5.08E-17**	0.54	599	599	599	High-grade serous[c]	ovary
			6.44	**1.21E-10**	0.68	49	49	49		cross-tissue
17q21.31	*LRRC37A2*	ENSG00000238083.3	8.26	**1.44E-16**	0.55	371	371	371	High-grade serous[c]	ovary
			7.76	**8.42E-15**	0.79	293	293	293		cross-tissue
17q21.31	*NSF*	ENSG00000073969.14	-5.55	**2.78E-08**	0.02	23	23	23	High-grade serous[c]	ovary
			-1.63	1.02E-01	0.03	7	7	7		cross-tissue
17q21.31	*WNT3*	ENSG00000108379.5	6.81	**9.82E-12**	0.40	14	14	14	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary

17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.54	**3.04E-08**	0.02	28	28	28	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	5.93	**3.00E-09**	0.19	19	19	19	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.32	*PNPO*	ENSG00000108439.5	5.34	**9.38E-08**	0.30	27	27	27	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.32	*PRR15L*	ENSG00000167183.2	-4.91	**9.18E-07**	0.04	12	12	12	High-grade serous[c]	cross-tissue
			-2.34	1.93E-02	0.05	48	48	48		ovary
17q21.32	*HOXB2*	ENSG00000173917.9	-5.48	**4.28E-08**	0.40	26	26	26	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-5.15	**2.59E-07**	0.29	31	31	31	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
17q21.32	*HOXB3*	ENSG00000120093.7	-5.59	**2.30E-08**	0.12	29	29	29	High-grade serous[c]	cross-tissue
			-	-	-	-	-	-		ovary
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-5.53	**3.13E-08**	0.11	14	14	14	Serous: low grade + borderline[d]	cross-tissue
			-1.05	2.93E-01	0.04	1	1	1		ovary
19p13.11	*ABHD8*	ENSG00000127220.5	4.79	**1.69E-06**	0.23	33	33	33	High-grade serous[c]	cross-tissue
			2.37	1.77E-02	0.08	71	71	71		ovary
19q13.2	*ZNF546*	ENSG00000187187.9	7.14	**9.07E-13**	0.01	22	22	22	Invasive/borderline mucinous[d]	ovary
			-	-	-	-	-	-		cross-tissue

a r^2 of tissue model's correlation to gene's measured transcriptome (prediction performance)

b N: number of snps from GWAS that were used in MetaXcan analysis; covariance_N: number of snps in the covariance matrix; model_N: number of snps in the model.

c The analyses were based on high-grade serous summary statistics from Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA);

d The analyses were based on summary statistics from OCAC.

Supplementary Table S3. Known common variants identified from genome-wide assocation studies and their bioinformatically predicted target genes.[a]

Locus#	Locus	SNP	Position (hg37)	Histotype	Nearby gene[b]	Highlighted target gene	Method used to assess potential causal genes	Reference	TWAS identified gene
1	1p36.12	rs56318008	22,470,407	Serous : invasive	*WNT4*	*WNT4, CDC42, LINC00339, RAP1GAP*	literature, differential gene expression between cancer tissue and normal tissue	Kuchenbaecker 2015	
2	1p34.3	rs58722170	38,096,421	Serous : invasive	*RSPO1*	*RSPO1, C1orf109, FHL3*	literature	Kuchenbaecker 2015	*DNALI1*
3	2q13	rs2165109	111,818,658	Serous : high-grade + *BRCA1/2* [c]	*ACOXL*	*BUB1, BCL2L11*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
	2q13	rs17041869	111,896,243	Serous	*BCL2L11*	*BCL2L11*	Enhancer enrichement, *cis* -Eqtl, pathway analysis,literature,	Kar 2016	
4	2q13	rs752590	113,972,945	Mucinous	*PAX8*	*PAX8*	cis-Eqtl, functional element annotation	Kelemen 2015	
5	2q31.1	rs2072590	177,042,633	Serous : invasive	*HOXD-AS1*	*HOXD3, HOXD1*	literature, differential gene expression between cancer tissue and normal tissue	Goode 2010	*HOXD3, HOXD1*
	2q31.1	rs711830	177,037,311	Mucinous	*HOXD3*	*HOXD9*	cis-Eqtl, chromosome conformation capture, in vitro over expression, functional element annotation	Kelemen 2015	
6	3q23	rs112071820	138,849,110	Mucinous : invasive + borderline	*MRPS22*	*FOXL2, RBP1*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
7	3q25.31	rs2665390	156,397,749	Serous : invasive	*TIPARP*	*TIPARP*	literature, differential gene expression between cancer tissue and normal tissue, in vitro model	Goode 2010	*LEKR1*
	3q25.31	rs7651446	156,406,997	Serous : invasive	*TIPARP*	-	-	Pharoah 2013	
	3q25.31	rs62273959	156,570,680	Serous : invasive	*LEKR1*	*LEKR1*	coding variant	Permuth 2016	
8	3q28	rs9870207	190,525,516	Serous : low-grade + borderline	*RP11-332P22.2*	*GMNC*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
9	4q26	rs17329882	119,949,960	Serous : invasive	*SYNPO2*	*SYNPO2*	literature, differential gene expression between cancer tissue and normal tissue	Kuchenbaecker 2015	
10	4q32.3	rs4691139	165,908,721	*BRCA1* [c]	*TRIM61*	*TRIM60, c4orf39, TMEM192*	Expressed in ovarian epithelium and/or ovarian tumors	Couch 2013	
11	4q32.3	rs13113999	167,187,046	Serous : borderline	*AC093874.1*	-	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
12	5p15.33	rs10069690	1,279,790	Serous : invasive	*TERT*	*TERT*	Promoter activity, alternative splicing of TERT, open chromatin analysis, methylation, association with telomere lenghth	Bojesen 2013	
	5p15.33	rs2242652	1,280,028	Serous : invasive	*TERT*	*TERT*	Promoter activity, alternative splicing of TERT, open chromatin analysis, methylation, association with telomere lenghth	Bojesen 2013	
	5p15.33	rs7705526	1,285,974	Serous: borderline	*TERT*	*TERT*	Promoter activity, alternative splicing of TERT, open chromatin analysis, methylation, association with telomere lenghth	Bojesen 2013	
13	5q12.3	rs555025179	66,121,089	Endometrioid	*MAST4*	-	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
14	6p22.1	rs116133110 (rs6456822)	28,480,635	Serous : invasive	*GPX6*	*ZKSCAN3, TRIM27*	literature	Kuchenbaecker 2015	
15	8q21.11	rs150293538	77,320,354	Serous : low-grade + borderline	*LINC01111, LINC01109*	-	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
16	8q21.13	rs11782652	82,653,644	Serous : invasive	*CHMP4C*	*CHMP4C*	cis-Eqtl, methylation, literature	Pharoah 2013	*CHMP4C*
17	8q24.21	rs9886651	128,817,883	Serous : high-grade + *BRCA1/2* [c]	*PVT1*	*PVT1 , MYC*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
	8q24.21	rs10088218	129,543,949	Serous : invasive	*RP11-89M16.1*	*MYC*	literature	Goode 2010	
18	9p22.2	rs3814113	16,915,021	Serous : invasive	*BNC2*	*BNC2*	literature, differential gene expression between cancer tissue and normal tissue, in vitro model	Song 2009, Permuth 2016, Goode 2010	*CCDC171, C9orf92*
19	9q31.1	rs320203	104,943,226	Mucinous : invasive + borderline	*RNU6-329P*	-	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
20	9q31.1	rs200182588	106,856,690	Serous : invasive	*SMC2*	*SMC2*	cis-Eqtl, literature	Kar 2016	
21	9q34.2	rs635634	136,155,000	Serous : invasive	*ABO*	*ABO, TSC1, RALGDS,RPL7A, VAV2*	literature, differential gene expression between cancer tissue and normal tissue	Kuchenbaecker 2015	*ABO*
22	10p12.31	rs1243180	21,915,619	Serous : invasive	*MLLT10*	*NEBL, C10orf114, SKIDA1, MLLT10*	cis-Eqtl, methylation, differential gene expression between cancer tissue and normal tissue, CNV, literature	Pharoah 2013	
23	10q24.33	rs7902587	105,694,301	Serous : low-grade + borderline	*OBFC1*	*OBFC1*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	*OBFC1*
24	11q12.3	rs7937840	61,893,972	Serous : invasive	*INCENP*	*INCENP, MTA2*	literature	Kar 2016	
25	12q24.31	rs7953249	121,403,724	Serous : high-grade + *BRCA1/2* [c]	*HNF1A-AS1*	*HNF1A, ORAI1*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	
26	15q26.1	rs8037137	91,506,637	Serous : invasive	*RCCD1*	*RCCD1*	cis-Eqtl	Kar 2016	*RCCD1*
27	17q11.2	rs199661266 (chr17:29181220:I)	29,181,221	Serous : invasive	*ATAD5*	*NF1, ATAD5*	literature	Kuchenbaecker 2015	
28	17q12	rs7405776	36,093,022	Serous : invasive	*HNF1B*	*HNF1B*	methylation, protein expression	Shen 2013	
	17q12	rs757210	36,096,515	Serous : invasive	*HNF1B*	*HNF1B*	methylation, differential gene expression between cancer tissue and normal tissue, literature	Pharoah 2013	
	17q12	rs11651755	36,099,840	Clear cell	*HNF1B*	*HNF1B*	methylation, protein expression, in vitro model	Shen 2013	
29	17q21.31	rs2960000	43,499,839	Serous : invasive	*ARHGAP27*	*ARHGAP27, PLEKHM1*	cis-Eqtl, differential gene expression between cancer tissue and normal tissue, CNV, methylation	Permuth-Wey 2013	*798G7.8, CRHR1, RP11-105N13.4, MAPT-AS1, KANSL1, RP11-669E14.6, KANSL1-AS1, LRRC37A, LRRC37A2, NSF, WNT3*
	17q21.31	rs17631303	43,516,402	*BRCA1* [c]	*PLEKHM1*	*PLEKHM1, c17orf69, ARHGAP27, MAPT, KANSL1, WNT3*	cis-Eqtl	Couch 2013	
30	17q21.32	rs9303542	46,411,500	Serous : invasive	*SKAP1*	*SKAP1*	literature, differential gene expression between cancer tissue and normal tissue, in vitro model	Pharoah 2013, Goode 2010	*RP11-138C9.1, RP11-6N17.6, PNPO, PRR15L, HOXB2, HOXB-AS1, HOXB3*
31	18q11.2	rs8098244	21,405,553	Serous : LG + borderline	*LAMA3*	*LAMA3, TTC39C*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	*RP11-403A21.1*
32	19p13.11	rs8170	17,389,704	Serous : invasive	*BABAM1*	*C19orf62 (MERIT40), ANKLE1, ABHD8*	literature, CNV, cis-Eqtl, Chromosome conformation capture, functional annotation, functional analysis of promoter and enhancer SNPs, *in vitro* overexpression	Bolton 2011, Lawrenson 2016	*ABHD8*
	19p13.11	rs2363956	17,394,124	Serous : invasive	*ANKLE1*	*C19orf62 (MERIT40), ANKLE1, ABHD8*	literature, CNV, cis-Eqtl, Chromosome conformation capture, functional annotation, functional analysis of promoter and enhancer SNPs, *in vitro* overexpression	Bolton 2011, Lawrenson 2016	
33	19p13.11	rs1469713	19,528,806	Serous : invasive	*GATAD2A*	*GATAD2A*	cis-Eqtl, Enhancer enrichement, literature	Kar 2016	
34	19q13.2	rs688187	39,732,752	Mucinous	*IFNL3*	*IFNL3*	coding variant annotation	Kelemen 2015	*ZNF546*
35	22q12.1	rs6005807	28,934,313	Serous : invasive	*TTC28*	*TTC28, CHEK2, XPB1*	Functional annotation, cis-Eqtl, methylation, literature	Phelan 2017	

a Rows highlighted in grey indicate that nearby genes were assocated with ovarian cancer risk in current transcriptome-wide association analysis.

b GENCODE V19

c *BRCA* mutation carriers

Supplementary Table S4. Results after the adjustment for nearby GWAS index SNPs for genes with predicted gene expression levels associated with ovarian cancer risk at $P < 2.21 \times 10^{-6}$

Region	Gene ID	Gencode ID	Gene location (hg19)	GWAS-index SNP	Position (hg19)	*Z value* after adjusting for index SNPs	*P value* after adjusting for index SNPs	N[c]	covariance_N[c]	model_N[c]	Histotype	Model
1p34.3	*DNALI1*	ENSG00000163879.9	Chromosome 1: 38,022,520-38,032,458	rs58722170	38,096,421	3.27	1.08E-03	90	90	90	High-grade serous[d]	cross-tissue
2q31.1	*HOXD3*	ENSG00000128652.7	Chromosome 2: 177,001,340-177,037,830	rs711830[a]	177,037,311	3.81	1.40E-04	52	52	52	Borderline mucinous[e]	cross-tissue
2q31.1	*HOXD1*	ENSG00000128645.11	Chromosome 2: 177,053,307-177,055,688			2.65	7.99E-03	42	42	42	High-grade serous[d]	cross-tissue
3q25.31	*LEKR1*	ENSG00000197980.7	Chromosome 3: 156,543,270-156,763,918	rs62274041[b]	156,435,640	0.74	4.60E-01	33	33	33	High-grade serous[d]	cross-tissue
8q21.13	*CHMP4C*	ENSG00000164695.4	Chromosome 8: 82,644,669-82,671,750	rs11782652	82,653,644	-0.48	6.33E-01	***38***	39	39	High-grade serous[e]	cross-tissue
9p22.3	*CCDC171*	ENSG00000164989.11	Chromosome 9: 15,552,895-16,061,661	rs10962692[b]	16,915,874	-4.18	2.90E-05	8	8	8	High-grade serous[d]	ovary
9p22.3	*C9orf92*	ENSG00000205549.4	Chromosome 9: 16,203,933-16,276,311			-2.25	2.44E-02	51	51	51	High-grade serous[d]	ovary
9q34.2	*ABO*	ENSG00000175164.9	Chromosome 9: 136,125,788-136,150,617	rs635634	136,155,000	1.97	4.92E-02	53	53	53	High-grade serous[d]	ovary
10q24.33	*OBFC1*	ENSG00000107960.6	Chromosome 10: 105,642,300-105,677,963	rs7902587	105,694,301	-2.32	2.06E-02	28	28	28	Borderline serous[e]	cross-tissue
15q26.1	*RCCD1*	ENSG00000166965.8	Chromosome 15: 91,498,100-91,506,349	rs8037137	91,506,637	-1.02	3.10E-01	***35***	38	38	High-grade serous[e]	cross-tissue
17q21.31	*ADAM11*	ENSG00000073670.9	Chromosome 17: 42,836,399-42,859,214	rs1879586[b]	43,567,337	-0.95	3.43E-01	12	12	12	High-grade serous[d]	ovary
17q21.31	*AC091132.1*	ENSG00000236234.1	Chromosome 17: 43,530,210-43,541,431			-1.49	1.36E-01	25	28	28	High-grade serous[d]	cross-tissue
17q21.31	*PLEKHM1*	ENSG00000225190.4	Chromosome 17: 43,513,266-43,568,115			0.04	9.72E-01	***4***	11	11	High-grade serous[d]	cross-tissue
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	Chromosome 17: 43,608,943-43,611,204			0.12	9.01E-01	210	210	210	High-grade serous[d]	ovary
17q21.31	*CRHR1*	ENSG00000120088.10	Chromosome 17: 43,699,267-43,913,194			1.32	1.88E-01	467	467	467	High-grade serous[d]	cross-tissue
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	Chromosome 17: 43,699,274-43,893,909			1.07	2.83E-01	19	19	19	High-grade serous[d]	ovary
17q21.31	*MAPT-AS1*	ENSG00000264589.1	Chromosome 17: 43,921,017-43,972,966			-0.39	6.98E-01	30	30	30	High-grade serous[d]	cross-tissue
17q21.31	*KANSL1*	ENSG00000120071.8	Chromosome 17: 44,107,282-44,302,733			1.46	1.44E-01	***65***	75	75	High-grade serous[d]	ovary
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	Chromosome 17: 44,112,679-44,113,136			-1.13	2.58E-01	370	370	370	High-grade serous[d]	cross-tissue
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	Chromosome 17: 44,270,942-44,274,089			0.91	3.61E-01	58	58	58	High-grade serous[d]	cross-tissue
17q21.31	*LRRC37A*	ENSG00000176681.10	Chromosome 17: 44,370,099-44,415,160			1.18	2.37E-01	599	599	599	High-grade serous[d]	ovary
17q21.31	*LRRC37A2*	ENSG00000238083.3	Chromosome 17: 44,588,877-44,633,016			1.20	2.32E-01	371	371	371	High-grade serous[d]	ovary
17q21.31	*NSF*	ENSG00000073969.14	Chromosome 17: 44,668,035-44,834,830			-1.06	2.90E-01	23	23	23	High-grade serous[d]	ovary
17q21.31	*WNT3*	ENSG00000108379.5	Chromosome 17: 44,839,872-44,910,520			1.02	3.10E-01	14	14	14	High-grade serous[d]	cross-tissue
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	Chromosome 17: 45,759,783-45,760,049	rs7207826[b]	46,500,673	0.52	6.05E-01	28	28	28	High-grade serous[d]	cross-tissue
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	Chromosome 17: 46,024,168-46,025,641			1.12	2.63E-01	19	19	19	High-grade serous[d]	cross-tissue
17q21.32	*PNPO*	ENSG00000108439.5	Chromosome 17: 46,018,872-46,025,654			1.01	3.12E-01	27	27	27	High-grade serous[d]	cross-tissue
17q21.32	*PRR15L*	ENSG00000167183.2	Chromosome 17: 46,029,333-46,035,244			0.19	8.48E-01	12	12	12	High-grade serous[d]	cross-tissue
17q21.32	*HOXB2*	ENSG00000173917.9	Chromosome 17: 46,618,256-46,623,441			0.13	8.97E-01	26	26	26	High-grade serous[d]	cross-tissue
17q21.32	*HOXB-AS1*	ENSG00000230148.4	Chromosome 17: 46,620,913-46,628,610			0.28	7.83E-01	31	31	31	High-grade serous[d]	cross-tissue
17q21.32	*HOXB3*	ENSG00000120093.7	Chromosome 17: 46,626,232-46,682,274			0.18	8.58E-01	29	29	29	High-grade serous[d]	cross-tissue
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	Chromosome 18: 21,537,718-21,562,520	rs8098244	21,405,553	-2.50	1.23E-02	14	14	14	Low grade/borderline serous[e]	cross-tissue
19p13.11	*ABHD8*	ENSG00000127220.5	Chromosome 19: 17,402,940-17,421,045	rs4808075[b]	17,390,291	-0.26	7.98E-01	33	33	33	High-grade serous[d]	cross-tissue
19q13.2	*ZNF546*	ENSG00000187187.9	Chromosome 19: 40,490,041-40,523,514	rs688187	39,732,752	-0.36	7.16E-01	***21***	22	22	Mucinous all[e]	ovary

a One additional SNP of rs6755777 (Phelan 2017) was also selected but was not included in the conditional analysis due to the multicollinearity.

b These GWAS index SNPs were based on the lastest GWAS of EOC risk (Phelan 2017); otherwise, they were reported in other studies (See Table S3 for details).

c N: number of snps from GWAS that were used in conditional MetaXcan analysis and fewer SNPs were included for genes of *CHMP4C, RCCD1, AC091132.1, PLEKHM1, KANSL1 and ZNF546* due to multicollinearity; covariance_N: number of snps in the covariance matrix; model_N: number of snps in the model.

d The analyses were based on high-grade serous summary statistics from Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA);

e The analyses were based on summary statistics from OCAC.

Supplementary Table S5. Genes coregulated in predicted expression at 2q31.1, 9p22.3, 17q21.31 and 17q21.32.$^{a, b}$

2q31.1			
Ovarian			***HOXD1***
	HOXD3	Rho	0.0955
		P	0.4388
Cross-tissue			***HOXD1***
	HOXD3	Rho	**0.5346**
		P	**<.0001**

9p22.3			
Ovarian			*C9orf92*
	CCDC171	Rho	0.0426
		P	0.7302

17q21.31														
Ovarian			***AC091132.1***	***PLEKHM1***	***RP11-798G7.8***	***CRHR1***	***RP11-105N13.4***	***KANSL1***	***RP11-669E14.6***	***KANSL1-AS1***	***LRRC37A***	***LRRC37A2***	***NSF***	***WNT3***
	ADAM11	Rho	-0.0133	-0.0164	**-0.4649**	**-0.4488**	**-0.5950**	**-0.3205**	0.0819	**-0.4508**	**-0.4861**	**-0.5234**	**0.4001**	0.0415
		P	0.9141	0.8947	**<.0001**	**0.0001**	**<.0001**	**0.0077**	0.5067	**0.0001**	**<.0001**	**<.0001**	**0.0007**	0.7368
	AC091132.1	Rho		0.0872	-0.2128	-0.2089	-0.0284	-0.3080	0.0192	-0.2447	-0.2029	-0.2001	0.2931	0.0509
		P		0.4797	0.0815	0.0873	0.8180	0.0106	0.8768	0.0443	0.0970	0.1018	0.0153	0.6801
	PLEKHM1	Rho			-0.1104	-0.0952	0.0313	-0.0567	0.1410	-0.0652	-0.0880	-0.0745	0.0730	-0.0588
		P			0.3703	0.4400	0.8000	0.6460	0.2516	0.5976	0.4756	0.5459	0.5540	0.6338
	RP11-798G7.8	Rho				**0.7765**	**0.4518**	**0.5264**	0.0418	**0.8640**	**0.8161**	**0.8122**	**-0.4974**	0.0543
		P				**<.0001**	**0.0001**	**<.0001**	0.7351	**<.0001**	**<.0001**	**<.0001**	**<.0001**	0.6603
	CRHR1	Rho					**0.5856**	**0.4071**	0.0477	**0.8468**	**0.8969**	**0.8598**	**-0.5378**	-0.1067
		P					**<.0001**	**0.0006**	0.6996	**<.0001**	**<.0001**	**<.0001**	**<.0001**	0.3864
	RP11-105N13.4	Rho						0.1459	-0.0816	**0.5291**	**0.6396**	**0.6279**	-0.1462	-0.0796
		P						0.2352	0.5085	**<.0001**	**<.0001**	**<.0001**	0.2341	0.5186
	KANSL1	Rho							-0.1135	**0.5948**	**0.4120**	**0.5110**	**-0.3578**	0.0005
		P							0.3566	**<.0001**	**0.0005**	**<.0001**	**0.0027**	0.9966
	RP11-669E14.6	Rho								-0.0046	0.0071	-0.0476	-0.1837	0.0838
		P								0.9706	0.9541	0.7001	0.1338	0.4970
	KANSL1-AS1	Rho									**0.9324**	**0.9387**	**-0.5447**	0.0058
		P									**<.0001**	**<.0001**	**<.0001**	0.9629
	LRRC37A	Rho										**0.9589**	**-0.4614**	0.0087
		P										**<.0001**	**<.0001**	0.9438
	LRRC37A2	Rho											**-0.4543**	0.0101
		P											**<.0001**	0.9351
	NSF	Rho												0.1803
		P												0.1413
Cross-tissue			***AC091132.1***	***PLEKHM1***	***CRHR1***	***RP11-105N13.4***	***MAPT-AS1***	***KANSL1***	***RP11-669E14.6***	***KANSL1-AS1***	***LRRC37A***	***LRRC37A2***	***NSF***	***WNT3***
	ADAM11	Rho	0.0996	**-0.1329**	0.0481	0.0781	0.0695	-0.0124	-0.0600	0.0860	0.0381	0.0602	-0.0341	0.0988
		P	0.0560	**0.0106**	0.3568	0.1341	0.1831	0.8119	0.2504	0.0989	0.4662	0.2489	0.5140	0.0579
	AC091132.1	Rho		**-0.2585**	**-0.6308**	**-0.5420**	**-0.6259**	**0.1034**	**0.6448**	**-0.5845**	**-0.4882**	**-0.6064**	**0.1175**	**-0.5199**
		P		**<.0001**	**<.0001**	**<.0001**	**<.0001**	**0.0471**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**0.0240**	**<.0001**
	PLEKHM1	Rho			**0.3951**	**0.2752**	**0.3796**	0.0510	**-0.3908**	**0.3711**	**0.2270**	**0.3398**	**-0.1864**	**0.2994**
		P			**<.0001**	**<.0001**	**<.0001**	0.3286	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**0.0003**	**<.0001**
	CRHR1	Rho				**0.7671**	**0.9657**	-0.0206	**-0.9880**	**0.9503**	**0.8056**	**0.9496**	**-0.2351**	**0.7993**
		P				**<.0001**	**<.0001**	0.6934	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**
	RP11-105N13.4	Rho					**0.7521**	-0.0172	**-0.7556**	**0.7483**	**0.6320**	**0.7530**	**-0.1765**	**0.6500**
		P					**<.0001**	0.7420	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**0.0007**	**<.0001**
	MAPT-AS1	Rho						-0.0264	**-0.9655**	**0.9438**	**0.7839**	**0.9342**	**-0.2304**	**0.7983**

	P	0.6137	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**
KANSL1	Rho		0.0178	**0.2089**	**-0.1765**	-0.0232	**-0.6977**	**-0.2555**
	P		0.7331	**<.0001**	**0.0007**	0.6571	**<.0001**	**<.0001**
RP11-669E14.6	Rho			**-0.9504**	**-0.8036**	**-0.9506**	**0.2373**	**-0.7934**
	P			**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**
KANSL1-AS1	Rho				**0.7497**	**0.9263**	**-0.4006**	**0.7504**
	P				**<.0001**	**<.0001**	**<.0001**	**<.0001**
LRRC37A	Rho					**0.9164**	**0.1618**	**0.7460**
	P					**<.0001**	**0.0018**	**<.0001**
LRRC37A2	Rho						**-0.1384**	**0.8184**
	P						**0.0078**	**<.0001**
NSF	Rho							-0.0329
	P							0.5285

17q21.32								
Ovarian			***RP11-6N17.6***	***PNPO***	***PRR15L***	***HOXB2***	***HOXB-AS1***	***HOXB3***
	RP11-138C9.1	Rho	-0.0120	0.2001	0.0065	-0.0921	0.1196	-0.1411
		P	0.9224	0.1019	0.9583	0.4549	0.3315	0.2512
	RP11-6N17.6	Rho		0.1692	0.0192	-0.1377	-0.1288	-0.1540
		P		0.1677	0.8766	0.2627	0.2954	0.2099
	PNPO	Rho			0.0616	0.0201	0.0889	0.0573
		P			0.6177	0.8706	0.4709	0.6424
	PRR15L	Rho				-0.0491	-0.0872	-0.0273
		P				0.6907	0.4796	0.8254
	HOXB2	Rho					**0.3128**	0.1399
		P					**0.0094**	0.2553
	HOXB-AS1	Rho						-0.0200
		P						0.8716
Cross-tissue			***RP11-6N17.6***	***PNPO***	***PRR15L***	***HOXB2***	***HOXB-AS1***	***HOXB3***
	RP11-138C9.1	Rho	**0.4014**	**0.4199**	**-0.2260**	**-0.5598**	**-0.5491**	**-0.5024**
		P	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**
	RP11-6N17.6	Rho		**0.9118**	**-0.5565**	**-0.4650**	**-0.4509**	**-0.5138**
		P		**<.0001**	**<.0001**	**<.0001**	**<.0001**	**<.0001**
	PNPO	Rho			**-0.3830**	**-0.4151**	**-0.4128**	**-0.4602**
		P			**<.0001**	**<.0001**	**<.0001**	**<.0001**
	PRR15L	Rho				**0.3465**	**0.3297**	**0.4446**
		P				**<.0001**	**<.0001**	**<.0001**
	HOXB2	Rho					**0.9683**	**0.9120**
		P					**<.0001**	**<.0001**
	HOXB-AS1	Rho						**0.8973**
								<.0001

a The analysis was based on the predicted expression data from Genotype-Tissue Expression Project (See Online Supplementary Material for details).

b The genes highly correlated in expression were highlighed in bold (based on Pearson correlation).

Supplementary Table S6. Association results between associated genes with $P < 2.21 \times 10^{-6}$ and risk of different histotypes of epithelial ovarian cancer.

Region	Gene ID	Gencode ID	Z-score	*P value* [a]	r^2[b]	N[c]	covariance_N[c]	model_N[c]	Model	Histotype
1p34.3	*DNALI1*	ENSG00000163879.9	6.13	**8.57E-10**	0.29	90	90	90	cross-tissue	Combined all[d]
1p34.3	*DNALI1*	ENSG00000163879.9	6.84	**7.84E-12**	0.29	90	90	90	cross-tissue	Serous: high-grade[d]
1p34.3	*DNALI1*	ENSG00000163879.9	-0.46	6.47E-01	0.29	90	90	90	cross-tissue	Clear cell[e]
1p34.3	*DNALI1*	ENSG00000163879.9	-0.77	4.41E-01	0.29	90	90	90	cross-tissue	Endometrioid[e]
1p34.3	*DNALI1*	ENSG00000163879.9	2.28	2.26E-02	0.29	90	90	90	cross-tissue	Invasive mucinous[e]
1p34.3	*DNALI1*	ENSG00000163879.9	2.10	3.54E-02	0.29	90	90	90	cross-tissue	Invasive/borderline mucinous[e]
1p34.3	*DNALI1*	ENSG00000163879.9	0.64	5.23E-01	0.29	90	90	90	cross-tissue	Mucinous: borderline[e]
1p34.3	*DNALI1*	ENSG00000163879.9	4.32	1.54E-05	0.29	90	90	90	cross-tissue	All: invasive[e]
1p34.3	*DNALI1*	ENSG00000163879.9	1.82	6.91E-02	0.29	90	90	90	cross-tissue	Serous: low-grade + borderline[e]
1p34.3	*DNALI1*	ENSG00000163879.9	4.99	**6.09E-07**	0.29	90	90	90	cross-tissue	Serous: invasive[e]
1p34.3	*DNALI1*	ENSG00000163879.9	5.27	**1.36E-07**	0.29	90	90	90	cross-tissue	Serous: high-grade[e]
1p34.3	*DNALI1*	ENSG00000163879.9	2.15	3.18E-02	0.29	90	90	90	cross-tissue	Serous: borderline[e]
1p34.3	*DNALI1*	ENSG00000163879.9	0.31	7.59E-01	0.29	90	90	90	cross-tissue	Serous: low-grade[e]
2q31.1	*HOXD3*	ENSG00000128652.7	4.16	3.17E-05	0.04	52	52	52	cross-tissue	Combined all[d]
2q31.1	*HOXD3*	ENSG00000128652.7	4.24	2.22E-05	0.04	52	52	52	cross-tissue	Serous: high-grade[d]
2q31.1	*HOXD3*	ENSG00000128652.7	0.59	5.52E-01	0.04	52	52	52	cross-tissue	Clear cell[e]
2q31.1	*HOXD3*	ENSG00000128652.7	1.12	2.64E-01	0.04	52	52	52	cross-tissue	Endometrioid[e]
2q31.1	*HOXD3*	ENSG00000128652.7	0.33	7.40E-01	0.04	52	52	52	cross-tissue	Invasive mucinous[e]
2q31.1	*HOXD3*	ENSG00000128652.7	3.77	1.65E-04	0.04	52	52	52	cross-tissue	Invasive/borderline mucinous[e]
2q31.1	*HOXD3*	ENSG00000128652.7	5.16	**2.42E-07**	0.04	52	52	52	cross-tissue	Mucinous: borderline[e]
2q31.1	*HOXD3*	ENSG00000128652.7	3.58	3.48E-04	0.04	52	52	52	cross-tissue	All: invasive[e]
2q31.1	*HOXD3*	ENSG00000128652.7	1.40	1.61E-01	0.04	52	52	52	cross-tissue	Serous: low-grade + borderline[e]
2q31.1	*HOXD3*	ENSG00000128652.7	3.67	2.44E-04	0.04	52	52	52	cross-tissue	Serous: invasive[e]
2q31.1	*HOXD3*	ENSG00000128652.7	3.35	8.09E-04	0.04	52	52	52	cross-tissue	Serous: high-grade[e]
2q31.1	*HOXD3*	ENSG00000128652.7	0.39	6.97E-01	0.04	52	52	52	cross-tissue	Serous: borderline[e]
2q31.1	*HOXD3*	ENSG00000128652.7	1.63	1.03E-01	0.04	52	52	52	cross-tissue	Serous: low-grade[e]
2q31.1	*HOXD1*	ENSG00000128645.11	5.73	**9.97E-09**	0.04	42	42	42	cross-tissue	Combined all[d]
2q31.1	*HOXD1*	ENSG00000128645.11	6.07	**1.31E-09**	0.04	42	42	42	cross-tissue	Serous: high-grade[d]
2q31.1	*HOXD1*	ENSG00000128645.11	-0.30	7.68E-01	0.04	42	42	42	cross-tissue	Clear cell[e]
2q31.1	*HOXD1*	ENSG00000128645.11	3.11	1.84E-03	0.04	42	42	42	cross-tissue	Endometrioid[e]
2q31.1	*HOXD1*	ENSG00000128645.11	1.32	1.87E-01	0.04	42	42	42	cross-tissue	Invasive mucinous[e]
2q31.1	*HOXD1*	ENSG00000128645.11	4.45	8.77E-06	0.04	42	42	42	cross-tissue	Invasive/borderline mucinous[e]
2q31.1	*HOXD1*	ENSG00000128645.11	5.24	**1.59E-07**	0.04	42	42	42	cross-tissue	Mucinous: borderline[e]
2q31.1	*HOXD1*	ENSG00000128645.11	4.59	4.46E-06	0.04	42	42	42	cross-tissue	All: invasive[e]
2q31.1	*HOXD1*	ENSG00000128645.11	3.53	4.11E-04	0.04	42	42	42	cross-tissue	Serous: low-grade + borderline[e]
2q31.1	*HOXD1*	ENSG00000128645.11	4.92	**8.55E-07**	0.04	42	42	42	cross-tissue	Serous: invasive[e]
2q31.1	*HOXD1*	ENSG00000128645.11	4.55	5.37E-06	0.04	42	42	42	cross-tissue	Serous: high-grade[e]
2q31.1	*HOXD1*	ENSG00000128645.11	2.76	5.85E-03	0.04	42	42	42	cross-tissue	Serous: borderline[e]
2q31.1	*HOXD1*	ENSG00000128645.11	2.18	2.94E-02	0.04	42	42	42	cross-tissue	Serous: low-grade[e]

3q25.31	*LEKR1*	ENSG00000197980.7	-5.70	**1.22E-08**	0.46	33	33	33	cross-tissue	Combined all[d]
3q25.31	*LEKR1*	ENSG00000197980.7	-5.81	**6.24E-09**	0.46	33	33	33	cross-tissue	Serous: high-grade[d]
3q25.31	*LEKR1*	ENSG00000197980.7	-1.96	5.05E-02	0.46	33	33	33	cross-tissue	Clear cell[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-1.61	1.08E-01	0.46	33	33	33	cross-tissue	Endometrioid[e]
3q25.31	*LEKR1*	ENSG00000197980.7	0.33	7.38E-01	0.46	33	33	33	cross-tissue	Invasive mucinous[e]
3q25.31	*LEKR1*	ENSG00000197980.7	0.43	6.69E-01	0.46	33	33	33	cross-tissue	Invasive/borderline mucinous[e]
3q25.31	*LEKR1*	ENSG00000197980.7	0.41	6.81E-01	0.46	33	33	33	cross-tissue	Mucinous: borderline[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-5.29	**1.22E-07**	0.46	33	33	33	cross-tissue	All: invasive[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-0.13	8.99E-01	0.46	33	33	33	cross-tissue	Serous: low-grade + borderline[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-5.47	**4.45E-08**	0.46	33	33	33	cross-tissue	Serous: invasive[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-5.32	**1.03E-07**	0.46	33	33	33	cross-tissue	Serous: high-grade[e]
3q25.31	*LEKR1*	ENSG00000197980.7	1.02	3.06E-01	0.46	33	33	33	cross-tissue	Serous: borderline[e]
3q25.31	*LEKR1*	ENSG00000197980.7	-1.46	1.45E-01	0.46	33	33	33	cross-tissue	Serous: low-grade[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.24	**4.48E-10**	0.47	39	39	39	cross-tissue	Combined all[d]
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.59	**4.40E-11**	0.47	39	39	39	cross-tissue	Serous: high-grade[d]
8q21.13	*CHMP4C*	ENSG00000164695.4	-0.97	3.31E-01	0.47	39	39	39	cross-tissue	Clear cell[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	0.02	9.85E-01	0.47	39	39	39	cross-tissue	Endometrioid[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-0.39	7.00E-01	0.47	39	39	39	cross-tissue	Invasive mucinous[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	0.25	8.03E-01	0.47	39	39	39	cross-tissue	Invasive/borderline mucinous[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	0.90	3.69E-01	0.47	39	39	39	cross-tissue	Mucinous: borderline[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.04	**1.56E-09**	0.47	39	39	39	cross-tissue	All: invasive[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	0.64	5.21E-01	0.47	39	39	39	cross-tissue	Serous: low-grade + borderline[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.53	**6.54E-11**	0.47	39	39	39	cross-tissue	Serous: invasive[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-6.69	**2.24E-11**	0.47	39	39	39	cross-tissue	Serous: high-grade[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	1.23	2.20E-01	0.47	39	39	39	cross-tissue	Serous: borderline[e]
8q21.13	*CHMP4C*	ENSG00000164695.4	-0.55	5.86E-01	0.47	39	39	39	cross-tissue	Serous: low-grade[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-8.17	**3.12E-16**	0.02	8	8	8	ovary	Combined all[d]
9p22.3	*CCDC171*	ENSG00000164989.11	-8.60	**8.08E-18**	0.02	8	8	8	ovary	Serous: high-grade[d]
9p22.3	*CCDC171*	ENSG00000164989.11	-1.43	1.52E-01	0.02	8	8	8	ovary	Clear cell[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-2.47	1.36E-02	0.02	8	8	8	ovary	Endometrioid[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-1.98	4.82E-02	0.26	92	92	92	cross-tissue	Invasive mucinous[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-0.88	3.81E-01	0.26	92	92	92	cross-tissue	Invasive/borderline mucinous[e]
9p22.3	*CCDC171*	ENSG00000164989.11	1.43	1.53E-01	0.02	8	8	8	ovary	Mucinous: borderline[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-6.97	**3.16E-12**	0.02	8	8	8	ovary	All: invasive[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-0.82	4.11E-01	0.02	8	8	8	ovary	Serous: low-grade + borderline[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-7.46	**8.69E-14**	0.02	8	8	8	ovary	Serous: invasive[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-7.46	**8.45E-14**	0.02	8	8	8	ovary	Serous: high-grade[e]
9p22.3	*CCDC171*	ENSG00000164989.11	0.60	5.46E-01	0.26	92	92	92	cross-tissue	Serous: borderline[e]
9p22.3	*CCDC171*	ENSG00000164989.11	-1.28	2.00E-01	0.02	8	8	8	ovary	Serous: low-grade[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-4.43	9.33E-06	0.15	51	51	51	ovary	Combined all[d]
9p22.3	*C9orf92*	ENSG00000205549.4	-5.16	**2.45E-07**	0.15	51	51	51	ovary	Serous: high-grade[d]

9p22.3	*C9orf92*	ENSG00000205549.4	0.68	4.98E-01	0.15	51	51	51	ovary	Clear cell[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-0.71	4.77E-01	0.15	51	51	51	ovary	Endometrioid[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-0.37	7.10E-01	0.15	51	51	51	ovary	Invasive mucinous[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-0.08	9.35E-01	0.15	51	51	51	ovary	Invasive/borderline mucinous[e]
9p22.3	*C9orf92*	ENSG00000205549.4	0.41	6.82E-01	0.15	51	51	51	ovary	Mucinous: borderline[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-3.24	1.21E-03	0.15	51	51	51	ovary	All: invasive[e]
9p22.3	*C9orf92*	ENSG00000205549.4	0.70	4.83E-01	0.15	51	51	51	ovary	Serous: low-grade + borderline[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-4.00	6.38E-05	0.15	51	51	51	ovary	Serous: invasive[e]
9p22.3	*C9orf92*	ENSG00000205549.4	-4.25	2.11E-05	0.15	51	51	51	ovary	Serous: high-grade[e]
9p22.3	*C9orf92*	ENSG00000205549.4	0.70	4.84E-01	0.15	51	51	51	ovary	Serous: borderline[e]
9p22.3	*C9orf92*	ENSG00000205549.4	0.47	6.40E-01	0.15	51	51	51	ovary	Serous: low-grade[e]
9q34.2	*ABO*	ENSG00000175164.9	5.21	**1.91E-07**	0.49	53	53	53	ovary	Combined all[d]
9q34.2	*ABO*	ENSG00000175164.9	5.44	**5.37E-08**	0.49	53	53	53	ovary	Serous: high-grade[d]
9q34.2	*ABO*	ENSG00000175164.9	0.19	8.47E-01	0.52	68	69	69	cross-tissue	Clear cell[e]
9q34.2	*ABO*	ENSG00000175164.9	1.67	9.51E-02	0.49	53	53	53	ovary	Endometrioid[e]
9q34.2	*ABO*	ENSG00000175164.9	1.51	1.30E-01	0.49	53	53	53	ovary	Invasive mucinous[e]
9q34.2	*ABO*	ENSG00000175164.9	-2.12	3.42E-02	0.52	68	69	69	cross-tissue	Invasive/borderline mucinous[e]
9q34.2	*ABO*	ENSG00000175164.9	-1.93	5.40E-02	0.52	68	69	69	cross-tissue	Mucinous: borderline[e]
9q34.2	*ABO*	ENSG00000175164.9	4.79	**1.69E-06**	0.49	53	53	53	ovary	All: invasive[e]
9q34.2	*ABO*	ENSG00000175164.9	0.98	3.28E-01	0.52	68	69	69	cross-tissue	Serous: low-grade + borderline[e]
9q34.2	*ABO*	ENSG00000175164.9	5.10	**3.44E-07**	0.49	53	53	53	ovary	Serous: invasive[e]
9q34.2	*ABO*	ENSG00000175164.9	5.02	**5.12E-07**	0.49	53	53	53	ovary	Serous: high-grade[e]
9q34.2	*ABO*	ENSG00000175164.9	-0.77	4.44E-01	0.49	53	53	53	ovary	Serous: borderline[e]
9q34.2	*ABO*	ENSG00000175164.9	2.69	7.09E-03	0.52	68	69	69	cross-tissue	Serous: low-grade[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-2.16	3.05E-02	0.01	28	28	28	cross-tissue	Combined all[d]
10q24.33	*OBFC1*	ENSG00000107960.6	-2.31	2.10E-02	0.01	28	28	28	cross-tissue	Serous: high-grade[d]
10q24.33	*OBFC1*	ENSG00000107960.6	0.09	9.28E-01	0.01	28	28	28	cross-tissue	Clear cell[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-1.71	8.66E-02	0.01	28	28	28	cross-tissue	Endometrioid[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-0.89	3.73E-01	0.01	28	28	28	cross-tissue	Invasive mucinous[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-0.37	7.11E-01	0.01	28	28	28	cross-tissue	Invasive/borderline mucinous[e]
10q24.33	*OBFC1*	ENSG00000107960.6	0.46	6.48E-01	0.01	28	28	28	cross-tissue	Mucinous: borderline[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-2.00	4.57E-02	0.01	28	28	28	cross-tissue	All: invasive[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-4.68	2.85E-06	0.01	28	28	28	cross-tissue	Serous: low-grade + borderline[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-2.19	2.89E-02	0.01	28	28	28	cross-tissue	Serous: invasive[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-2.02	4.36E-02	0.01	28	28	28	cross-tissue	Serous: high-grade[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-5.09	**3.66E-07**	0.01	28	28	28	cross-tissue	Serous: borderline[e]
10q24.33	*OBFC1*	ENSG00000107960.6	-1.04	2.99E-01	0.01	28	28	28	cross-tissue	Serous: low-grade[e]
11q14.2	*FZD4*	ENSG00000174804.3	3.91	9.31E-05	0.07	8	8	8	cross-tissue	Combined all[d]
11q14.2	*FZD4*	ENSG00000174804.3	5.08	**3.83E-07**	0.07	8	8	8	cross-tissue	Serous: high-grade[d]
11q14.2	*FZD4*	ENSG00000174804.3	0.04	9.68E-01	0.13	56	56	56	ovary	Clear cell[e]
11q14.2	*FZD4*	ENSG00000174804.3	0.42	6.74E-01	0.13	56	56	56	ovary	Endometrioid[e]

11q14.2	*FZD4*	ENSG00000174804.3	0.75	4.56E-01	0.13	56	56	56	ovary	Invasive mucinous[e]
11q14.2	*FZD4*	ENSG00000174804.3	0.50	6.14E-01	0.07	8	8	8	cross-tissue	Invasive/borderline mucinous[e]
11q14.2	*FZD4*	ENSG00000174804.3	1.45	1.47E-01	0.07	8	8	8	cross-tissue	Mucinous: borderline[e]
11q14.2	*FZD4*	ENSG00000174804.3	3.39	6.95E-04	0.07	8	8	8	cross-tissue	All: invasive[e]
11q14.2	*FZD4*	ENSG00000174804.3	1.55	1.21E-01	0.07	8	8	8	cross-tissue	Serous: low-grade + borderline[e]
11q14.2	*FZD4*	ENSG00000174804.3	4.75	**2.02E-06**	0.07	8	8	8	cross-tissue	Serous: invasive[e]
11q14.2	*FZD4*	ENSG00000174804.3	4.42	1.00E-05	0.07	8	8	8	cross-tissue	Serous: high-grade[e]
11q14.2	*FZD4*	ENSG00000174804.3	1.39	1.64E-01	0.13	56	56	56	ovary	Serous: borderline[e]
11q14.2	*FZD4*	ENSG00000174804.3	2.74	6.19E-03	0.07	8	8	8	cross-tissue	Serous: low-grade[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-4.38	1.17E-05	0.59	38	38	38	cross-tissue	Combined all[d]
15q26.1	*RCCD1*	ENSG00000166965.8	-4.51	6.38E-06	0.59	38	38	38	cross-tissue	Serous: high-grade[d]
15q26.1	*RCCD1*	ENSG00000166965.8	0.36	7.18E-01	0.59	38	38	38	cross-tissue	Clear cell[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-1.74	8.25E-02	0.08	22	22	22	ovary	Endometrioid[e]
15q26.1	*RCCD1*	ENSG00000166965.8	1.04	2.99E-01	0.08	22	22	22	ovary	Invasive mucinous[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-0.84	4.03E-01	0.59	38	38	38	cross-tissue	Invasive/borderline mucinous[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-1.15	2.52E-01	0.59	38	38	38	cross-tissue	Mucinous: borderline[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-5.05	**4.32E-07**	0.59	38	38	38	cross-tissue	All: invasive[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-1.56	1.20E-01	0.59	38	38	38	cross-tissue	Serous: low-grade + borderline[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-5.41	**6.36E-08**	0.59	38	38	38	cross-tissue	Serous: invasive[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-5.46	**4.64E-08**	0.59	38	38	38	cross-tissue	Serous: high-grade[e]
15q26.1	*RCCD1*	ENSG00000166965.8	-1.49	1.35E-01	0.59	38	38	38	cross-tissue	Serous: borderline[e]
15q26.1	*RCCD1*	ENSG00000166965.8	1.58	1.14E-01	0.08	22	22	22	ovary	Serous: low-grade[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-4.15	3.31E-05	0.05	12	12	12	ovary	Combined all[d]
17q21.31	*ADAM11*	ENSG00000073670.9	-4.86	**1.19E-06**	0.05	12	12	12	ovary	Serous: high-grade[d]
17q21.31	*ADAM11*	ENSG00000073670.9	-0.07	9.42E-01	0.05	12	12	12	ovary	Clear cell[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-0.44	6.59E-01	0.16	12	12	12	cross-tissue	Endometrioid[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-0.33	7.38E-01	0.05	12	12	12	ovary	Invasive mucinous[e]
17q21.31	*ADAM11*	ENSG00000073670.9	1.43	1.54E-01	0.16	12	12	12	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*ADAM11*	ENSG00000073670.9	2.02	4.31E-02	0.16	12	12	12	cross-tissue	Mucinous: borderline[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-2.60	9.34E-03	0.05	12	12	12	ovary	All: invasive[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-1.10	2.73E-01	0.16	12	12	12	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-3.27	1.09E-03	0.05	12	12	12	ovary	Serous: invasive[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-3.52	4.32E-04	0.05	12	12	12	ovary	Serous: high-grade[e]
17q21.31	*ADAM11*	ENSG00000073670.9	-1.27	2.05E-01	0.16	12	12	12	cross-tissue	Serous: borderline[e]
17q21.31	*ADAM11*	ENSG00000073670.9	0.30	7.64E-01	0.05	12	12	12	ovary	Serous: low-grade[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-6.73	**1.65E-11**	0.03	28	28	28	cross-tissue	Combined all[d]
17q21.31	*AC091132.1*	ENSG00000236234.1	-7.18	**7.02E-13**	0.03	28	28	28	cross-tissue	Serous: high-grade[d]
17q21.31	*AC091132.1*	ENSG00000236234.1	-1.34	1.80E-01	0.03	28	28	28	cross-tissue	Clear cell[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-2.41	1.58E-02	0.03	28	28	28	cross-tissue	Endometrioid[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-0.56	5.73E-01	0.03	28	28	28	cross-tissue	Invasive mucinous[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	0.06	9.53E-01	0.03	28	28	28	cross-tissue	Invasive/borderline mucinous[e]

17q21.31	*AC091132.1*	ENSG00000236234.1	1.07	2.86E-01	0.03	28	28	28	cross-tissue	Mucinous: borderline[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-5.42	**5.81E-08**	0.03	28	28	28	cross-tissue	All: invasive[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-0.14	8.87E-01	0.03	28	28	28	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-5.88	**4.12E-09**	0.03	28	28	28	cross-tissue	Serous: invasive[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-6.21	**5.16E-10**	0.03	28	28	28	cross-tissue	Serous: high-grade[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	-0.23	8.15E-01	0.03	28	28	28	cross-tissue	Serous: borderline[e]
17q21.31	*AC091132.1*	ENSG00000236234.1	0.24	8.12E-01	0.03	28	28	28	cross-tissue	Serous: low-grade[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	4.38	1.21E-05	0.01	11	11	11	cross-tissue	Combined all[d]
17q21.31	*PLEKHM1*	ENSG00000225190.4	4.80	**1.59E-06**	0.01	11	11	11	cross-tissue	Serous: high-grade[d]
17q21.31	*PLEKHM1*	ENSG00000225190.4	0.92	3.55E-01	0.01	11	11	11	cross-tissue	Clear cell[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	0.93	3.52E-01	0.01	11	11	11	cross-tissue	Endometrioid[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	-2.01	4.45E-02	0.01	29	29	29	ovary	Invasive mucinous[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	-1.57	1.18E-01	0.01	29	29	29	ovary	Invasive/borderline mucinous[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	-1.71	8.70E-02	0.01	11	11	11	cross-tissue	Mucinous: borderline[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	2.43	1.50E-02	0.01	11	11	11	cross-tissue	All: invasive[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	1.56	1.19E-01	0.01	29	29	29	ovary	Serous: low-grade + borderline[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	2.71	6.67E-03	0.01	11	11	11	cross-tissue	Serous: invasive[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	2.77	5.69E-03	0.01	11	11	11	cross-tissue	Serous: high-grade[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	0.73	4.64E-01	0.01	29	29	29	ovary	Serous: borderline[e]
17q21.31	*PLEKHM1*	ENSG00000225190.4	1.63	1.03E-01	0.01	29	29	29	ovary	Serous: low-grade[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	6.61	**3.91E-11**	0.05	210	210	210	ovary	Combined all[d]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	6.58	**4.77E-11**	0.05	210	210	210	ovary	Serous: high-grade[d]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	0.52	6.06E-01	0.05	210	210	210	ovary	Clear cell[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	2.28	2.28E-02	0.05	210	210	210	ovary	Endometrioid[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	1.84	6.64E-02	0.05	210	210	210	ovary	Invasive mucinous[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	0.84	4.01E-01	0.05	210	210	210	ovary	Invasive/borderline mucinous[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	-0.88	3.79E-01	0.05	210	210	210	ovary	Mucinous: borderline[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	5.03	**4.98E-07**	0.05	210	210	210	ovary	All: invasive[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	-1.12	2.62E-01	0.05	210	210	210	ovary	Serous: low-grade + borderline[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	4.88	**1.05E-06**	0.05	210	210	210	ovary	Serous: invasive[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	5.18	**2.21E-07**	0.05	210	210	210	ovary	Serous: high-grade[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	-1.41	1.58E-01	0.05	210	210	210	ovary	Serous: borderline[e]
17q21.31	*RP11-798G7.8*	ENSG00000266918.1	-0.09	9.29E-01	0.05	210	210	210	ovary	Serous: low-grade[e]
17q21.31	*CRHR1*	ENSG00000120088.10	9.09	**1.02E-19**	0.60	467	467	467	cross-tissue	Combined all[d]
17q21.31	*CRHR1*	ENSG00000120088.10	8.61	**7.23E-18**	0.60	467	467	467	cross-tissue	Serous: high-grade[d]
17q21.31	*CRHR1*	ENSG00000120088.10	1.23	2.20E-01	0.49	36	36	36	ovary	Clear cell[e]
17q21.31	*CRHR1*	ENSG00000120088.10	3.41	6.61E-04	0.60	467	467	467	cross-tissue	Endometrioid[e]
17q21.31	*CRHR1*	ENSG00000120088.10	2.48	1.30E-02	0.60	467	467	467	cross-tissue	Invasive mucinous[e]
17q21.31	*CRHR1*	ENSG00000120088.10	1.19	2.36E-01	0.60	467	467	467	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*CRHR1*	ENSG00000120088.10	-1.15	2.50E-01	0.49	36	36	36	ovary	Mucinous: borderline[e]
17q21.31	*CRHR1*	ENSG00000120088.10	7.35	**1.96E-13**	0.60	467	467	467	cross-tissue	All: invasive[e]

17q21.31	*CRHR1*	ENSG00000120088.10	-1.29	1.96E-01	0.60	467	467	467	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*CRHR1*	ENSG00000120088.10	6.71	**1.93E-11**	0.60	467	467	467	cross-tissue	Serous: invasive[e]
17q21.31	*CRHR1*	ENSG00000120088.10	7.05	**1.76E-12**	0.60	467	467	467	cross-tissue	Serous: high-grade[e]
17q21.31	*CRHR1*	ENSG00000120088.10	-1.70	8.88E-02	0.60	467	467	467	cross-tissue	Serous: borderline[e]
17q21.31	*CRHR1*	ENSG00000120088.10	0.10	9.20E-01	0.60	467	467	467	cross-tissue	Serous: low-grade[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	6.56	**5.54E-11**	0.05	19	19	19	ovary	Combined all[d]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	6.77	**1.33E-11**	0.05	19	19	19	ovary	Serous: high-grade[d]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	0.49	6.22E-01	0.05	19	19	19	ovary	Clear cell[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	0.84	4.00E-01	0.05	19	19	19	ovary	Endometrioid[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	1.19	2.35E-01	0.05	19	19	19	ovary	Invasive mucinous[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	-0.32	7.47E-01	0.05	19	19	19	ovary	Invasive/borderline mucinous[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	-1.88	6.01E-02	0.05	19	19	19	ovary	Mucinous: borderline[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	5.10	**3.38E-07**	0.05	19	19	19	ovary	All: invasive[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	-1.22	2.21E-01	0.05	19	19	19	ovary	Serous: low-grade + borderline[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	5.25	**1.50E-07**	0.05	19	19	19	ovary	Serous: invasive[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	5.53	**3.18E-08**	0.05	19	19	19	ovary	Serous: high-grade[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	-1.40	1.60E-01	0.05	19	19	19	ovary	Serous: borderline[e]
17q21.31	*RP11-105N13.4*	ENSG00000263715.2	-0.27	7.87E-01	0.05	19	19	19	ovary	Serous: low-grade[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	8.33	**7.93E-17**	0.10	30	30	30	cross-tissue	Combined all[d]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	7.74	**9.60E-15**	0.10	30	30	30	cross-tissue	Serous: high-grade[d]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	0.53	5.95E-01	0.10	30	30	30	cross-tissue	Clear cell[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	3.12	1.79E-03	0.10	30	30	30	cross-tissue	Endometrioid[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	2.29	2.23E-02	0.10	30	30	30	cross-tissue	Invasive mucinous[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	1.28	2.01E-01	0.10	30	30	30	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	-0.76	4.48E-01	0.10	30	30	30	cross-tissue	Mucinous: borderline[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	6.62	**3.57E-11**	0.10	30	30	30	cross-tissue	All: invasive[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	-1.15	2.52E-01	0.10	30	30	30	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	5.84	**5.31E-09**	0.10	30	30	30	cross-tissue	Serous: invasive[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	6.13	**8.58E-10**	0.10	30	30	30	cross-tissue	Serous: high-grade[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	-1.53	1.25E-01	0.10	30	30	30	cross-tissue	Serous: borderline[e]
17q21.31	*MAPT-AS1*	ENSG00000264589.1	0.10	9.23E-01	0.10	30	30	30	cross-tissue	Serous: low-grade[e]
17q21.31	*KANSL1*	ENSG00000120071.8	4.70	2.59E-06	0.18	75	75	75	ovary	Combined all[d]
17q21.31	*KANSL1*	ENSG00000120071.8	4.74	**2.15E-06**	0.18	75	75	75	ovary	Serous: high-grade[d]
17q21.31	*KANSL1*	ENSG00000120071.8	0.66	5.06E-01	0.18	75	75	75	ovary	Clear cell[e]
17q21.31	*KANSL1*	ENSG00000120071.8	1.73	8.39E-02	0.18	75	75	75	ovary	Endometrioid[e]
17q21.31	*KANSL1*	ENSG00000120071.8	2.00	4.55E-02	0.18	75	75	75	ovary	Invasive mucinous[e]
17q21.31	*KANSL1*	ENSG00000120071.8	1.79	7.32E-02	0.18	75	75	75	ovary	Invasive/borderline mucinous[e]
17q21.31	*KANSL1*	ENSG00000120071.8	0.51	6.08E-01	0.43	39	39	39	cross-tissue	Mucinous: borderline[e]
17q21.31	*KANSL1*	ENSG00000120071.8	4.39	1.13E-05	0.18	75	75	75	ovary	All: invasive[e]
17q21.31	*KANSL1*	ENSG00000120071.8	-0.51	6.10E-01	0.43	39	39	39	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*KANSL1*	ENSG00000120071.8	4.48	7.40E-06	0.18	75	75	75	ovary	Serous: invasive[e]

17q21.31	*KANSL1*	ENSG00000120071.8	4.64	3.45E-06	0.18	75	75	75	ovary	Serous: high-grade[e]
17q21.31	*KANSL1*	ENSG00000120071.8	-1.13	2.57E-01	0.43	39	39	39	cross-tissue	Serous: borderline[e]
17q21.31	*KANSL1*	ENSG00000120071.8	0.83	4.05E-01	0.43	39	39	39	cross-tissue	Serous: low-grade[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-8.84	**9.51E-19**	0.30	370	370	370	cross-tissue	Combined all[d]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-8.35	**6.64E-17**	0.30	370	370	370	cross-tissue	Serous: high-grade[d]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-0.65	5.18E-01	0.30	370	370	370	cross-tissue	Clear cell[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-3.23	1.25E-03	0.30	370	370	370	cross-tissue	Endometrioid[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-2.52	1.18E-02	0.30	370	370	370	cross-tissue	Invasive mucinous[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-1.26	2.09E-01	0.30	370	370	370	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	1.03	3.05E-01	0.30	370	370	370	cross-tissue	Mucinous: borderline[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-7.12	**1.08E-12**	0.30	370	370	370	cross-tissue	All: invasive[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	1.19	2.32E-01	0.30	370	370	370	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-6.46	**1.03E-10**	0.30	370	370	370	cross-tissue	Serous: invasive[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-6.78	**1.17E-11**	0.30	370	370	370	cross-tissue	Serous: high-grade[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	1.62	1.06E-01	0.30	370	370	370	cross-tissue	Serous: borderline[e]
17q21.31	*RP11-669E14.6*	ENSG00000262372.1	-0.14	8.86E-01	0.30	370	370	370	cross-tissue	Serous: low-grade[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	8.45	**2.81E-17**	0.85	58	58	58	cross-tissue	Combined all[d]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	8.26	**1.48E-16**	0.85	58	58	58	cross-tissue	Serous: high-grade[d]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	0.46	6.44E-01	0.85	58	58	58	cross-tissue	Clear cell[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	2.75	5.95E-03	0.85	58	58	58	cross-tissue	Endometrioid[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	2.56	1.03E-02	0.85	58	58	58	cross-tissue	Invasive mucinous[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	1.50	1.34E-01	0.85	58	58	58	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	-0.75	4.53E-01	0.51	172	172	172	ovary	Mucinous: borderline[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	6.57	**5.16E-11**	0.85	58	58	58	cross-tissue	All: invasive[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	-1.39	1.63E-01	0.51	172	172	172	ovary	Serous: low-grade + borderline[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	6.22	**5.09E-10**	0.85	58	58	58	cross-tissue	Serous: invasive[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	6.52	**7.04E-11**	0.85	58	58	58	cross-tissue	Serous: high-grade[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	-1.87	6.12E-02	0.85	58	58	58	cross-tissue	Serous: borderline[e]
17q21.31	*KANSL1-AS1*	ENSG00000214401.4	0.24	8.08E-01	0.85	58	58	58	cross-tissue	Serous: low-grade[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	8.88	**6.54E-19**	0.54	599	599	599	ovary	Combined all[d]
17q21.31	*LRRC37A*	ENSG00000176681.10	8.38	**5.08E-17**	0.54	599	599	599	ovary	Serous: high-grade[d]
17q21.31	*LRRC37A*	ENSG00000176681.10	0.67	5.06E-01	0.54	599	599	599	ovary	Clear cell[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	3.22	1.27E-03	0.54	599	599	599	ovary	Endometrioid[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	2.55	1.09E-02	0.54	599	599	599	ovary	Invasive mucinous[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	1.92	5.45E-02	0.68	49	49	49	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	-1.05	2.95E-01	0.54	599	599	599	ovary	Mucinous: borderline[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	7.17	**7.30E-13**	0.54	599	599	599	ovary	All: invasive[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	-1.19	2.36E-01	0.54	599	599	599	ovary	Serous: low-grade + borderline[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	6.51	**7.65E-11**	0.54	599	599	599	ovary	Serous: invasive[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	6.83	**8.42E-12**	0.54	599	599	599	ovary	Serous: high-grade[e]
17q21.31	*LRRC37A*	ENSG00000176681.10	-1.60	1.09E-01	0.54	599	599	599	ovary	Serous: borderline[e]

17q21.31	*LRRC37A*	ENSG00000176681.10	0.33	7.43E-01	0.68	49	49	49	cross-tissue	Serous: low-grade[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	8.71	**3.02E-18**	0.55	371	371	371	ovary	Combined all[d]
17q21.31	*LRRC37A2*	ENSG00000238083.3	8.26	**1.44E-16**	0.55	371	371	371	ovary	Serous: high-grade[d]
17q21.31	*LRRC37A2*	ENSG00000238083.3	0.48	6.29E-01	0.55	371	371	371	ovary	Clear cell[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	3.05	2.30E-03	0.55	371	371	371	ovary	Endometrioid[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	2.62	8.82E-03	0.79	293	293	293	cross-tissue	Invasive mucinous[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	1.55	1.21E-01	0.79	293	293	293	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	-0.95	3.44E-01	0.55	371	371	371	ovary	Mucinous: borderline[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	7.11	**1.17E-12**	0.55	371	371	371	ovary	All: invasive[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	-0.88	3.78E-01	0.79	293	293	293	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	6.51	**7.39E-11**	0.55	371	371	371	ovary	Serous: invasive[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	6.72	**1.80E-11**	0.55	371	371	371	ovary	Serous: high-grade[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	-1.35	1.77E-01	0.79	293	293	293	cross-tissue	Serous: borderline[e]
17q21.31	*LRRC37A2*	ENSG00000238083.3	0.62	5.38E-01	0.55	371	371	371	ovary	Serous: low-grade[e]
17q21.31	*NSF*	ENSG00000073969.14	-5.38	**7.65E-08**	0.02	23	23	23	ovary	Combined all[d]
17q21.31	*NSF*	ENSG00000073969.14	-5.55	**2.78E-08**	0.02	23	23	23	ovary	Serous: high-grade[d]
17q21.31	*NSF*	ENSG00000073969.14	-0.97	3.32E-01	0.02	23	23	23	ovary	Clear cell[e]
17q21.31	*NSF*	ENSG00000073969.14	-2.18	2.92E-02	0.02	23	23	23	ovary	Endometrioid[e]
17q21.31	*NSF*	ENSG00000073969.14	-1.27	2.05E-01	0.03	7	7	7	cross-tissue	Invasive mucinous[e]
17q21.31	*NSF*	ENSG00000073969.14	0.50	6.20E-01	0.02	23	23	23	ovary	Invasive/borderline mucinous[e]
17q21.31	*NSF*	ENSG00000073969.14	1.82	6.94E-02	0.02	23	23	23	ovary	Mucinous: borderline[e]
17q21.31	*NSF*	ENSG00000073969.14	-3.69	2.27E-04	0.02	23	23	23	ovary	All: invasive[e]
17q21.31	*NSF*	ENSG00000073969.14	2.03	4.19E-02	0.02	23	23	23	ovary	Serous: low-grade + borderline[e]
17q21.31	*NSF*	ENSG00000073969.14	-3.74	1.87E-04	0.02	23	23	23	ovary	Serous: invasive[e]
17q21.31	*NSF*	ENSG00000073969.14	-4.01	6.20E-05	0.02	23	23	23	ovary	Serous: high-grade[e]
17q21.31	*NSF*	ENSG00000073969.14	2.45	1.44E-02	0.02	23	23	23	ovary	Serous: borderline[e]
17q21.31	*NSF*	ENSG00000073969.14	0.39	6.96E-01	0.02	23	23	23	ovary	Serous: low-grade[e]
17q21.31	*WNT3*	ENSG00000108379.5	7.33	**2.38E-13**	0.40	14	14	14	cross-tissue	Combined all[d]
17q21.31	*WNT3*	ENSG00000108379.5	6.81	**9.82E-12**	0.40	14	14	14	cross-tissue	Serous: high-grade[d]
17q21.31	*WNT3*	ENSG00000108379.5	1.00	3.19E-01	0.40	14	14	14	cross-tissue	Clear cell[e]
17q21.31	*WNT3*	ENSG00000108379.5	2.12	3.39E-02	0.40	14	14	14	cross-tissue	Endometrioid[e]
17q21.31	*WNT3*	ENSG00000108379.5	1.92	5.50E-02	0.40	14	14	14	cross-tissue	Invasive mucinous[e]
17q21.31	*WNT3*	ENSG00000108379.5	0.92	3.57E-01	0.40	14	14	14	cross-tissue	Invasive/borderline mucinous[e]
17q21.31	*WNT3*	ENSG00000108379.5	-0.80	4.25E-01	0.40	14	14	14	cross-tissue	Mucinous: borderline[e]
17q21.31	*WNT3*	ENSG00000108379.5	5.90	**3.74E-09**	0.40	14	14	14	cross-tissue	All: invasive[e]
17q21.31	*WNT3*	ENSG00000108379.5	-1.21	2.26E-01	0.40	14	14	14	cross-tissue	Serous: low-grade + borderline[e]
17q21.31	*WNT3*	ENSG00000108379.5	5.22	**1.81E-07**	0.40	14	14	14	cross-tissue	Serous: invasive[e]
17q21.31	*WNT3*	ENSG00000108379.5	5.61	**2.03E-08**	0.40	14	14	14	cross-tissue	Serous: high-grade[e]
17q21.31	*WNT3*	ENSG00000108379.5	-1.22	2.22E-01	0.40	14	14	14	cross-tissue	Serous: borderline[e]
17q21.31	*WNT3*	ENSG00000108379.5	-0.35	7.29E-01	0.40	14	14	14	cross-tissue	Serous: low-grade[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.57	**2.55E-08**	0.02	28	28	28	cross-tissue	Combined all[d]

17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.54	**3.04E-08**	0.02	28	28	28	cross-tissue	Serous: high-grade[d]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	2.05	4.07E-02	0.02	28	28	28	cross-tissue	Clear cell[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	2.97	2.96E-03	0.02	28	28	28	cross-tissue	Endometrioid[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	0.28	7.79E-01	0.02	28	28	28	cross-tissue	Invasive mucinous[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	1.28	1.99E-01	0.02	28	28	28	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	1.64	1.01E-01	0.02	28	28	28	cross-tissue	Mucinous: borderline[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.65	**1.58E-08**	0.02	28	28	28	cross-tissue	All: invasive[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.45	**5.11E-08**	0.02	28	28	28	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.74	**9.62E-09**	0.02	28	28	28	cross-tissue	Serous: invasive[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	5.20	**1.97E-07**	0.02	28	28	28	cross-tissue	Serous: high-grade[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	4.27	1.94E-05	0.02	28	28	28	cross-tissue	Serous: borderline[e]
17q21.32	*RP11-138C9.1*	ENSG00000264558.1	3.50	4.64E-04	0.02	28	28	28	cross-tissue	Serous: low-grade[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	6.07	**1.30E-09**	0.19	19	19	19	cross-tissue	Combined all[d]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	5.93	**3.00E-09**	0.19	19	19	19	cross-tissue	Serous: high-grade[d]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	1.68	9.23E-02	0.19	19	19	19	cross-tissue	Clear cell[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	1.64	1.01E-01	0.19	19	19	19	cross-tissue	Endometrioid[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	1.29	1.99E-01	0.19	19	19	19	cross-tissue	Invasive mucinous[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	0.64	5.21E-01	0.19	19	19	19	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	-0.32	7.52E-01	0.19	19	19	19	cross-tissue	Mucinous: borderline[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	5.75	**8.81E-09**	0.19	19	19	19	cross-tissue	All: invasive[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	4.06	4.88E-05	0.19	19	19	19	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	5.66	**1.50E-08**	0.19	19	19	19	cross-tissue	Serous: invasive[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	5.49	**3.95E-08**	0.19	19	19	19	cross-tissue	Serous: high-grade[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	3.59	3.36E-04	0.19	19	19	19	cross-tissue	Serous: borderline[e]
17q21.32	*RP11-6N17.6*	ENSG00000264019.1	2.09	3.69E-02	0.19	19	19	19	cross-tissue	Serous: low-grade[e]
17q21.32	*PNPO*	ENSG00000108439.5	5.37	**7.70E-08**	0.30	27	27	27	cross-tissue	Combined all[d]
17q21.32	*PNPO*	ENSG00000108439.5	5.34	**9.38E-08**	0.30	27	27	27	cross-tissue	Serous: high-grade[d]
17q21.32	*PNPO*	ENSG00000108439.5	1.33	1.83E-01	0.30	27	27	27	cross-tissue	Clear cell[e]
17q21.32	*PNPO*	ENSG00000108439.5	1.69	9.04E-02	0.30	27	27	27	cross-tissue	Endometrioid[e]
17q21.32	*PNPO*	ENSG00000108439.5	1.04	2.96E-01	0.30	27	27	27	cross-tissue	Invasive mucinous[e]
17q21.32	*PNPO*	ENSG00000108439.5	0.55	5.79E-01	0.30	27	27	27	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*PNPO*	ENSG00000108439.5	-0.22	8.29E-01	0.30	27	27	27	cross-tissue	Mucinous: borderline[e]
17q21.32	*PNPO*	ENSG00000108439.5	5.33	**9.96E-08**	0.30	27	27	27	cross-tissue	All: invasive[e]
17q21.32	*PNPO*	ENSG00000108439.5	4.10	4.09E-05	0.30	27	27	27	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*PNPO*	ENSG00000108439.5	5.38	**7.33E-08**	0.30	27	27	27	cross-tissue	Serous: invasive[e]
17q21.32	*PNPO*	ENSG00000108439.5	5.03	**5.00E-07**	0.30	27	27	27	cross-tissue	Serous: high-grade[e]
17q21.32	*PNPO*	ENSG00000108439.5	3.14	1.68E-03	0.30	27	27	27	cross-tissue	Serous: borderline[e]
17q21.32	*PNPO*	ENSG00000108439.5	2.68	7.34E-03	0.30	27	27	27	cross-tissue	Serous: low-grade[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-5.12	**3.06E-07**	0.04	12	12	12	cross-tissue	Combined all[d]
17q21.32	*PRR15L*	ENSG00000167183.2	-4.91	**9.18E-07**	0.04	12	12	12	cross-tissue	Serous: high-grade[d]
17q21.32	*PRR15L*	ENSG00000167183.2	-1.60	1.09E-01	0.04	12	12	12	cross-tissue	Clear cell[e]

17q21.32	*PRR15L*	ENSG00000167183.2	-1.95	5.07E-02	0.04	12	12	12	cross-tissue	Endometrioid[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-1.38	1.66E-01	0.04	12	12	12	cross-tissue	Invasive mucinous[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-0.90	3.71E-01	0.04	12	12	12	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*PRR15L*	ENSG00000167183.2	0.38	7.02E-01	0.05	48	48	48	ovary	Mucinous: borderline[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-4.85	**1.23E-06**	0.04	12	12	12	cross-tissue	All: invasive[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-4.05	5.02E-05	0.04	12	12	12	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-4.66	3.13E-06	0.04	12	12	12	cross-tissue	Serous: invasive[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-4.54	5.65E-06	0.04	12	12	12	cross-tissue	Serous: high-grade[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-3.89	9.90E-05	0.04	12	12	12	cross-tissue	Serous: borderline[e]
17q21.32	*PRR15L*	ENSG00000167183.2	-3.05	2.26E-03	0.05	48	48	48	ovary	Serous: low-grade[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-5.27	**1.38E-07**	0.40	26	26	26	cross-tissue	Combined all[d]
17q21.32	*HOXB2*	ENSG00000173917.9	-5.48	**4.28E-08**	0.40	26	26	26	cross-tissue	Serous: high-grade[d]
17q21.32	*HOXB2*	ENSG00000173917.9	-0.52	6.03E-01	0.40	26	26	26	cross-tissue	Clear cell[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-1.04	2.97E-01	0.40	26	26	26	cross-tissue	Endometrioid[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-0.37	7.11E-01	0.40	26	26	26	cross-tissue	Invasive mucinous[e]
17q21.32	*HOXB2*	ENSG00000173917.9	0.04	9.65E-01	0.40	26	26	26	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*HOXB2*	ENSG00000173917.9	0.51	6.13E-01	0.40	26	26	26	cross-tissue	Mucinous: borderline[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-5.21	**1.89E-07**	0.40	26	26	26	cross-tissue	All: invasive[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-2.97	2.95E-03	0.40	26	26	26	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-5.55	**2.92E-08**	0.40	26	26	26	cross-tissue	Serous: invasive[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-5.09	**3.51E-07**	0.40	26	26	26	cross-tissue	Serous: high-grade[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-1.52	1.28E-01	0.40	26	26	26	cross-tissue	Serous: borderline[e]
17q21.32	*HOXB2*	ENSG00000173917.9	-2.96	3.03E-03	0.40	26	26	26	cross-tissue	Serous: low-grade[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-5.13	**2.83E-07**	0.29	31	31	31	cross-tissue	Combined all[d]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-5.15	**2.59E-07**	0.29	31	31	31	cross-tissue	Serous: high-grade[d]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-0.99	3.23E-01	0.29	31	31	31	cross-tissue	Clear cell[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-1.31	1.89E-01	0.29	31	31	31	cross-tissue	Endometrioid[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-0.61	5.39E-01	0.29	31	31	31	cross-tissue	Invasive mucinous[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-0.02	9.81E-01	0.29	31	31	31	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	0.64	5.19E-01	0.29	31	31	31	cross-tissue	Mucinous: borderline[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-5.08	**3.84E-07**	0.29	31	31	31	cross-tissue	All: invasive[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-3.11	1.88E-03	0.29	31	31	31	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-5.18	**2.19E-07**	0.29	31	31	31	cross-tissue	Serous: invasive[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-4.72	2.33E-06	0.29	31	31	31	cross-tissue	Serous: high-grade[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-1.73	8.41E-02	0.29	31	31	31	cross-tissue	Serous: borderline[e]
17q21.32	*HOXB-AS1*	ENSG00000230148.4	-2.90	3.72E-03	0.29	31	31	31	cross-tissue	Serous: low-grade[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-5.39	**7.11E-08**	0.12	29	29	29	cross-tissue	Combined all[d]
17q21.32	*HOXB3*	ENSG00000120093.7	-5.59	**2.30E-08**	0.12	29	29	29	cross-tissue	Serous: high-grade[d]
17q21.32	*HOXB3*	ENSG00000120093.7	-0.82	4.10E-01	0.12	29	29	29	cross-tissue	Clear cell[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-0.75	4.53E-01	0.12	29	29	29	cross-tissue	Endometrioid[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-0.89	3.75E-01	0.12	29	29	29	cross-tissue	Invasive mucinous[e]

17q21.32	*HOXB3*	ENSG00000120093.7	-0.31	7.54E-01	0.12	29	29	29	cross-tissue	Invasive/borderline mucinous[e]
17q21.32	*HOXB3*	ENSG00000120093.7	0.54	5.87E-01	0.12	29	29	29	cross-tissue	Mucinous: borderline[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-5.24	**1.64E-07**	0.12	29	29	29	cross-tissue	All: invasive[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-3.84	1.23E-04	0.12	29	29	29	cross-tissue	Serous: low-grade + borderline[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-5.55	**2.90E-08**	0.12	29	29	29	cross-tissue	Serous: invasive[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-4.97	**6.70E-07**	0.12	29	29	29	cross-tissue	Serous: high-grade[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-2.37	1.80E-02	0.12	29	29	29	cross-tissue	Serous: borderline[e]
17q21.32	*HOXB3*	ENSG00000120093.7	-3.31	9.24E-04	0.12	29	29	29	cross-tissue	Serous: low-grade[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-1.79	7.30E-02	0.11	14	14	14	cross-tissue	Combined all[d]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-2.43	1.52E-02	0.11	14	14	14	cross-tissue	Serous: high-grade[d]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-0.91	3.64E-01	0.04	1	1	1	ovary	Clear cell[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	0.47	6.41E-01	0.11	14	14	14	cross-tissue	Endometrioid[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	1.66	9.74E-02	0.11	14	14	14	cross-tissue	Invasive mucinous[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	0.95	3.43E-01	0.11	14	14	14	cross-tissue	Invasive/borderline mucinous[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	0.55	5.82E-01	0.04	1	1	1	ovary	Mucinous: borderline[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-1.33	1.84E-01	0.11	14	14	14	cross-tissue	All: invasive[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-5.53	**3.13E-08**	0.11	14	14	14	cross-tissue	Serous: low-grade + borderline[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-2.03	4.19E-02	0.11	14	14	14	cross-tissue	Serous: invasive[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	1.86	6.25E-02	0.04	1	1	1	ovary	Serous: high-grade[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-4.13	3.64E-05	0.11	14	14	14	cross-tissue	Serous: borderline[e]
18q11.2	*RP11-403A21.1*	ENSG00000265752.2	-3.93	8.52E-05	0.11	14	14	14	cross-tissue	Serous: low-grade[e]
19p13.11	*ABHD8*	ENSG00000127220.5	3.89	9.86E-05	0.23	33	33	33	cross-tissue	Combined all[d]
19p13.11	*ABHD8*	ENSG00000127220.5	4.79	**1.69E-06**	0.23	33	33	33	cross-tissue	Serous: high-grade[d]
19p13.11	*ABHD8*	ENSG00000127220.5	-0.74	4.59E-01	0.08	71	71	71	ovary	Clear cell[e]
19p13.11	*ABHD8*	ENSG00000127220.5	-0.50	6.16E-01	0.23	33	33	33	cross-tissue	Endometrioid[e]
19p13.11	*ABHD8*	ENSG00000127220.5	-0.85	3.95E-01	0.23	33	33	33	cross-tissue	Invasive mucinous[e]
19p13.11	*ABHD8*	ENSG00000127220.5	0.71	4.75E-01	0.08	71	71	71	ovary	Invasive/borderline mucinous[e]
19p13.11	*ABHD8*	ENSG00000127220.5	0.93	3.53E-01	0.08	71	71	71	ovary	Mucinous: borderline[e]
19p13.11	*ABHD8*	ENSG00000127220.5	4.49	7.07E-06	0.23	33	33	33	cross-tissue	All: invasive[e]
19p13.11	*ABHD8*	ENSG00000127220.5	-1.95	5.12E-02	0.08	71	71	71	ovary	Serous: low-grade + borderline[e]
19p13.11	*ABHD8*	ENSG00000127220.5	5.71	**1.12E-08**	0.23	33	33	33	cross-tissue	Serous: invasive[e]
19p13.11	*ABHD8*	ENSG00000127220.5	5.66	**1.51E-08**	0.23	33	33	33	cross-tissue	Serous: high-grade[e]
19p13.11	*ABHD8*	ENSG00000127220.5	-1.43	1.53E-01	0.08	71	71	71	ovary	Serous: borderline[e]
19p13.11	*ABHD8*	ENSG00000127220.5	-1.61	1.07E-01	0.08	71	71	71	ovary	Serous: low-grade[e]
19q13.2	*ZNF546*	ENSG00000187187.9	-0.87	3.84E-01	0.01	22	22	22	ovary	Combined all[d]
19q13.2	*ZNF546*	ENSG00000187187.9	-1.68	9.28E-02	0.01	22	22	22	ovary	Serous: high-grade[d]
19q13.2	*ZNF546*	ENSG00000187187.9	0.42	6.78E-01	0.01	22	22	22	ovary	Clear cell[e]
19q13.2	*ZNF546*	ENSG00000187187.9	-0.84	4.02E-01	0.01	22	22	22	ovary	Endometrioid[e]
19q13.2	*ZNF546*	ENSG00000187187.9	4.49	7.29E-06	0.01	22	22	22	ovary	Invasive mucinous[e]
19q13.2	*ZNF546*	ENSG00000187187.9	7.14	**9.07E-13**	0.01	22	22	22	ovary	Invasive/borderline mucinous[e]
19q13.2	*ZNF546*	ENSG00000187187.9	5.99	**2.14E-09**	0.01	22	22	22	ovary	Mucinous: borderline[e]

19q13.2	*ZNF546*	ENSG00000187187.9	-0.68	4.99E-01	0.01	22	22	22	ovary	All: invasive[e]
19q13.2	*ZNF546*	ENSG00000187187.9	0.63	5.29E-01	0.01	22	22	22	ovary	Serous: low-grade + borderline[e]
19q13.2	*ZNF546*	ENSG00000187187.9	-1.61	1.07E-01	0.01	22	22	22	ovary	Serous: invasive[e]
19q13.2	*ZNF546*	ENSG00000187187.9	-1.57	1.16E-01	0.01	22	22	22	ovary	Serous: high-grade[e]
19q13.2	*ZNF546*	ENSG00000187187.9	1.13	2.58E-01	0.01	22	22	22	ovary	Serous: borderline[e]
19q13.2	*ZNF546*	ENSG00000187187.9	-0.41	6.80E-01	0.01	22	22	22	ovary	Serous: low-grade[e]

a P values < 2.21×10^{-6} were in bold.

b r^2 of tissue model's correlation to gene's measured transcriptome (prediction performance)

c N: number of snps from GWAS that were used in MetaXcan analysis; covariance_N: number of snps in the covariance matrix; model_N: number of snps in the model.

d The analyses were based on invasive-combined or high-grade serous summary statistics from Ovarian Cancer Association Consortium (OCAC) and Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA);

e The analyses were based on summary statistics from OCAC.

Supplementary Table S7. Variants with *P* < 5E-8 either in BCAC or OCAC between 42,836,399 and 44,910,520 on the chromosome 17.[a,b]

Variant_name	Chr	Position_b37	Effect allele (mino	Effect allele freq_BCAC	Beta_BCAC	SE_BCAC	*P*_BCAC	Effect allele freq_OCAC	Beta_OCAC	SE_OCAC	*P*_OCAC	1KG_Phase3_ID
17_43460181_G_A	17	43460181	A	0.1414	-0.0479	0.0091	1.26E-07	0.1372	0.1175	0.01856	2.45E-10	rs62064594:43460181:G:A
17_43460374_A_G	17	43460374	G	0.1434	-0.0482	0.009	8.99E-08	0.1388	0.1192	0.01842	9.87E-11	rs62064595:43460374:A:G
17_43463493_A_C	17	43463493	C	0.1741	-0.0446	0.0082	6.10E-08	0.1757	0.1122	0.01697	3.83E-11	rs79724577:43463493:A:C
17_43471489_G_A	17	43471489	A	0.1745	-0.0464	0.0083	1.86E-08	0.1752	0.1129	0.017	3.11E-11	rs4763:43471489:G:A
17_43473307_C_G	17	43473307	G	0.1738	-0.0451	0.0083	4.81E-08	0.1751	0.1182	0.01702	3.79E-12	rs62064597:43473307:C:G
17_43474668_C_G	17	43474668	G	0.176	-0.0451	0.0082	3.73E-08	0.1769	0.116	0.0169	6.59E-12	rs62064598:43474668:C:G
17_43475929_G_A	17	43475929	A	0.176	-0.0455	0.0082	2.79E-08	0.1771	0.1171	0.01691	4.34E-12	rs2028078:43475929:G:A
17_43476807_A_G	17	43476807	G	0.1748	-0.0456	0.0082	2.89E-08	0.1765	0.1191	0.01695	2.06E-12	rs56220387:43476807:A:G
17_43479748_T_C	17	43479748	C	0.1762	-0.0451	0.0082	3.73E-08	0.1777	0.116	0.01689	6.55E-12	rs55793500:43479748:T:C
17_43480701_G_A	17	43480701	A	0.1759	-0.0448	0.0082	4.52E-08	0.1777	0.1165	0.0169	5.57E-12	rs62064600:43480701:G:A
17_43483551_C_T	17	43483551	T	0.1761	-0.0448	0.0082	4.63E-08	0.1781	0.1178	0.0169	3.22E-12	rs56236914:43483551:C:T
17_43484496_C_T	17	43484496	T	0.1771	-0.0448	0.0082	4.28E-08	0.1797	0.1168	0.01689	4.75E-12	rs62064603:43484496:C:T
17_43484598_G_T	17	43484598	T	0.1767	-0.0444	0.0082	5.74E-08	0.1788	0.1175	0.01689	3.47E-12	rs73984391:43484598:G:T
17_43484903_T_C	17	43484903	C	0.1767	-0.0444	0.0082	5.75E-08	0.1789	0.1165	0.01689	5.33E-12	rs1808189:43484903:T:C
17_43485551_T_G	17	43485551	G	0.1763	-0.0442	0.0082	6.70E-08	0.1782	0.1176	0.01689	3.42E-12	rs62064637:43485551:T:G
17_43487217_G_A	17	43487217	A	0.1767	-0.0446	0.0082	4.66E-08	0.1785	0.1185	0.01687	2.17E-12	rs36078910:43487217:G:A
17_43487424_T_C	17	43487424	C	0.1768	-0.0445	0.0082	5.07E-08	0.1785	0.1189	0.01687	1.86E-12	rs35389313:43487424:T:C
17_43487574_C_A	17	43487574	A	0.1757	-0.0446	0.0082	5.36E-08	0.1781	0.119	0.01692	2.04E-12	rs35327136:43487574:C:A
17_43488382_C_T	17	43488382	T	0.177	-0.0439	0.0082	7.47E-08	0.1785	0.1202	0.01686	1.03E-12	rs8071011:43488382:C:T
17_43488792_T_C	17	43488792	C	0.1775	-0.0434	0.0082	1.06E-07	0.1786	0.1214	0.01684	5.51E-13	rs62064641:43488792:T:C
17_43489161_T_TCACACA	17	43489161	TCACACA	0.1756	-0.0426	0.0083	2.54E-07	0.1777	0.1217	0.01691	6.33E-13	17:43489161:T:TCACACA
17_43490853_G_A	17	43490853	A	0.1757	-0.0436	0.0082	9.91E-08	0.1779	0.1225	0.0169	4.11E-13	rs62064643:43490853:G:A
17_43491003_G_A	17	43491003	A	0.1771	-0.0439	0.0082	7.26E-08	0.1786	0.1208	0.01685	7.36E-13	rs34063617:43491003:G:A
17_43492357_C_T	17	43492357	T	0.177	-0.044	0.0082	7.08E-08	0.1784	0.1203	0.01686	9.64E-13	rs12940792:43492357:C:T
17_43493101_G_A	17	43493101	A	0.177	-0.044	0.0082	7.17E-08	0.1784	0.1202	0.01686	1.00E-12	rs12947718:43493101:G:A
17_43493398_G_GTT	17	43493398	GTT	0.1729	-0.0433	0.0084	2.55E-07	0.175	0.1251	0.01725	4.07E-13	17:43493398:G:GTT
17_43493504_C_T	17	43493504	T	0.177	-0.044	0.0082	6.87E-08	0.1784	0.1202	0.01686	1.02E-12	rs71373560:43493504:C:T
17_43493560_C_G	17	43493560	G	0.177	-0.044	0.0082	6.86E-08	0.1784	0.1202	0.01686	1.02E-12	rs34915103:43493560:C:G
17_43493835_T_C	17	43493835	C	0.1739	-0.0458	0.0083	3.05E-08	0.1743	0.1209	0.01707	1.43E-12	rs12942951:43493835:T:C
17_43495119_C_CAA	17	43495119	CAA	0.1265	-0.0523	0.0101	2.33E-07	0.1324	0.1527	0.0209	2.71E-13	rs34796153:43495119:C:CAA
17_43495216_G_A	17	43495216	A	0.177	-0.0442	0.0082	6.18E-08	0.1784	0.1201	0.01686	1.05E-12	rs35884427:43495216:G:A
17_43495235_C_G	17	43495235	G	0.177	-0.0441	0.0082	6.30E-08	0.1784	0.1202	0.01686	1.02E-12	rs12952504:43495235:C:G
17_43495420_A_T	17	43495420	T	0.1779	-0.0426	0.0083	2.61E-07	0.1795	0.12	0.0171	2.23E-12	rs12936645:43495420:A:T
17_43495852_A_G	17	43495852	G	0.1767	-0.0441	0.0082	6.80E-08	0.1783	0.1204	0.01687	9.73E-13	rs34286926:43495852:A:G
17_43496465_T_C	17	43496465	C	0.1769	-0.0444	0.0082	5.39E-08	0.1783	0.1202	0.01686	1.00E-12	rs56378631:43496465:T:C
17_43496828_C_T	17	43496828	T	0.1769	-0.0444	0.0082	5.26E-08	0.1784	0.1202	0.01687	1.02E-12	rs12946723:43496828:C:T
17_43497210_G_A	17	43497210	A	0.1769	-0.0445	0.0082	5.02E-08	0.1783	0.1205	0.01687	8.87E-13	rs12952764:43497210:G:A
17_43498180_C_T	17	43498180	T	0.1769	-0.0445	0.0082	4.88E-08	0.1783	0.1202	0.01687	1.02E-12	rs35420583:43498180:C:T
17_43498181_A_G	17	43498181	G	0.1769	-0.0445	0.0082	4.88E-08	0.1783	0.1202	0.01687	1.02E-12	rs34792542:43498181:A:G
17_43499328_T_C	17	43499328	C	0.1769	-0.0446	0.0082	4.61E-08	0.1783	0.1202	0.01687	1.03E-12	rs35519908:43499328:T:C
17_43499839_A_G[c]	**17**	**43499839**	**G**	**0.1771**	**-0.0444**	**0.0082**	**5.04E-08**	**0.1783**	**0.1195**	**0.01686**	**1.36E-12**	**rs12942666:43499839:A:G**
17_43500477_G_A	17	43500477	A	0.1757	-0.0444	0.0082	5.53E-08	0.1777	0.1222	0.0169	4.89E-13	rs62064645:43500477:G:A
17_43500587_G_A	17	43500587	A	0.1773	-0.0446	0.0082	4.52E-08	0.1787	0.1198	0.01686	1.19E-12	rs62064646:43500587:G:A
17_43500621_G_A	17	43500621	A	0.177	-0.0446	0.0082	4.46E-08	0.1783	0.1204	0.01687	9.48E-13	rs62064647:43500621:G:A
17_43501442_T_C	17	43501442	C	0.177	-0.0445	0.0082	4.82E-08	0.1783	0.1201	0.01687	1.09E-12	rs7222389:43501442:T:C
17_43501591_T_C	17	43501591	C	0.1773	-0.0444	0.0082	5.17E-08	0.1787	0.1201	0.01686	1.07E-12	rs55648326:43501591:T:C
17_43501940_G_A	17	43501940	A	0.1769	-0.0439	0.0082	7.43E-08	0.1785	0.1201	0.01687	1.07E-12	rs56212100:43501940:G:A
17_43502012_T_C	17	43502012	C	0.1769	-0.0444	0.0082	5.20E-08	0.1783	0.1202	0.01686	1.02E-12	rs55914643:43502012:T:C
17_43502044_AG_A	17	43502044	A	0.177	-0.0433	0.0082	1.40E-07	0.1783	0.1202	0.01686	1.02E-12	rs55874939:43502044:AG:A
17_43502111_A_G	17	43502111	G	0.1769	-0.0444	0.0082	5.22E-08	0.1783	0.1202	0.01686	1.02E-12	rs62064649:43502111:A:G
17_43502241_T_C	17	43502241	C	0.177	-0.0443	0.0082	5.59E-08	0.1783	0.12	0.01686	1.13E-12	rs35626715:43502241:T:C
17_43503000_G_A	17	43503000	A	0.1758	-0.0442	0.0082	6.38E-08	0.1777	0.1224	0.0169	4.38E-13	rs62064651:43503000:G:A
17_43503284_G_A	17	43503284	A	0.1757	-0.0442	0.0082	6.55E-08	0.1777	0.1224	0.0169	4.45E-13	rs76344126:43503284:G:A

17_43503294_A_C	17	43503294	C	0.1766	-0.044	0.0082	7.21E-08	0.1781	0.1207	0.01688	8.54E-13	rs7209501:43503294:A:C
17_43504525_A_AC	17	43504525	AC	0.1793	-0.0431	0.0082	1.48E-07	0.1803	0.1199	0.01681	9.72E-13	rs199883901:43504525:A:AC
17_43507297_C_T	17	43507297	T	0.1758	-0.0439	0.0082	7.92E-08	0.1777	0.1227	0.0169	3.82E-13	rs12949256:43507297:C:T
17_43507403_G_A	17	43507403	A	0.1758	-0.044	0.0082	7.58E-08	0.1777	0.1228	0.0169	3.78E-13	rs7220206:43507403:G:A
17_43507649_A_G	17	43507649	G	0.1758	-0.0439	0.0082	7.66E-08	0.1777	0.1228	0.0169	3.75E-13	rs7222444:43507649:A:G
17_43508223_G_T	17	43508223	T	0.1758	-0.0439	0.0082	7.84E-08	0.1776	0.1228	0.0169	3.69E-13	rs12939187:43508223:G:T
17_43508303_A_G	17	43508303	G	0.1759	-0.0442	0.0082	6.22E-08	0.1777	0.1227	0.0169	3.79E-13	rs34018943:43508303:A:G
17_43508616_G_T	17	43508616	T	0.1758	-0.0439	0.0082	7.91E-08	0.1776	0.1228	0.0169	3.69E-13	rs34104358:43508616:G:T
17_43509310_A_G	17	43509310	G	0.1751	-0.0442	0.0082	7.08E-08	0.1768	0.1225	0.01696	5.21E-13	rs62064652:43509310:A:G
17_43509316_C_T	17	43509316	T	0.175	-0.0442	0.0082	6.90E-08	0.1768	0.1225	0.01696	5.25E-13	rs62064653:43509316:C:T
17_43509778_C_T	17	43509778	T	0.1757	-0.0439	0.0082	7.67E-08	0.1776	0.1226	0.0169	3.99E-13	rs56020833:43509778:C:T
17_43510187_G_C	17	43510187	C	0.1757	-0.0439	0.0082	7.70E-08	0.1776	0.1226	0.0169	4.01E-13	rs55642947:43510187:G:C
17_43511281_TGGCTAACA	17	43511281	T	0.142	-0.0476	0.0096	6.62E-07	0.1415	0.1353	0.01953	4.23E-12	511281:TGGCTAACACGGTGAAACCCC:T
17_43511435_C_A	17	43511435	A	0.1758	-0.0438	0.0082	8.23E-08	0.1776	0.1228	0.0169	3.73E-13	rs34465449:43511435:C:A
17_43512206_A_G	17	43512206	G	0.1758	-0.0438	0.0082	8.33E-08	0.1776	0.1228	0.0169	3.74E-13	rs12946900:43512206:A:G
17_43512318_G_A	17	43512318	A	0.1757	-0.0439	0.0082	7.71E-08	0.1776	0.1226	0.0169	4.07E-13	rs56168933:43512318:G:A
17_43512439_G_C	17	43512439	C	0.1758	-0.0438	0.0082	8.36E-08	0.1776	0.1228	0.0169	3.74E-13	rs55790407:43512439:G:C
17_43513441_C_T	17	43513441	T	0.1763	-0.0441	0.0082	7.09E-08	0.1778	0.1223	0.0169	4.50E-13	rs11012:43513441:C:T
17_43513551_C_G	17	43513551	G	0.1759	-0.044	0.0082	7.51E-08	0.1776	0.1225	0.0169	4.24E-13	rs9730:43513551:C:G
17_43513896_C_T	17	43513896	T	0.1757	-0.0439	0.0082	8.06E-08	0.1776	0.1223	0.0169	4.68E-13	rs62064654:43513896:C:T
17_43514954_G_A	17	43514954	A	0.1758	-0.0438	0.0082	8.43E-08	0.1776	0.1228	0.0169	3.74E-13	rs62064655:43514954:G:A
17_43515846_C_T	17	43515846	T	0.1758	-0.0438	0.0082	8.46E-08	0.1776	0.1228	0.0169	3.70E-13	rs34363898:43515846:C:T
17_43515885_A_G	17	43515885	G	0.1758	-0.0438	0.0082	8.46E-08	0.1776	0.1228	0.0169	3.70E-13	rs36114997:43515885:A:G
17_43515927_C_T	17	43515927	T	0.1798	-0.0451	0.0081	2.88E-08	0.1821	0.1191	0.01681	1.40E-12	rs35354512:43515927:C:T
17_43516402_A_G[c]	**17**	**43516402**	**G**	**0.1758**	**-0.0437**	**0.0082**	**8.67E-08**	**0.1777**	**0.122**	**0.01689**	**5.11E-13**	**rs17631303:43516402:A:G**
17_43516739_G_A	17	43516739	A	0.1758	-0.0437	0.0082	8.85E-08	0.1777	0.1227	0.0169	3.90E-13	17:43516739:G:A
17_43517054_G_A	17	43517054	A	0.1755	-0.0437	0.0082	9.59E-08	0.1776	0.1229	0.01693	3.91E-13	rs62064657:43517054:G:A
17_43517252_T_C	17	43517252	C	0.1758	-0.0437	0.0082	8.84E-08	0.1777	0.1227	0.0169	3.95E-13	rs35489312:43517252:T:C
17_43519564_C_A	17	43519564	A	0.1759	-0.0445	0.0082	5.38E-08	0.1776	0.123	0.01691	3.45E-13	rs34887474:43519564:C:A
17_43520118_A_G	17	43520118	G	0.176	-0.0441	0.0082	7.29E-08	0.1776	0.1231	0.01691	3.45E-13	rs2684641:43520118:A:G
17_43520272_G_A	17	43520272	A	0.1757	-0.0439	0.0082	8.16E-08	0.1776	0.1225	0.01691	4.28E-13	rs141943637:43520272:G:A
17_43520675_T_C	17	43520675	C	0.1617	-0.0446	0.0087	2.59E-07	0.1634	0.1207	0.01792	1.62E-11	rs370245477:43520675:T:C
17_43521161_C_G	17	43521161	G	0.1759	-0.0438	0.0082	8.39E-08	0.1778	0.1221	0.0169	5.15E-13	rs62065376:43521161:C:G
17_43521193_A_G	17	43521193	G	0.176	-0.0437	0.0082	8.93E-08	0.1779	0.1223	0.0169	4.73E-13	rs117793085:43521193:A:G
17_43522361_T_C	17	43522361	C	0.1758	-0.0437	0.0082	8.98E-08	0.1776	0.1227	0.01691	3.90E-13	rs62065378:43522361:T:C
17_43522775_TTGTG_T	17	43522775	T	0.1698	-0.0416	0.0085	8.60E-07	0.1708	0.1215	0.01728	2.07E-12	17:43522775:TTGTG:T
17_43523385_T_TC	17	43523385	TC	0.1757	-0.0424	0.0083	2.75E-07	0.1774	0.1222	0.01691	5.05E-13	rs55668920:43523385:T:TC
17_43524526_C_T	17	43524526	T	0.1757	-0.0438	0.0082	8.79E-08	0.1776	0.1225	0.01691	4.23E-13	rs113575082:43524526:C:T
17_43525022_G_A	17	43525022	A	0.1758	-0.0437	0.0082	9.41E-08	0.1776	0.1227	0.01691	3.88E-13	rs71373572:43525022:G:A
17_43525166_C_CT	17	43525166	CT	0.1769	-0.0442	0.0084	1.45E-07	0.1809	0.1258	0.01715	2.16E-13	rs67636342:43525166:C:CT
17_43525346_TAG_T	17	43525346	T	0.1758	-0.0425	0.0082	2.62E-07	0.1776	0.1227	0.01691	3.87E-13	rs67974075:43525346:TAG:T
17_43525365_C_T	17	43525365	T	0.1756	-0.0437	0.0082	8.93E-08	0.1776	0.1226	0.01691	4.22E-13	rs62065379:43525365:C:T
17_43527025_C_T	17	43527025	T	0.1757	-0.0437	0.0082	9.39E-08	0.1776	0.1224	0.01691	4.47E-13	rs62065380:43527025:C:T
17_43527323_C_T	17	43527323	T	0.1758	-0.0436	0.0082	9.75E-08	0.1776	0.1227	0.01691	3.86E-13	rs112538459:43527323:C:T
17_43529293_G_A	17	43529293	A	0.1758	-0.0434	0.0082	1.09E-07	0.1776	0.1215	0.01692	7.10E-13	rs2077606:43529293:G:A
17_43529687_T_C	17	43529687	C	0.1758	-0.0436	0.0082	1.01E-07	0.1776	0.1228	0.01691	3.85E-13	rs1079434:43529687:T:C
17_43529769_G_T	17	43529769	T	0.1758	-0.0436	0.0082	1.00E-07	0.1776	0.1228	0.01691	3.85E-13	rs1079432:43529769:G:T
17_43531926_C_T	17	43531926	T	0.1758	-0.0436	0.0082	9.69E-08	0.1776	0.1227	0.01691	3.88E-13	rs112257723:43531926:C:T
17_43532804_C_T	17	43532804	T	0.1756	-0.0437	0.0082	9.05E-08	0.1776	0.1226	0.01691	4.24E-13	rs374201867:43532804:C:T
17_43534353_T_C	17	43534353	C	0.1781	-0.0437	0.0082	8.17E-08	0.1796	0.1222	0.01684	4.12E-13	rs2960000:43534353:T:C
17_43534694_C_T	17	43534694	T	0.1757	-0.044	0.0082	7.64E-08	0.1777	0.1224	0.01691	4.46E-13	rs62065385:43534694:C:T
17_43536408_C_T	17	43536408	T	0.1758	-0.0437	0.0082	9.04E-08	0.1776	0.1227	0.01691	3.94E-13	rs55703888:43536408:C:T
17_43536743_C_T	17	43536743	T	0.1758	-0.0441	0.0082	7.08E-08	0.1776	0.1215	0.0169	6.66E-13	rs56005713:43536743:C:T
17_43536970_G_A	17	43536970	A	0.1758	-0.0437	0.0082	8.92E-08	0.1776	0.1227	0.01691	3.92E-13	rs56314414:43536970:G:A
17_43537711_C_T	17	43537711	T	0.1756	-0.0439	0.0082	8.23E-08	0.1776	0.1226	0.01691	4.09E-13	rs368067814:43537711:C:T

17_43538523_G_A	17	43538523	A	0.1756	-0.0439	0.0082	8.13E-08	0.1776	0.1228	0.01691	3.89E-13	rs111423688:43538523:G:A
17_43538807_T_G	17	43538807	G	0.1756	-0.0439	0.0082	8.05E-08	0.1776	0.1228	0.01691	3.84E-13	rs62065389:43538807:T:G
17_43538991_G_A	17	43538991	A	0.1758	-0.0438	0.0082	8.39E-08	0.1776	0.1229	0.01691	3.68E-13	rs142488006:43538991:G:A
17_43538993_G_C	17	43538993	C	0.1758	-0.0438	0.0082	8.39E-08	0.1776	0.1229	0.01691	3.68E-13	rs145932064:43538993:G:C
17_43539035_G_A	17	43539035	A	0.1758	-0.0441	0.0082	6.99E-08	0.1776	0.1227	0.0169	3.85E-13	rs71369809:43539035:G:A
17_43539437_C_G	17	43539437	G	0.1757	-0.0439	0.0082	7.89E-08	0.1776	0.1227	0.01691	4.00E-13	rs117169618:43539437:C:G
17_43539723_C_T	17	43539723	T	0.1758	-0.0438	0.0082	8.44E-08	0.1776	0.1229	0.01691	3.67E-13	rs148807263:43539723:C:T
17_43539968_G_A	17	43539968	A	0.1758	-0.0438	0.0082	8.51E-08	0.1776	0.1229	0.01691	3.67E-13	rs77099723:43539968:G:A
17_43540273_C_A	17	43540273	A	0.1758	-0.0438	0.0082	8.54E-08	0.1776	0.1229	0.01691	3.67E-13	rs62065394:43540273:C:A
17_43540472_A_T	17	43540472	T	0.1758	-0.0438	0.0082	8.57E-08	0.1776	0.1229	0.01691	3.67E-13	rs148269941:43540472:A:T
17_43540732_T_C	17	43540732	C	0.1757	-0.0439	0.0082	8.18E-08	0.1776	0.1228	0.01691	3.81E-13	rs145328646:43540732:T:C
17_43541627_C_A	17	43541627	A	0.1759	-0.0442	0.0082	6.39E-08	0.1776	0.123	0.01691	3.51E-13	rs2139890:43541627:C:A
17_43541656_C_T	17	43541656	T	0.1757	-0.0439	0.0082	8.18E-08	0.1776	0.1227	0.01691	3.99E-13	rs3946526:43541656:C:T
17_43542037_T_C	17	43542037	C	0.1748	-0.0428	0.0082	1.86E-07	0.177	0.1233	0.01695	3.57E-13	rs145553563:43542037:T:C
17_43543083_T_A	17	43543083	A	0.1769	-0.0447	0.0082	5.44E-08	0.1793	0.1251	0.01697	1.74E-13	rs77319632:43543083:T:A
17_43543207_T_C	17	43543207	C	0.1775	-0.0431	0.0082	1.39E-07	0.1799	0.1245	0.01692	1.92E-13	rs62065396:43543207:T:C
17_43544206_G_C	17	43544206	C	0.1765	-0.0437	0.0082	9.59E-08	0.1791	0.1252	0.01694	1.46E-13	rs56227760:43544206:G:C
17_43544379_G_A	17	43544379	A	0.1765	-0.0437	0.0082	9.70E-08	0.1791	0.1252	0.01694	1.46E-13	rs55663797:43544379:G:A
17_43545893_T_C	17	43545893	C	0.1767	-0.0435	0.0082	1.06E-07	0.1792	0.1251	0.01693	1.48E-13	rs1879581:43545893:T:C
17_43546057_G_T	17	43546057	T	0.1766	-0.0435	0.0082	1.08E-07	0.1792	0.125	0.01693	1.53E-13	rs62065399:43546057:G:T
17_43548321_T_C	17	43548321	C	0.1769	-0.0434	0.0082	1.14E-07	0.1793	0.1251	0.01691	1.40E-13	rs55930887:43548321:T:C
17_43548424_A_G	17	43548424	G	0.1768	-0.0434	0.0082	1.14E-07	0.1792	0.1245	0.01691	1.84E-13	rs55671319:43548424:A:G
17_43548481_A_G	17	43548481	G	0.1768	-0.0433	0.0082	1.19E-07	0.1792	0.1248	0.01691	1.63E-13	rs55652155:43548481:A:G
17_43549526_A_G	17	43549526	G	0.1769	-0.0437	0.0082	9.52E-08	0.1794	0.1245	0.01692	1.85E-13	rs17631676:43549526:A:G
17_43549608_G_A	17	43549608	A	0.1767	-0.0431	0.0082	1.43E-07	0.1792	0.1244	0.01691	1.84E-13	rs149366495:43549608:G:A
17_43550107_A_G	17	43550107	G	0.1768	-0.0432	0.0082	1.31E-07	0.1792	0.1248	0.01691	1.58E-13	rs2090847:43550107:A:G
17_43551083_C_T	17	43551083	T	0.1767	-0.0432	0.0082	1.28E-07	0.1792	0.1247	0.01691	1.65E-13	rs55746869:43551083:C:T
17_43551151_C_G	17	43551151	G	0.1768	-0.0432	0.0082	1.34E-07	0.1792	0.125	0.01691	1.47E-13	rs12950965:43551151:C:G
17_43551321_G_C	17	43551321	C	0.1771	-0.0432	0.0082	1.28E-07	0.1792	0.1244	0.0169	1.80E-13	rs56015792:43551321:G:C
17_43551523_T_C	17	43551523	C	0.1768	-0.0432	0.0082	1.35E-07	0.1792	0.125	0.01691	1.42E-13	rs62065403:43551523:T:C
17_43551546_C_T	17	43551546	T	0.1767	-0.0433	0.0082	1.25E-07	0.1792	0.125	0.01691	1.46E-13	rs77132763:43551546:C:T
17_43551613_C_T	17	43551613	T	0.1768	-0.0432	0.0082	1.35E-07	0.1792	0.1251	0.01691	1.41E-13	rs62065404:43551613:C:T
17_43552537_G_A	17	43552537	A	0.1769	-0.0427	0.0082	1.81E-07	0.1792	0.1262	0.0169	7.94E-14	rs71238846:43552537:G:A
17_43552717_G_C	17	43552717	C	0.1768	-0.0431	0.0082	1.35E-07	0.1792	0.1252	0.01691	1.29E-13	rs147243132:43552717:G:C
17_43552812_A_G	17	43552812	G	0.1613	-0.0438	0.0087	5.25E-07	0.1639	0.1285	0.0181	1.24E-12	rs71227520:43552812:A:G
17_43552921_C_T	17	43552921	T	0.1768	-0.0431	0.0082	1.35E-07	0.1792	0.1252	0.01691	1.29E-13	rs12452273:43552921:C:T
17_43553496_AAT_A	17	43553496	A	0.1786	-0.043	0.0083	1.86E-07	0.1802	0.1189	0.0169	1.98E-12	rs67051615:43553496:AAT:A
17_43553564_TTA_T	17	43553564	T	0.1842	-0.0427	0.0082	1.83E-07	0.1862	0.1235	0.01683	2.16E-13	rs370357825:43553564:TTA:T
17_43555253_A_G	17	43555253	G	0.1768	-0.0431	0.0082	1.35E-07	0.1792	0.1253	0.01691	1.27E-13	rs56192752:43555253:A:G
17_43556652_G_A	17	43556652	A	0.1767	-0.0433	0.0082	1.24E-07	0.1792	0.1251	0.01691	1.43E-13	rs62065436:43556652:G:A
17_43556807_T_C	17	43556807	C	0.1781	-0.043	0.0082	1.42E-07	0.18	0.1233	0.01688	2.69E-13	rs55925547:43556807:T:C
17_43556862_C_T	17	43556862	T	0.1767	-0.0433	0.0082	1.23E-07	0.1792	0.1251	0.01691	1.43E-13	rs56159231:43556862:C:T
17_43556982_G_A	17	43556982	A	0.1768	-0.0432	0.0082	1.34E-07	0.1792	0.1253	0.01691	1.25E-13	rs55643511:43556982:G:A
17_43557054_A_AAAAACA	17	43557054	AAAAACAAAAC	0.1696	-0.0434	0.0085	3.18E-07	0.1714	0.1223	0.01743	2.24E-12	17:43557054:A:AAAAACAAAAC
17_43557612_G_A	17	43557612	A	0.1768	-0.0432	0.0082	1.34E-07	0.1792	0.1253	0.01691	1.25E-13	rs62065437:43557612:G:A
17_43557856_ACAAAAAAA	17	43557856	A	0.1772	-0.0422	0.0083	3.21E-07	0.1797	0.1249	0.01691	1.51E-13	17:43557856:ACAAAAAAA:A
17_43558092_C_T	17	43558092	T	0.1767	-0.0433	0.0082	1.22E-07	0.1792	0.1251	0.01692	1.42E-13	rs62065438:43558092:C:T
17_43563093_A_G	17	43563093	G	0.1769	-0.0431	0.0082	1.39E-07	0.1792	0.1252	0.01691	1.32E-13	rs62065441:43563093:A:G
17_43563304_A_C	17	43563304	C	0.1759	-0.043	0.0082	1.65E-07	0.1781	0.1267	0.01699	8.89E-14	rs112275793:43563304:A:C
17_43563305_T_G	17	43563305	G	0.1759	-0.043	0.0082	1.65E-07	0.1781	0.1267	0.01699	8.89E-14	rs112995489:43563305:T:G
17_43563349_G_A	17	43563349	A	0.1759	-0.043	0.0082	1.65E-07	0.1781	0.1267	0.01699	8.89E-14	rs111960572:43563349:G:A
17_43563606_A_T	17	43563606	T	0.205	-0.0353	0.0079	7.19E-06	0.2065	0.1051	0.01628	1.07E-10	rs142925250:43563606:A:T
17_43563894_T_C	17	43563894	C	0.1769	-0.0432	0.0082	1.32E-07	0.1792	0.1252	0.01691	1.31E-13	rs62065442:43563894:T:C
17_43564222_T_G	17	43564222	G	0.1771	-0.0431	0.0082	1.36E-07	0.1793	0.1243	0.0169	1.97E-13	rs144733372:43564222:T:G
17_43564357_C_T	17	43564357	T	0.1769	-0.0432	0.0082	1.34E-07	0.1792	0.1253	0.01691	1.29E-13	rs148532951:43564357:C:T

17_43565599_T_C	17	43565599	C	0.1772	-0.0438	0.0082	8.24E-08	0.1792	0.1255	0.01691	1.20E-13	rs62065444:43565599:T:C
17_43565840_G_A	17	43565840	A	0.1769	-0.0428	0.0082	1.63E-07	0.1793	0.125	0.01691	1.45E-13	rs62065445:43565840:G:A
17_43566931_A_G	17	43566931	G	0.1768	-0.0428	0.0082	1.68E-07	0.1793	0.1249	0.01694	1.62E-13	rs117416586:43566931:A:G
17_43567175_T_G	17	43567175	G	0.1764	-0.0428	0.0082	1.80E-07	0.1792	0.1253	0.01695	1.44E-13	rs1879585:43567175:T:G
17_43567337_C_G	17	43567337	G	0.1765	-0.0428	0.0082	1.76E-07	0.1792	0.125	0.01695	1.62E-13	rs1879586:43567337:C:G
17_43568278_T_TGA	17	43568278	TGA	0.1759	-0.042	0.0083	3.97E-07	0.1787	0.1242	0.01699	2.65E-13	17:43568278:T:TGA
17_43568280_G_GA	17	43568280	GA	0.1759	-0.042	0.0083	3.97E-07	0.1787	0.1242	0.01699	2.65E-13	17:43568280:G:GA
17_43568928_T_A	17	43568928	A	0.1758	-0.0427	0.0082	2.14E-07	0.1785	0.1247	0.017	2.25E-13	rs111392251:43568928:T:A
17_43569001_CA_C	17	43569001	C	0.1766	-0.0414	0.0083	5.34E-07	0.1794	0.1246	0.01695	1.95E-13	rs67553647:43569001:CA:C
17_43569083_C_T	17	43569083	T	0.1765	-0.0425	0.0082	2.09E-07	0.1794	0.1246	0.01695	1.98E-13	rs62065447:43569083:C:T
17_43569245_T_A	17	43569245	A	0.1765	-0.0425	0.0082	2.12E-07	0.1794	0.1245	0.01695	2.03E-13	rs113322852:43569245:T:A
17_43569770_C_T	17	43569770	T	0.176	-0.0456	0.0082	3.13E-08	0.1818	0.1191	0.01706	2.93E-12	rs147866440:43569770:C:T
17_43569909_T_C	17	43569909	C	0.1765	-0.0426	0.0082	2.09E-07	0.1794	0.1237	0.01697	3.02E-13	rs146746174:43569909:T:C
17_43570407_C_T	17	43570407	T	0.1769	-0.0422	0.0082	2.69E-07	0.1796	0.1226	0.017	5.58E-13	rs62065450:43570407:C:T
17_43570680_C_T	17	43570680	T	0.1768	-0.0425	0.0082	2.19E-07	0.1795	0.1221	0.01701	6.90E-13	rs1879582:43570680:C:T
17_43570893_C_T	17	43570893	T	0.1769	-0.0425	0.0082	2.31E-07	0.1796	0.1217	0.01701	8.48E-13	rs1879583:43570893:C:T
17_43572419_C_T	17	43572419	T	0.2096	-0.0481	0.0077	3.72E-10	0.2154	0.1148	0.0158	3.66E-13	rs56328224:43572419:C:T
17_43572896_T_G	17	43572896	G	0.2108	-0.0484	0.0077	2.74E-10	0.2157	0.1127	0.01578	9.08E-13	rs5026246:43572896:T:G
17_43573061_T_C	17	43573061	C	0.2089	-0.0479	0.0077	4.64E-10	0.2128	0.1137	0.01582	6.51E-13	rs62065452:43573061:T:C
17_43573231_C_G	17	43573231	G	0.21	-0.0478	0.0077	4.71E-10	0.2156	0.1144	0.01578	4.24E-13	rs2903705:43573231:C:G
17_43573419_C_T	17	43573419	T	0.2091	-0.0482	0.0077	3.51E-10	0.2135	0.1144	0.01581	4.54E-13	rs62065453:43573419:C:T
17_43573649_C_T	17	43573649	T	0.21	-0.0479	0.0077	4.10E-10	0.2158	0.1135	0.01578	6.42E-13	rs188710438:43573649:C:T
17_43574016_A_G	17	43574016	G	0.2083	-0.0482	0.0077	3.97E-10	0.2139	0.1137	0.01588	8.16E-13	rs117590192:43574016:A:G
17_43574229_T_C	17	43574229	C	0.2099	-0.0479	0.0077	4.34E-10	0.2157	0.1139	0.01578	5.30E-13	rs189777036:43574229:T:C
17_43574611_G_A	17	43574611	A	0.2096	-0.0479	0.0077	4.56E-10	0.215	0.1143	0.0158	4.59E-13	rs377004743:43574611:G:A
17_43574935_C_T	17	43574935	T	0.21	-0.0479	0.0077	4.15E-10	0.2157	0.1139	0.01578	5.24E-13	rs62066460:43574935:C:T
17_43575452_A_G	17	43575452	G	0.2101	-0.0478	0.0077	4.55E-10	0.2157	0.114	0.01578	5.12E-13	17:43575452:A:G
17_43575946_G_T	17	43575946	T	0.2099	-0.0479	0.0077	4.33E-10	0.2157	0.1139	0.01578	5.31E-13	rs112556326:43575946:G:T
17_43576046_T_TG	17	43576046	TG	0.21	-0.0471	0.0077	1.05E-09	0.2154	0.1134	0.01579	6.79E-13	rs200133133:43576046:T:TG
17_43576081_T_<CN0>	17	43576081	<CN0>	0.2101	-0.0469	0.0077	1.28E-09	0.2157	0.1139	0.01578	5.24E-13	17:43576081:T:<CN0>:0
17_43647443_A_<CN0>	17	43647443	<CN0>	0.2001	-0.0556	0.0081	7.60E-12	0.2024	0.1124	0.01663	1.41E-11	17:43647443:A:<CN0>:43649234
17_43650834_A_AAAACAA	17	43650834	AAAACAAAC	0.2675	-0.0462	0.0082	1.66E-08	0.2791	0.07468	0.01698	0.00001089	8337455:43650834:A:AAAACAAAC
17_43654108_T_C	17	43654108	C	0.4981	-0.0291	0.0074	0.00007716	0.4955	0.08689	0.01553	2.20E-08	rs2693366:43654108:T:C
17_43654468_C_T	17	43654468	T	0.2076	-0.0528	0.0079	1.87E-11	0.2086	0.1138	0.01621	2.15E-12	rs62064364:43654468:C:T
17_43656176_C_A	17	43656176	A	0.1853	-0.054	0.0085	1.87E-10	0.1839	0.1255	0.01737	4.97E-13	17:43656176:C:A
17_43656895_G_A	17	43656895	A	0.1883	-0.0542	0.0083	8.41E-11	0.1867	0.1245	0.01712	3.47E-13	17:43656895:G:A
17_43657257_C_T	17	43657257	T	0.1861	-0.0554	0.0084	4.59E-11	0.1838	0.1255	0.01724	3.28E-13	17:43657257:C:T
17_43657267_A_G	17	43657267	G	0.1861	-0.0554	0.0084	4.58E-11	0.1838	0.1255	0.01724	3.28E-13	17:43657267:A:G
17_43657393_A_G	17	43657393	G	0.1836	-0.0542	0.0085	1.91E-10	0.1803	0.1253	0.01744	6.73E-13	rs2693362:43657393:A:G
17_43657437_A_G	***17***	***43657437***	***A***	***0.4983***	***0.033***	***0.0073***	***5.42E-06***	***0.4993***	***-0.08573***	***0.01534***	***2.29E-08***	***rs2696467:43657437:A:G***
17_43657440_C_G	17	43657440	G	0.1836	-0.0542	0.0085	1.91E-10	0.1803	0.1253	0.01744	6.73E-13	17:43657440:C:G
17_43658409_G_A	17	43658409	A	0.1735	-0.0589	0.0086	5.69E-12	0.1804	0.1315	0.01765	9.49E-14	17:43658409:G:A
17_43658516_C_T	17	43658516	T	0.1751	-0.0587	0.0085	4.67E-12	0.182	0.1321	0.01747	3.96E-14	17:43658516:C:T
17_43658721_T_G	17	43658721	G	0.4951	-0.0399	0.0073	4.96E-08	0.4999	0.06697	0.01537	0.0000132	rs2693361:43658721:T:G
17_43658778_C_A	17	43658778	A	0.1756	-0.0576	0.0085	1.05E-11	0.1823	0.1312	0.01745	5.55E-14	17:43658778:C:A
17_43659251_C_A	17	43659251	A	0.1764	-0.058	0.0084	6.31E-12	0.1832	0.131	0.01738	4.83E-14	17:43659251:C:A
17_43659526_C_T	17	43659526	T	0.1886	-0.0534	0.0083	1.45E-10	0.1869	0.1244	0.01708	3.25E-13	17:43659526:C:T
17_43659738_T_C	17	43659738	C	0.1894	-0.0538	0.0083	8.94E-11	0.1876	0.123	0.01703	5.18E-13	17:43659738:T:C
17_43659975_T_C	17	43659975	C	0.1893	-0.0536	0.0083	1.17E-10	0.1878	0.1236	0.01704	4.02E-13	17:43659975:T:C
17_43660209_C_A	17	43660209	A	0.1893	-0.0535	0.0083	1.20E-10	0.1878	0.1229	0.01705	5.74E-13	17:43660209:C:A
17_43660599_A_<INS:ME:S	17	43660599	<INS:ME:SVA>	0.0772	-0.073	0.0146	6.05E-07	0.08681	0.1735	0.02954	4.23E-09	3660599:A:<INS:ME:SVA>:43662157
17_43661378_C_T	17	43661378	T	0.1888	-0.0535	0.0083	1.22E-10	0.1873	0.1232	0.01707	5.33E-13	17:43661378:C:T
17_43661751_T_A	17	43661751	A	0.1872	-0.0544	0.0084	7.81E-11	0.186	0.1228	0.01716	8.39E-13	rs2693359:43661751:T:A
17_43661801_T_G	17	43661801	G	0.1864	-0.0552	0.0084	4.87E-11	0.1848	0.1248	0.01723	4.24E-13	17:43661801:T:G
17_43661959_T_C	17	43661959	C	0.1877	-0.0552	0.0084	3.96E-11	0.1863	0.1235	0.01712	5.48E-13	17:43661959:T:C

17_43662020_A_G	17	43662020	G	0.1852	-0.0555	0.0084	4.83E-11	0.1837	0.124	0.01732	8.05E-13	17:43662020:A:G
17_43663169_T_C	17	43663169	C	0.2135	-0.0506	0.0077	4.27E-11	0.2171	0.1107	0.01585	2.86E-12	17:43663169:T:C
17_43663213_C_CA	17	43663213	CA	0.2096	-0.0485	0.0078	4.52E-10	0.2119	0.1102	0.01595	4.95E-12	17:43663213:C:CA
17_43663247_C_A	17	43663247	A	0.2147	-0.05	0.0077	7.11E-11	0.2182	0.1099	0.01586	4.21E-12	rs1724390:43663247:C:A
17_43663455_C_CT	17	43663455	CT	0.2554	-0.0487	0.0076	1.63E-10	0.2612	0.1109	0.01574	1.80E-12	17:43663455:C:CT
17_43663780_C_G	17	43663780	G	0.1967	-0.0519	0.0081	1.22E-10	0.2005	0.12	0.01667	6.08E-13	17:43663780:C:G
17_43663843_C_T	17	43663843	T	0.1868	-0.053	0.0084	2.36E-10	0.1896	0.1198	0.01726	3.82E-12	17:43663843:C:T
17_43664231_T_G	17	43664231	G	0.2025	-0.0498	0.0079	3.74E-10	0.206	0.1138	0.01647	4.97E-12	rs28428892:43664231:T:G
17_43664335_C_G	17	43664335	G	0.2126	-0.0494	0.0077	1.25E-10	0.2155	0.1132	0.01588	9.96E-13	17:43664335:C:G
17_43664978_A_G	17	43664978	G	0.2133	-0.0494	0.0076	1.08E-10	0.2166	0.1124	0.01584	1.29E-12	17:43664978:A:G
17_43665322_C_T	17	43665322	T	0.2172	-0.0476	0.0076	4.42E-10	0.2204	0.1111	0.01581	2.16E-12	17:43665322:C:T
17_43665343_T_G	17	43665343	G	0.2148	-0.0494	0.0076	1.09E-10	0.2183	0.1114	0.01584	2.04E-12	17:43665343:T:G
17_43665379_T_C	17	43665379	C	0.2144	-0.0491	0.0076	1.38E-10	0.2178	0.1119	0.01585	1.65E-12	17:43665379:T:C
17_43665468_T_G	17	43665468	G	0.2159	-0.0492	0.0076	1.17E-10	0.2196	0.1135	0.01583	7.41E-13	17:43665468:T:G
17_43665809_C_T	17	43665809	T	0.2134	-0.0493	0.0076	1.13E-10	0.2168	0.1125	0.01582	1.16E-12	17:43665809:C:T
17_43665838_A_G	17	43665838	G	0.2134	-0.0493	0.0076	1.11E-10	0.2168	0.1125	0.01582	1.16E-12	17:43665838:A:G
17_43665906_C_G	17	43665906	G	0.2141	-0.0487	0.0076	1.79E-10	0.2188	0.1128	0.01582	9.86E-13	17:43665906:C:G
17_43666001_A_C	17	43666001	C	0.2217	-0.0498	0.0076	5.88E-11	0.2264	0.1076	0.01573	7.83E-12	rs369572480:43666001:A:C
17_43666002_AT_A	17	43666002	A	0.2174	-0.0474	0.0076	5.82E-10	0.2191	0.1081	0.01572	6.01E-12	rs367637729:43666002:AT:A
17_43666244_A_G	17	43666244	G	0.2134	-0.0493	0.0076	1.12E-10	0.2168	0.1124	0.01582	1.17E-12	17:43666244:A:G
17_43666251_C_G	17	43666251	G	0.2116	-0.0482	0.0076	2.59E-10	0.2147	0.1138	0.01578	5.58E-13	17:43666251:C:G
17_43666385_C_T	17	43666385	T	0.2066	-0.0525	0.0078	1.92E-11	0.2067	0.1143	0.0161	1.25E-12	17:43666385:C:T
17_43666431_T_C	17	43666431	C	0.2134	-0.0493	0.0076	1.07E-10	0.2168	0.1124	0.01582	1.17E-12	17:43666431:T:C
17_43666492_C_T	17	43666492	T	0.2127	-0.0489	0.0077	1.72E-10	0.2162	0.113	0.01584	1.00E-12	rs112010353:43666492:C:T
17_43666511_A_T	17	43666511	T	0.2133	-0.0493	0.0076	1.06E-10	0.2167	0.1126	0.01582	1.12E-12	17:43666511:A:T
17_43666820_G_A	17	43666820	A	0.2007	-0.0522	0.008	6.59E-11	0.1985	0.1156	0.01637	1.63E-12	17:43666820:G:A
17_43666906_G_C	17	43666906	C	0.2145	-0.0481	0.0076	2.74E-10	0.2174	0.112	0.01579	1.32E-12	17:43666906:G:C
17_43667365_T_C	17	43667365	C	0.2147	-0.0494	0.0076	1.01E-10	0.2182	0.1121	0.01581	1.37E-12	17:43667365:T:C
17_43667413_CTT_C	17	43667413	C	0.2171	-0.0472	0.0077	7.38E-10	0.2211	0.1115	0.01575	1.50E-12	rs376183404:43667413:CTT:C
17_43667537_C_T	17	43667537	T	0.2006	-0.0519	0.008	8.43E-11	0.1986	0.1157	0.01637	1.57E-12	17:43667537:C:T
17_43667635_A_G	17	43667635	G	0.2238	-0.0514	0.0076	1.29E-11	0.2281	0.1096	0.01571	3.12E-12	17:43667635:A:G
17_43667792_C_T	17	43667792	T	0.218	-0.0523	0.0076	7.18E-12	0.2234	0.1104	0.01577	2.61E-12	17:43667792:C:T
17_43667836_C_A	17	43667836	A	0.2155	-0.0502	0.0076	4.79E-11	0.2202	0.1137	0.01581	6.56E-13	17:43667836:C:A
17_43667915_T_C	17	43667915	C	0.2142	-0.0497	0.0076	7.84E-11	0.2173	0.1127	0.01582	1.03E-12	17:43667915:T:C
17_43667922_G_C	17	43667922	C	0.2127	-0.0483	0.0076	2.41E-10	0.2158	0.114	0.01578	5.07E-13	17:43667922:G:C
17_43667934_C_G	17	43667934	G	0.2144	-0.0496	0.0076	8.28E-11	0.2176	0.113	0.01582	9.19E-13	17:43667934:C:G
17_43668017_G_A	17	43668017	A	0.2151	-0.0498	0.0076	6.74E-11	0.2186	0.113	0.01581	8.85E-13	17:43668017:G:A
17_43668187_A_G	17	43668187	G	0.214	-0.0497	0.0076	7.75E-11	0.2176	0.1132	0.01581	7.95E-13	17:43668187:A:G
17_43668239_T_C	17	43668239	C	0.214	-0.0498	0.0076	6.95E-11	0.2172	0.1124	0.01583	1.25E-12	17:43668239:T:C
17_43668455_T_G	17	43668455	G	0.2175	-0.0505	0.0076	3.86E-11	0.2222	0.1127	0.01581	1.02E-12	17:43668455:T:G
17_43668512_C_CAAA	17	43668512	CAAA	0.1798	-0.0459	0.0086	8.37E-08	0.1808	0.1169	0.01763	3.32E-11	17:43668512:C:CAAA
17_43668539_T_G	17	43668539	G	0.2115	-0.0481	0.0076	2.80E-10	0.2145	0.1138	0.01579	5.52E-13	17:43668539:T:G
17_43668815_A_G	17	43668815	G	0.2095	-0.0493	0.0078	2.01E-10	0.2115	0.1156	0.01601	5.31E-13	17:43668815:A:G
17_43668850_T_C	17	43668850	C	0.1576	-0.0573	0.0092	4.33E-10	0.1646	0.1342	0.01913	2.28E-12	17:43668850:T:C
17_43668852_C_T	17	43668852	T	0.1576	-0.0573	0.0092	4.33E-10	0.1646	0.1342	0.01913	2.28E-12	17:43668852:C:T
17_43668853_A_G	17	43668853	G	0.1576	-0.0573	0.0092	4.33E-10	0.1646	0.1342	0.01913	2.28E-12	17:43668853:A:G
17_43669049_A_AC	17	43669049	AC	0.2118	-0.0472	0.0077	7.62E-10	0.2146	0.1139	0.01579	5.27E-13	17:43669049:A:AC
17_43669250_A_G	17	43669250	G	0.2139	-0.0495	0.0076	9.40E-11	0.2175	0.1121	0.01582	1.38E-12	17:43669250:A:G
17_43669491_A_G	17	43669491	G	0.2082	-0.0477	0.0078	9.53E-10	0.2114	0.1146	0.01612	1.18E-12	rs112327620:43669491:A:G
17_43669704_C_A	17	43669704	A	0.2119	-0.0491	0.0077	1.49E-10	0.2151	0.1141	0.01589	6.81E-13	17:43669704:C:A
17_43669800_A_G	17	43669800	G	0.211	-0.0502	0.0077	7.03E-11	0.2141	0.1131	0.01595	1.31E-12	rs369043198:43669800:A:G
17_43669879_A_G	17	43669879	G	0.2134	-0.0498	0.0077	7.97E-11	0.2167	0.1149	0.01588	4.72E-13	17:43669879:A:G
17_43669923_T_C	17	43669923	C	0.212	-0.0491	0.0077	1.49E-10	0.2151	0.1141	0.01589	6.90E-13	17:43669923:T:C
17_43669931_T_C	17	43669931	C	0.217	-0.0473	0.0076	5.77E-10	0.2198	0.1103	0.01583	3.20E-12	17:43669931:T:C
17_43670018_G_A	17	43670018	A	0.2144	-0.0492	0.0076	1.18E-10	0.2181	0.113	0.01583	9.30E-13	17:43670018:G:A

17_43670073_G_T	17	43670073	T	0.2145	-0.0482	0.0077	3.17E-10	0.2181	0.1121	0.01584	1.46E-12	17:43670073:G:T
17_43670097_T_<INS:ME:S	17	43670097	<INS:ME:SVA>	0.0983	-0.0846	0.0126	2.27E-11	0.107	0.1611	0.02548	2.56E-10	3670097:T:<INS:ME:SVA>:43670458
17_43670225_A_G	17	43670225	G	0.1638	-0.0521	0.0091	1.06E-08	0.1609	0.1107	0.01851	2.25E-09	17:43670225:A:G
17_43670337_C_CT	17	43670337	CT	0.2203	-0.0468	0.0076	8.89E-10	0.2251	0.1126	0.01572	8.18E-13	rs144755808:43670337:C:CT
17_43670536_A_G	17	43670536	G	0.2022	-0.0531	0.008	2.84E-11	0.2037	0.1124	0.01641	7.50E-12	17:43670536:A:G
17_43670696_G_C	17	43670696	C	0.1981	-0.0526	0.0081	6.84E-11	0.1978	0.1144	0.01657	5.10E-12	17:43670696:G:C
17_43670754_G_A	17	43670754	A	0.2224	-0.0481	0.0076	2.86E-10	0.2263	0.1089	0.01582	5.84E-12	17:43670754:G:A
17_43670940_A_G	17	43670940	G	0.2188	-0.0488	0.0076	1.72E-10	0.2214	0.1119	0.01585	1.64E-12	17:43670940:A:G
17_43671066_G_GA	17	43671066	GA	0.2098	-0.0464	0.0078	2.19E-09	0.2118	0.1151	0.01591	4.77E-13	17:43671066:G:GA
17_43671099_C_A	17	43671099	A	0.2118	-0.0496	0.0077	1.13E-10	0.2154	0.1131	0.01589	1.12E-12	17:43671099:C:A
17_43671174_A_G	17	43671174	G	0.2013	-0.0524	0.008	4.63E-11	0.2018	0.1116	0.01642	1.07E-11	17:43671174:A:G
17_43671235_C_T	17	43671235	T	0.2134	-0.0492	0.0076	1.24E-10	0.217	0.1119	0.01584	1.61E-12	17:43671235:C:T
17_43671471_T_C	17	43671471	C	0.2259	-0.0505	0.0076	3.20E-11	0.2341	0.1065	0.01576	1.40E-11	rs140012394:43671471:T:C
17_43671522_C_T	17	43671522	T	0.199	-0.053	0.008	4.36E-11	0.1987	0.1149	0.01653	3.65E-12	rs145472926:43671522:C:T
17_43671737_A_C	17	43671737	C	0.2278	-0.0486	0.0076	1.65E-10	0.2278	0.1113	0.01578	1.73E-12	17:43671737:A:C
17_43671739_A_G	17	43671739	G	0.2278	-0.0486	0.0076	1.65E-10	0.2278	0.1113	0.01578	1.73E-12	17:43671739:A:G
17_43671965_G_T	17	43671965	T	0.0745	-0.0484	0.0152	0.00145	0.08173	0.1791	0.03074	5.65E-09	rs117893837:43671965:G:T
17_43671986_T_C	17	43671986	C	0.0682	-0.0485	0.0154	0.001681	0.07453	0.1769	0.03141	1.78E-08	17:43671986:T:C
17_43672118_A_G	17	43672118	G	0.1615	-0.0554	0.009	6.61E-10	0.1696	0.1358	0.01857	2.57E-13	rs376389482:43672118:A:G
17_43673792_A_G	17	43673792	G	0.2076	-0.0506	0.0078	7.85E-11	0.2105	0.1139	0.01608	1.40E-12	17:43673792:A:G
17_43675431_T_A	17	43675431	A	0.196	-0.0523	0.0081	1.16E-10	0.1952	0.1148	0.01667	5.63E-12	rs374316043:43675431:T:A
17_43675462_G_T	17	43675462	T	0.2743	-0.0467	0.0075	4.49E-10	0.2728	0.09811	0.01558	3.02E-10	17:43675462:G:T
17_43675489_A_T	17	43675489	T	0.2477	-0.0491	0.0076	8.40E-11	0.2435	0.1055	0.01571	1.92E-11	17:43675489:A:T
17_43679121_G_A	17	43679121	A	0.2138	-0.0488	0.0076	1.53E-10	0.2171	0.112	0.0158	1.36E-12	17:43679121:G:A
17_43679132_A_G	17	43679132	G	0.215	-0.0486	0.0076	1.78E-10	0.2182	0.1111	0.01579	1.92E-12	17:43679132:A:G
17_43679193_G_A	17	43679193	A	0.2274	-0.0479	0.0075	1.89E-10	0.2351	0.1018	0.01558	6.32E-11	17:43679193:G:A
17_43680850_G_C	17	43680850	C	0.2132	-0.0487	0.0076	1.66E-10	0.2168	0.1124	0.01579	1.12E-12	rs369209138:43680850:G:C
17_43681149_C_CA	17	43681149	CA	0.2037	-0.0508	0.008	2.56E-10	0.2027	0.1128	0.01638	5.65E-12	17:43681149:C:CA
17_43681222_C_T	17	43681222	T	0.2139	-0.0485	0.0076	2.00E-10	0.2171	0.1111	0.01581	2.10E-12	17:43681222:C:T
17_43681304_G_A	17	43681304	A	0.2112	-0.0485	0.0076	2.24E-10	0.2148	0.1135	0.01582	7.33E-13	17:43681304:G:A
17_43681316_T_C	17	43681316	C	0.2112	-0.0485	0.0076	2.16E-10	0.2148	0.1135	0.01582	7.33E-13	17:43681316:T:C
17_43681738_C_T	17	43681738	T	0.1898	-0.0505	0.0083	9.67E-10	0.1904	0.1237	0.01697	3.07E-13	rs113311910:43681738:C:T
17_43681771_C_T	17	43681771	T	0.1676	-0.0575	0.0087	3.79E-11	0.1744	0.1245	0.01809	5.77E-12	17:43681771:C:T
17_43681796_G_A	17	43681796	A	0.187	-0.0515	0.0084	6.85E-10	0.1876	0.1244	0.01716	4.25E-13	17:43681796:G:A
17_43681824_A_G	17	43681824	G	0.187	-0.0515	0.0084	6.85E-10	0.1876	0.1244	0.01716	4.25E-13	17:43681824:A:G
17_43682010_C_T	17	43682010	T	0.187	-0.0514	0.0083	7.59E-10	0.1876	0.1246	0.01716	3.93E-13	17:43682010:C:T
17_43682098_A_C	17	43682098	C	0.199	-0.0491	0.008	7.21E-10	0.2001	0.1175	0.01647	9.94E-13	17:43682098:A:C
17_43682323_T_C	17	43682323	C	0.2113	-0.049	0.0076	1.40E-10	0.2158	0.113	0.01582	9.00E-13	17:43682323:T:C
17_43683392_A_G	17	43683392	G	0.2118	-0.0481	0.0076	2.84E-10	0.2156	0.1123	0.0158	1.18E-12	rs451737:43683392:A:G
17_43683597_T_G	17	43683597	G	0.212	-0.0481	0.0076	2.72E-10	0.2157	0.1131	0.01579	7.88E-13	rs4528616:43683597:T:G
17_43683611_G_T	17	43683611	T	0.212	-0.0481	0.0076	2.72E-10	0.2157	0.1131	0.01579	7.88E-13	rs4471725:43683611:G:T
17_43683627_C_G	17	43683627	G	0.2124	-0.0479	0.0076	3.17E-10	0.2167	0.113	0.01578	8.14E-13	rs4485406:43683627:C:G
17_43683792_ATGG_A	17	43683792	A	0.2118	-0.0471	0.0077	8.69E-10	0.2145	0.1138	0.01579	5.51E-13	rs201658835:43683792:ATGG:A
17_43684094_T_C	17	43684094	C	0.2155	-0.0494	0.0076	8.25E-11	0.2182	0.1118	0.01577	1.31E-12	17:43684094:T:C
17_43684209_C_G	17	43684209	G	0.2153	-0.0471	0.0076	5.42E-10	0.219	0.1104	0.01575	2.33E-12	rs1635285:43684209:C:G
17_43684267_AT_ATT	17	43684267	ATT	0.2123	-0.0474	0.0077	6.69E-10	0.2167	0.112	0.01578	1.29E-12	rs372301122:43684267:AT:ATT
17_43684425_AT_A	17	43684425	A	0.2363	-0.0465	0.0077	1.97E-09	0.2374	0.107	0.01591	1.71E-11	17:43684425:AT:A
17_43684563_T_C	17	43684563	C	0.212	-0.0481	0.0076	2.71E-10	0.2157	0.1131	0.01579	7.88E-13	rs2906009:43684563:T:C
17_43684920_C_T	17	43684920	T	0.212	-0.0481	0.0076	2.69E-10	0.2157	0.1131	0.01579	7.88E-13	rs2906007:43684920:C:T
17_43685021_C_T	17	43685021	T	0.2105	-0.0484	0.0077	2.61E-10	0.2138	0.1135	0.01585	8.08E-13	rs2906006:43685021:C:T
17_43685291_CA_C	17	43685291	C	0.2209	-0.0442	0.0076	6.42E-09	0.2219	0.11	0.01568	2.31E-12	17:43685291:CA:C
17_43685698_A_G	17	43685698	G	0.2124	-0.0474	0.0076	4.82E-10	0.2161	0.1127	0.01578	9.22E-13	rs444967:43685698:A:G
17_43685707_T_C	17	43685707	C	0.2107	-0.0485	0.0077	2.42E-10	0.2132	0.1144	0.01583	4.87E-13	rs430688:43685707:T:C
17_43685826_A_G	17	43685826	G	0.213	-0.0491	0.0076	1.15E-10	0.217	0.1128	0.01578	8.78E-13	rs413519:43685826:A:G
17_43686419_A_C	17	43686419	C	0.2135	-0.0481	0.0076	2.55E-10	0.2178	0.112	0.01576	1.21E-12	rs385199:43686419:A:C

17_43686420_A_G	17	43686420	G	0.212	-0.0481	0.0076	2.66E-10	0.2157	0.1131	0.01579	7.78E-13	rs440778:43686420:A:G
17_43687072_G_A	17	43687072	A	0.2112	-0.048	0.0076	3.44E-10	0.215	0.1134	0.01582	7.67E-13	rs2949997:43687072:G:A
17_43687181_CT_C	17	43687181	C	0.2531	-0.0462	0.0076	1.27E-09	0.2616	0.1112	0.01567	1.29E-12	17:43687181:CT:C
17_43687268_G_A	17	43687268	A	0.1973	-0.0516	0.008	1.28E-10	0.1968	0.1163	0.01648	1.68E-12	rs391338:43687268:G:A
17_43687393_C_T	17	43687393	T	0.191	-0.0532	0.0082	8.43E-11	0.1907	0.1222	0.01683	3.90E-13	rs411305:43687393:C:T
17_43687542_C_G	17	43687542	G	0.2121	-0.0477	0.0076	3.77E-10	0.2153	0.1129	0.01578	8.29E-13	rs378392:43687542:C:G
17_43688042_C_G	17	43688042	G	0.2024	-0.05	0.0079	2.17E-10	0.2029	0.1165	0.01624	7.32E-13	17:43688042:C:G
17_43688249_G_C	17	43688249	C	0.211	-0.0483	0.0076	2.68E-10	0.2149	0.113	0.01582	9.12E-13	rs62066085:43688249:G:C
17_43688317_A_G	17	43688317	G	0.2143	-0.0464	0.0076	1.01E-09	0.2177	0.1109	0.01575	1.91E-12	17:43688317:A:G
17_43688387_A_G	17	43688387	G	0.212	-0.0481	0.0076	2.66E-10	0.2157	0.1131	0.01579	7.86E-13	rs62066086:43688387:A:G
17_43688579_A_G	17	43688579	G	0.212	-0.0481	0.0076	2.67E-10	0.2157	0.1131	0.01579	7.89E-13	17:43688579:A:G
17_43688905_A_G	17	43688905	G	0.2142	-0.0463	0.0076	1.07E-09	0.2176	0.1107	0.01575	2.05E-12	rs28795799:43688905:A:G
17_43689090_T_C	17	43689090	C	0.2123	-0.0483	0.0076	2.37E-10	0.2162	0.1129	0.0158	9.07E-13	rs56340658:43689090:T:C
17_43689684_C_G	17	43689684	G	0.2035	-0.0489	0.0079	5.94E-10	0.2022	0.1138	0.01626	2.61E-12	17:43689684:C:G
17_43690468_C_T	17	43690468	T	0.212	-0.0481	0.0076	2.66E-10	0.2157	0.1131	0.01579	7.89E-13	rs148537841:43690468:C:T
17_43690637_T_C	17	43690637	C	0.2055	-0.0494	0.0078	2.35E-10	0.2069	0.1149	0.01605	8.35E-13	rs147670174:43690637:T:C
17_43691173_C_T	17	43691173	T	0.209	-0.0491	0.0077	1.62E-10	0.2119	0.1128	0.01594	1.48E-12	rs376775643:43691173:C:T
17_43691192_A_AT	17	43691192	AT	0.1168	-0.066	0.0112	3.94E-09	0.1209	0.1504	0.02317	8.67E-11	17:43691192:A:AT
17_43691195_G_T	17	43691195	T	0.1168	-0.0673	0.0111	1.58E-09	0.1209	0.1504	0.02317	8.67E-11	rs369761090:43691195:G:T
17_43691377_T_C	17	43691377	C	0.2138	-0.0463	0.0076	1.12E-09	0.2164	0.1115	0.01575	1.47E-12	17:43691377:T:C
17_43692338_T_C	17	43692338	C	0.2017	-0.0514	0.0079	7.99E-11	0.2033	0.1138	0.01625	2.50E-12	rs2668709:43692338:T:C
17_43692935_A_G	17	43692935	G	0.212	-0.0481	0.0076	2.64E-10	0.2157	0.1131	0.01579	7.90E-13	rs611351:43692935:A:G
17_43693341_A_G	17	43693341	G	0.212	-0.0481	0.0076	2.64E-10	0.2157	0.1131	0.01579	7.90E-13	17:43693341:A:G
17_43693379_TA_T	17	43693379	T	0.2137	-0.0472	0.0077	7.62E-10	0.2168	0.1141	0.01577	4.60E-13	17:43693379:TA:T
17_43693462_C_T	17	43693462	T	0.2009	-0.0519	0.0079	5.84E-11	0.2019	0.1144	0.01629	2.16E-12	17:43693462:C:T
17_43693538_G_T	17	43693538	T	0.2116	-0.0479	0.0076	3.27E-10	0.2145	0.1138	0.01578	5.62E-13	17:43693538:G:T
17_43695197_C_T	17	43695197	T	0.2123	-0.0487	0.0076	1.58E-10	0.2161	0.1115	0.01578	1.61E-12	17:43695197:C:T
17_43695263_T_G	17	43695263	G	0.2002	-0.0528	0.008	3.08E-11	0.2011	0.1133	0.01632	3.86E-12	rs112997627:43695263:T:G
17_43695967_A_G	17	43695967	G	0.2119	-0.0479	0.0076	3.13E-10	0.2157	0.113	0.01579	8.01E-13	17:43695967:A:G
17_43696159_A_T	17	43696159	T	0.1785	-0.0481	0.0086	2.34E-08	0.182	0.115	0.01797	1.55E-10	17:43696159:A:T
17_43696254_A_G	17	43696254	G	0.2119	-0.0479	0.0076	3.13E-10	0.2157	0.113	0.01579	8.01E-13	17:43696254:A:G
17_43696837_TC_T	17	43696837	T	0.2121	-0.047	0.0077	9.21E-10	0.2157	0.113	0.01579	8.02E-13	rs199505547:43696837:TC:T
17_43696920_C_T	17	43696920	T	0.2119	-0.0479	0.0076	3.12E-10	0.2157	0.113	0.01579	8.02E-13	rs143345034:43696920:C:T
17_43698899_A_G	17	43698899	G	0.2112	-0.0481	0.0076	2.94E-10	0.2141	0.1143	0.01581	4.99E-13	rs184745911:43698899:A:G
17_43699113_A_G	17	43699113	G	0.21	-0.0483	0.0077	2.97E-10	0.2129	0.116	0.01586	2.62E-13	17:43699113:A:G
17_43702296_T_C	17	43702296	C	0.2111	-0.0482	0.0076	2.64E-10	0.2139	0.1143	0.01582	4.86E-13	rs192252295:43702296:T:C
17_43702701_C_G	17	43702701	G	0.2136	-0.0461	0.0076	1.29E-09	0.2159	0.1116	0.01575	1.41E-12	rs62066125:43702701:C:G
17_43703555_A_G	17	43703555	G	0.2115	-0.0479	0.0076	3.11E-10	0.2142	0.1139	0.01579	5.52E-13	rs392116:43703555:A:G
17_43704031_C_A	17	43704031	A	0.2115	-0.0479	0.0076	3.10E-10	0.2142	0.1139	0.01579	5.52E-13	rs385383:43704031:C:A
17_43704235_T_C	17	43704235	C	0.1969	-0.0479	0.0081	3.11E-09	0.1993	0.115	0.01683	8.38E-12	rs446330:43704235:T:C
17_43704310_T_G	17	43704310	G	0.2104	-0.0489	0.0077	1.71E-10	0.2124	0.1139	0.01582	6.10E-13	17:43704310:T:G
17_43704419_T_C	17	43704419	C	0.2115	-0.0479	0.0076	3.10E-10	0.2142	0.1139	0.01579	5.52E-13	rs372526058:43704419:T:C
17_43704491_G_A	17	43704491	A	0.2115	-0.0479	0.0076	3.26E-10	0.2142	0.1139	0.01579	5.52E-13	rs375424530:43704491:G:A
17_43705356_G_A	17	43705356	A	0.2115	-0.0479	0.0076	3.09E-10	0.2142	0.1139	0.01579	5.52E-13	rs383241:43705356:G:A
17_43705518_A_G	17	43705518	G	0.2115	-0.0479	0.0076	3.09E-10	0.2142	0.1139	0.01579	5.52E-13	rs376120:43705518:A:G
17_43705601_A_G	17	43705601	G	0.2136	-0.0461	0.0076	1.25E-09	0.2159	0.1116	0.01575	1.41E-12	rs365825:43705601:A:G
17_43705756_G_C	17	43705756	C	0.2136	-0.0461	0.0076	1.25E-09	0.2159	0.1116	0.01575	1.41E-12	rs393838:43705756:G:C
17_43707619_C_A	17	43707619	A	0.2119	-0.0479	0.0076	3.26E-10	0.2143	0.1135	0.01578	6.28E-13	rs681485:43707619:C:A
17_43707620_G_T	17	43707620	T	0.212	-0.0478	0.0076	3.34E-10	0.2144	0.113	0.01578	8.12E-13	rs594591:43707620:G:T
17_43707838_TG_T	17	43707838	T	0.2122	-0.0461	0.0077	1.84E-09	0.2146	0.1142	0.01579	4.62E-13	17:43707838:TG:T
17_43707848_G_T	17	43707848	T	0.2115	-0.0479	0.0076	3.08E-10	0.2142	0.1139	0.01579	5.52E-13	rs593720:43707848:G:T
17_43707951_C_T	17	43707951	T	0.2115	-0.0479	0.0076	3.08E-10	0.2142	0.1139	0.01579	5.52E-13	rs444071:43707951:C:T
17_43707955_C_A	17	43707955	A	0.2115	-0.0479	0.0076	3.08E-10	0.2142	0.1139	0.01579	5.52E-13	rs396593:43707955:C:A
17_43708415_CA_C	17	43708415	C	0.2111	-0.0472	0.0077	8.31E-10	0.214	0.1154	0.01581	2.86E-13	rs67379001:43708415:CA:C
17_43708418_C_G	17	43708418	G	0.2109	-0.0482	0.0076	2.70E-10	0.214	0.1154	0.01581	2.86E-13	rs368673667:43708418:C:G

17_43709225_T_C	17	43709225	C	0.2136	-0.0461	0.0076	1.29E-09	0.2159	0.1116	0.01575	1.41E-12	rs450237:43709225:T:C
17_43709415_C_T	17	43709415	T	0.212	-0.0478	0.0076	3.48E-10	0.2144	0.1132	0.01578	7.38E-13	rs436667:43709415:C:T
17_43709867_T_G	17	43709867	G	0.2115	-0.0479	0.0076	3.07E-10	0.2142	0.1139	0.01579	5.52E-13	rs650927:43709867:T:G
17_43709893_A_G	17	43709893	G	0.2115	-0.0479	0.0076	3.07E-10	0.2142	0.1139	0.01579	5.52E-13	rs671740:43709893:A:G
17_43710127_T_A	17	43710127	A	0.2115	-0.0479	0.0076	3.03E-10	0.2142	0.1139	0.01579	5.53E-13	rs81632:43710127:T:A
17_43710371_G_A	17	43710371	A	0.2115	-0.0479	0.0076	3.07E-10	0.2142	0.1139	0.01579	5.52E-13	rs16940633:43710371:G:A
17_43710384_A_C	17	43710384	C	0.212	-0.0478	0.0076	3.47E-10	0.2144	0.1132	0.01578	7.46E-13	rs17686610:43710384:A:C
17_43711312_C_T	17	43711312	T	0.2115	-0.0479	0.0076	3.07E-10	0.2142	0.1139	0.01579	5.53E-13	rs2942170:43711312:C:T
17_43711539_G_C	17	43711539	C	0.212	-0.0479	0.0076	3.04E-10	0.2144	0.1126	0.01578	9.88E-13	rs2942169:43711539:G:C
17_43712337_C_T	17	43712337	T	0.2115	-0.0479	0.0076	3.04E-10	0.2142	0.1138	0.01579	5.55E-13	rs241045:43712337:C:T
17_43712464_G_A	17	43712464	A	0.212	-0.0476	0.0076	3.93E-10	0.2144	0.1132	0.01578	7.34E-13	rs241044:43712464:G:A
17_43712657_T_C	17	43712657	C	0.2115	-0.0479	0.0076	3.04E-10	0.2142	0.1138	0.01579	5.56E-13	rs241042:43712657:T:C
17_43713925_A_G	17	43713925	G	0.212	-0.0477	0.0076	3.68E-10	0.2144	0.113	0.01578	8.13E-13	rs241041:43713925:A:G
17_43714179_C_CT	17	43714179	CT	0.2116	-0.0471	0.0077	8.61E-10	0.214	0.1137	0.01579	5.91E-13	17:43714179:C:CT
17_43714190_A_T	17	43714190	T	0.2116	-0.0479	0.0076	3.02E-10	0.2142	0.1139	0.01579	5.42E-13	17:43714190:A:T
17_43714673_A_T	17	43714673	T	0.212	-0.0478	0.0076	3.26E-10	0.2144	0.113	0.01578	7.90E-13	rs241039:43714673:A:T
17_43714850_G_A	17	43714850	A	0.212	-0.0477	0.0076	3.54E-10	0.2144	0.1132	0.01578	7.45E-13	rs2942168:43714850:G:A
17_43715018_T_C	17	43715018	C	0.212	-0.0478	0.0076	3.41E-10	0.2144	0.113	0.01578	7.93E-13	rs2942167:43715018:T:C
17_43715427_T_C	17	43715427	C	0.2121	-0.0473	0.0076	4.98E-10	0.2146	0.1131	0.01578	7.69E-13	rs2942166:43715427:T:C
17_43715619_G_C	17	43715619	C	0.2116	-0.048	0.0076	2.99E-10	0.2142	0.1138	0.01579	5.58E-13	rs2942165:43715619:G:C
17_43715924_A_G	17	43715924	G	0.2121	-0.0479	0.0076	3.17E-10	0.2144	0.1132	0.01578	7.51E-13	rs117368197:43715924:A:G
17_43716229_G_T	17	43716229	T	0.1378	-0.0595	0.01	2.73E-09	0.1442	0.1371	0.02074	3.88E-11	rs372494195:43716229:G:T
17_43716234_G_T	17	43716234	T	0.1378	-0.0595	0.01	2.73E-09	0.1442	0.1371	0.02074	3.88E-11	rs187569028:43716234:G:T
17_43716239_G_T	17	43716239	T	0.1378	-0.0594	0.01	2.81E-09	0.1442	0.1371	0.02074	3.88E-11	rs190958065:43716239:G:T
17_43716244_G_T	17	43716244	T	0.1381	-0.06	0.01	1.96E-09	0.1446	0.1364	0.02073	4.77E-11	rs182784716:43716244:G:T
17_43716885_A_G	17	43716885	G	0.2121	-0.0478	0.0076	3.23E-10	0.2144	0.1132	0.01578	7.47E-13	rs413778:43716885:A:G
17_43717131_C_T	17	43717131	T	0.2121	-0.0478	0.0076	3.23E-10	0.2144	0.1132	0.01578	7.47E-13	rs389217:43717131:C:T
17_43717415_A_G	17	43717415	G	0.2117	-0.0478	0.0076	3.45E-10	0.2144	0.1138	0.01578	5.61E-13	rs389978:43717415:A:G
17_43717803_T_C	17	43717803	C	0.2123	-0.0475	0.0076	4.19E-10	0.2147	0.1121	0.01578	1.19E-12	rs439558:43717803:T:C
17_43718336_T_C	17	43718336	C	0.2137	-0.0462	0.0076	1.19E-09	0.2159	0.1116	0.01575	1.41E-12	rs434805:43718336:T:C
17_43719143_A_G	17	43719143	G	0.2137	-0.0461	0.0076	1.23E-09	0.2158	0.1114	0.01575	1.51E-12	rs393152:43719143:A:G
17_43719829_G_T	17	43719829	T	0.209	-0.0498	0.0077	9.12E-11	0.2104	0.1137	0.01585	7.16E-13	rs3108318:43719829:G:T
17_43719870_G_A	17	43719870	A	0.2116	-0.048	0.0076	2.94E-10	0.2142	0.1138	0.01579	5.63E-13	rs3108317:43719870:G:A
17_43721283_G_C	17	43721283	C	0.2121	-0.0478	0.0076	3.31E-10	0.2144	0.1132	0.01578	7.32E-13	rs2942164:43721283:G:C
17_43721457_C_T	17	43721457	T	0.2116	-0.048	0.0076	2.97E-10	0.2142	0.1138	0.01579	5.66E-13	rs1706746:43721457:C:T
17_43721690_CAAAAAAAA	17	43721690	C	0.2117	-0.047	0.0077	9.25E-10	0.2142	0.1138	0.01579	5.66E-13	17:43721690:CAAAAAAAA:C
17_43722509_C_G	17	43722509	G	0.2125	-0.0481	0.0076	2.58E-10	0.2156	0.1136	0.01578	6.06E-13	rs1706748:43722509:C:G
17_43723189_G_A	17	43723189	A	0.2121	-0.0478	0.0076	3.29E-10	0.2145	0.1136	0.01578	6.03E-13	rs413917:43723189:G:A
17_43723462_C_T	17	43723462	T	0.2116	-0.048	0.0076	2.98E-10	0.2142	0.1138	0.01579	5.68E-13	rs3418:43723462:C:T
17_43723605_T_C	17	43723605	C	0.2121	-0.0478	0.0076	3.33E-10	0.2144	0.1131	0.01578	7.55E-13	rs393675:43723605:T:C
17_43723929_G_A	17	43723929	A	0.2081	-0.0482	0.0077	4.00E-10	0.2122	0.1117	0.01599	2.90E-12	17:43723929:G:A
17_43723930_A_G	17	43723930	G	0.2081	-0.0482	0.0077	4.01E-10	0.2122	0.1117	0.01599	2.90E-12	17:43723930:A:G
17_43724245_G_A	17	43724245	A	0.2121	-0.0479	0.0076	3.18E-10	0.2144	0.113	0.01578	8.13E-13	rs669915:43724245:G:A
17_43724247_T_TA	17	43724247	TA	0.2111	-0.047	0.0077	1.04E-09	0.2123	0.1143	0.01581	4.90E-13	17:43724247:T:TA
17_43724555_G_A	17	43724555	A	0.2121	-0.0478	0.0076	3.46E-10	0.2145	0.1131	0.01578	7.75E-13	rs449501:43724555:G:A
17_43725212_G_A	17	43725212	A	0.2121	-0.0478	0.0076	3.45E-10	0.2144	0.113	0.01578	7.93E-13	rs448830:43725212:G:A
17_43725684_G_A	17	43725684	A	0.2121	-0.0477	0.0076	3.51E-10	0.2144	0.1131	0.01578	7.64E-13	rs434428:43725684:G:A
17_43725762_G_A	17	43725762	A	0.2121	-0.0477	0.0076	3.50E-10	0.2144	0.113	0.01578	7.89E-13	rs434598:43725762:G:A
17_43725992_G_A	17	43725992	A	0.2116	-0.0479	0.0076	2.99E-10	0.2142	0.1138	0.01579	5.72E-13	rs434971:43725992:G:A
17_43726125_A_C	17	43726125	C	0.2121	-0.0477	0.0076	3.63E-10	0.2144	0.1131	0.01578	7.77E-13	rs385691:43726125:A:C
17_43726574_T_C	17	43726574	C	0.2116	-0.0479	0.0076	2.99E-10	0.2142	0.1138	0.01579	5.73E-13	rs455028:43726574:T:C
17_43726588_C_T	17	43726588	T	0.2121	-0.0478	0.0076	3.36E-10	0.2144	0.1131	0.01578	7.84E-13	rs366858:43726588:C:T
17_43726659_A_C	17	43726659	A	0.2477	-0.0364	0.0072	4.17E-07	0.2512	0.09215	0.015	8.08E-10	rs439945:43726659:A:C
17_43727061_C_T	17	43727061	T	0.2121	-0.0478	0.0076	3.40E-10	0.2145	0.1133	0.01578	7.08E-13	rs453997:43727061:C:T
17_43727887_A_T	17	43727887	T	0.2116	-0.0479	0.0076	2.99E-10	0.2142	0.1138	0.01579	5.74E-13	rs424243:43727887:A:T

17_43728137_G_A	17	43728137	A	0.2116	-0.0479	0.0076	3.12E-10	0.2142	0.1137	0.01579	5.78E-13	rs422112:43728137:G:A
17_43728376_G_A	17	43728376	G	0.2478	-0.0362	0.0072	4.97E-07	0.2514	0.0918	0.015	9.33E-10	rs417968:43728376:G:A
17_43729384_G_A	17	43729384	A	0.212	-0.0477	0.0076	3.67E-10	0.2144	0.113	0.01578	7.92E-13	rs413844:43729384:G:A
17_43729432_C_T	17	43729432	T	0.2116	-0.0479	0.0076	2.99E-10	0.2142	0.1138	0.01579	5.74E-13	rs647483:43729432:C:T
17_43730598_G_A	17	43730598	A	0.2116	-0.0479	0.0076	2.99E-10	0.2143	0.1138	0.01579	5.72E-13	rs241038:43730598:G:A
17_43730636_G_T	17	43730636	T	0.2116	-0.0479	0.0076	3.00E-10	0.2142	0.1138	0.01579	5.62E-13	rs241037:43730636:G:T
17_43731719_A_C	17	43731719	C	0.2121	-0.0478	0.0076	3.46E-10	0.2144	0.1135	0.01578	6.49E-13	rs241036:43731719:A:C
17_43731896_C_T	17	43731896	T	0.2121	-0.0478	0.0076	3.44E-10	0.2144	0.1131	0.01578	7.63E-13	rs241035:43731896:C:T
17_43732780_CCCCTATGT_	17	43732780	CCCCTATGT	0.2476	-0.0349	0.0073	1.55E-06	0.2512	0.09228	0.01501	7.76E-10	11276875:43732780:CCCCTATGT:C
17_43733048_A_T	17	43733048	T	0.2116	-0.0479	0.0076	3.00E-10	0.2143	0.1138	0.01579	5.70E-13	rs241034:43733048:A:T
17_43733707_GC_G	17	43733707	G	0.2117	-0.047	0.0077	9.33E-10	0.2143	0.1138	0.01579	5.69E-13	17:43733707:GC:G
17_43733983_G_A	17	43733983	A	0.2121	-0.0477	0.0076	3.58E-10	0.2144	0.113	0.01578	8.16E-13	rs241033:43733983:G:A
17_43734145_T_C	17	43734145	C	0.2116	-0.048	0.0076	2.90E-10	0.2143	0.1138	0.01579	5.68E-13	rs241032:43734145:T:C
17_43734255_TA_T	17	43734255	T	0.2117	-0.047	0.0077	9.33E-10	0.2143	0.1138	0.01579	5.68E-13	17:43734255:TA:T
17_43734304_T_C	17	43734304	C	0.2121	-0.0478	0.0076	3.21E-10	0.2145	0.1126	0.01578	9.86E-13	rs241031:43734304:T:C
17_43734503_A_G	17	43734503	G	0.2116	-0.0479	0.0076	3.00E-10	0.2143	0.1138	0.01579	5.68E-13	rs241030:43734503:A:G
17_43734643_T_C	17	43734643	C	0.2116	-0.0479	0.0076	2.99E-10	0.2143	0.1138	0.01579	5.68E-13	rs241029:43734643:T:C
17_43735276_C_T	17	43735276	T	0.2119	-0.0481	0.0076	2.77E-10	0.214	0.113	0.01579	8.29E-13	rs241028:43735276:C:T
17_43735478_A_G	17	43735478	G	0.2116	-0.0479	0.0076	2.98E-10	0.2143	0.1138	0.01579	5.67E-13	rs241027:43735478:A:G
17_43735555_G_A	17	43735555	A	0.2116	-0.0479	0.0076	2.98E-10	0.2143	0.1138	0.01579	5.67E-13	rs241026:43735555:G:A
17_43736504_T_C	17	43736504	C	0.2046	-0.0505	0.0078	1.23E-10	0.2012	0.1129	0.01596	1.50E-12	rs241025:43736504:T:C
17_43736763_C_T	17	43736763	T	0.2116	-0.048	0.0076	2.96E-10	0.2142	0.1138	0.01579	5.63E-13	rs241024:43736763:C:T
17_43737040_G_A	17	43737040	A	0.2116	-0.0479	0.0076	2.99E-10	0.2143	0.1138	0.01579	5.66E-13	rs241023:43737040:G:A
17_43737730_T_C	17	43737730	C	0.212	-0.0475	0.0076	4.16E-10	0.2145	0.1132	0.01578	7.23E-13	rs241022:43737730:T:C
17_43738627_T_G	17	43738627	G	0.2121	-0.0477	0.0076	3.49E-10	0.2144	0.113	0.01578	8.25E-13	rs241021:43738627:T:G
17_43738676_C_A	17	43738676	A	0.2121	-0.048	0.0076	2.76E-10	0.2145	0.1127	0.01578	9.15E-13	rs241020:43738676:C:A
17_43740565_G_T	17	43740565	G	0.2464	-0.0363	0.0072	4.85E-07	0.2492	0.09029	0.01501	1.82E-09	rs1724409:43740565:G:T
17_43740856_C_T	17	43740856	T	0.2116	-0.0479	0.0076	3.08E-10	0.2143	0.1138	0.01579	5.56E-13	rs62053939:43740856:C:T
17_43740967_C_T	17	43740967	T	0.2116	-0.0479	0.0076	3.00E-10	0.2143	0.1138	0.01579	5.60E-13	rs111273167:43740967:C:T
17_43741028_A_G	17	43741028	G	0.2116	-0.0479	0.0076	3.00E-10	0.2143	0.1138	0.01579	5.59E-13	rs62053940:43741028:A:G
17_43741136_C_T	17	43741136	T	0.2128	-0.0482	0.0076	2.57E-10	0.2151	0.1135	0.0158	6.81E-13	rs55688739:43741136:C:T
17_43741452_C_T	17	43741452	T	0.2119	-0.0478	0.0076	3.35E-10	0.2143	0.1135	0.01579	6.52E-13	rs17760577:43741452:C:T
17_43741627_A_AT	17	43741627	AT	0.2117	-0.047	0.0077	9.38E-10	0.2143	0.1138	0.01579	5.56E-13	17:43741627:A:AT
17_43742454_AC_A	17	43742454	A	0.2124	-0.0469	0.0077	1.02E-09	0.2147	0.1133	0.01578	6.94E-13	17:43742454:AC:A
17_43743045_T_C	17	43743045	C	0.2121	-0.0478	0.0076	3.30E-10	0.2145	0.1131	0.01578	7.69E-13	rs17760631:43743045:T:C
17_43744203_C_T	17	43744203	T	0.1445	-0.0597	0.0092	7.05E-11	0.1498	0.122	0.01878	8.19E-11	rs62053943:43744203:C:T
17_43744344_T_A	17	43744344	T	0.234	-0.0397	0.0073	6.70E-08	0.2378	0.09471	0.01529	5.80E-10	rs1635298:43744344:T:A
17_43744990_C_T	17	43744990	T	0.2121	-0.0479	0.0076	3.11E-10	0.2145	0.1135	0.01578	6.39E-13	rs17687462:43744990:C:T
17_43746187_TC_T	17	43746187	T	0.2123	-0.0467	0.0077	1.18E-09	0.2145	0.1138	0.01578	5.54E-13	17:43746187:TC:T
17_43746276_G_T	17	43746276	T	0.212	-0.0478	0.0076	3.42E-10	0.2144	0.1134	0.01578	6.84E-13	rs17760733:43746276:G:T
17_43746418_T_A	17	43746418	A	0.2121	-0.0478	0.0076	3.40E-10	0.2145	0.1135	0.01578	6.51E-13	rs79675109:43746418:T:A
17_43746610_T_TATC	17	43746610	TATC	0.2117	-0.047	0.0077	9.40E-10	0.2143	0.114	0.01579	5.06E-13	rs142642115:43746610:T:TATC
17_43746721_A_G	17	43746721	G	0.2121	-0.0477	0.0076	3.78E-10	0.2145	0.113	0.01578	8.14E-13	rs17687504:43746721:A:G
17_43746839_T_C	17	43746839	C	0.2121	-0.0477	0.0076	3.49E-10	0.2145	0.1133	0.01578	6.99E-13	rs62053945:43746839:T:C
17_43747615_C_T	17	43747615	C	0.2344	-0.0399	0.0073	5.35E-08	0.2385	0.09267	0.01525	1.23E-09	rs1724407:43747615:C:T
17_43747677_C_T	17	43747677	T	0.2121	-0.0478	0.0076	3.44E-10	0.2145	0.1135	0.01578	6.40E-13	rs62053946:43747677:C:T
17_43747683_G_A	17	43747683	A	0.2116	-0.0479	0.0076	3.00E-10	0.2143	0.1141	0.01579	5.02E-13	rs62053947:43747683:G:A
17_43748046_C_T	17	43748046	T	0.2121	-0.0478	0.0076	3.45E-10	0.2145	0.1135	0.01578	6.30E-13	rs62053948:43748046:C:T
17_43748101_A_G	17	43748101	G	0.2116	-0.0479	0.0076	3.01E-10	0.2143	0.1141	0.01579	5.02E-13	rs62053949:43748101:A:G
17_43748412_A_G	17	43748412	G	0.2116	-0.0479	0.0076	3.02E-10	0.2143	0.1141	0.01579	5.02E-13	rs62053950:43748412:A:G
17_43749168_G_C	17	43749168	C	0.2121	-0.0478	0.0076	3.44E-10	0.2145	0.1125	0.01578	1.01E-12	rs62053951:43749168:G:C
17_43749261_T_C	17	43749261	C	0.2116	-0.0479	0.0076	3.08E-10	0.2143	0.1142	0.01579	4.80E-13	rs62053952:43749261:T:C
17_43749454_G_A	17	43749454	A	0.2121	-0.0478	0.0076	3.46E-10	0.2145	0.1134	0.01578	6.70E-13	rs62053953:43749454:G:A
17_43749579_T_C	17	43749579	C	0.2121	-0.0477	0.0076	3.49E-10	0.2145	0.1131	0.01578	7.62E-13	rs17687534:43749579:T:C
17_43749942_A_G	17	43749942	A	0.2344	-0.04	0.0073	4.86E-08	0.2385	0.09266	0.01525	1.23E-09	rs1631850:43749942:A:G

17_43749949_G_A	17	43749949	A	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.01E-13	rs62053954:43749949:G:A
17_43749980_T_C	17	43749980	C	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.01E-13	rs62053955:43749980:T:C
17_43750010_G_A	17	43750010	A	0.2121	-0.0477	0.0076	3.54E-10	0.2145	0.1133	0.01578	7.09E-13	rs17687571:43750010:G:A
17_43750137_G_C	17	43750137	C	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.01E-13	rs17760817:43750137:G:C
17_43750172_G_A	17	43750172	G	0.2344	-0.0399	0.0073	5.14E-08	0.2385	0.09288	0.01525	1.13E-09	rs1630095:43750172:G:A
17_43750238_A_G	17	43750238	G	0.2121	-0.0478	0.0076	3.37E-10	0.2145	0.1133	0.01578	7.08E-13	rs17687625:43750238:A:G
17_43750315_A_G	17	43750315	G	0.2121	-0.0477	0.0076	3.51E-10	0.2145	0.1132	0.01578	7.35E-13	rs62053956:43750315:A:G
17_43750910_C_T	17	43750910	C	0.2344	-0.0399	0.0073	5.16E-08	0.2385	0.09299	0.01525	1.08E-09	rs4792824:43750910:C:T
17_43750921_T_TA	17	43750921	T	0.2328	-0.0398	0.0074	8.55E-08	0.237	0.09457	0.01531	6.59E-10	rs1635293:43750921:T:TA
17_43750939_T_C	17	43750939	C	0.2116	-0.0479	0.0076	3.04E-10	0.2143	0.1141	0.01579	5.01E-13	rs62053957:43750939:T:C
17_43751101_A_G	17	43751101	G	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.01E-13	rs112637166:43751101:A:G
17_43751223_A_T	17	43751223	T	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.00E-13	rs62053958:43751223:A:T
17_43751246_C_T	17	43751246	T	0.2116	-0.048	0.0076	2.88E-10	0.2143	0.1141	0.01579	4.87E-13	rs62053959:43751246:C:T
17_43751308_T_C	17	43751308	C	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.00E-13	rs62055660:43751308:T:C
17_43751427_T_C	17	43751427	C	0.2116	-0.0479	0.0076	3.03E-10	0.2143	0.1141	0.01579	5.00E-13	rs113486004:43751427:T:C
17_43751598_GT_G	17	43751598	G	0.2117	-0.0471	0.0077	8.37E-10	0.2145	0.1144	0.01579	4.35E-13	17:43751598:GT:G
17_43751913_G_A	17	43751913	G	0.2344	-0.0401	0.0073	4.69E-08	0.2386	0.09342	0.01525	9.01E-10	rs1635291:43751913:G:A
17_43752039_C_T	17	43752039	T	0.2116	-0.0479	0.0076	3.10E-10	0.2143	0.1141	0.01579	5.00E-13	rs62055661:43752039:C:T
17_43752078_A_AC	17	43752078	AC	0.2117	-0.0469	0.0077	9.75E-10	0.2143	0.1141	0.01579	5.00E-13	rs113155081:43752078:A:AC
17_43752566_C_T	17	43752566	T	0.2121	-0.0477	0.0076	3.52E-10	0.2145	0.1134	0.01578	6.68E-13	rs62055662:43752566:C:T
17_43753454_A_G	17	43753454	G	0.2116	-0.0479	0.0076	3.11E-10	0.2143	0.1141	0.01579	5.00E-13	rs62055663:43753454:A:G
17_43753642_A_G	17	43753642	G	0.2116	-0.0479	0.0076	3.11E-10	0.2143	0.1141	0.01579	5.00E-13	rs62055664:43753642:A:G
17_43754010_T_C	17	43754010	C	0.2121	-0.0476	0.0076	3.92E-10	0.2145	0.1133	0.01578	6.90E-13	rs76717812:43754010:T:C
17_43754099_G_A	17	43754099	A	0.2121	-0.0476	0.0076	3.93E-10	0.2145	0.1133	0.01578	7.07E-13	rs17687667:43754099:G:A
17_43754209_G_C	17	43754209	C	0.2121	-0.0479	0.0076	3.04E-10	0.2145	0.1134	0.01578	6.66E-13	rs79073784:43754209:G:C
17_43754505_A_C	17	43754505	C	0.2116	-0.0479	0.0076	3.11E-10	0.2143	0.1141	0.01579	4.98E-13	rs62055665:43754505:A:C
17_43754569_G_A	17	43754569	A	0.2116	-0.0479	0.0076	3.10E-10	0.2143	0.1141	0.01579	4.98E-13	rs62055689:43754569:G:A
17_43754576_C_G	17	43754576	G	0.2117	-0.0479	0.0076	3.10E-10	0.2144	0.114	0.01579	5.10E-13	rs62055690:43754576:C:G
17_43754850_T_C	17	43754850	C	0.2116	-0.0479	0.0076	3.11E-10	0.2143	0.1141	0.01579	4.97E-13	rs62055691:43754850:T:C
17_43754909_A_G	17	43754909	G	0.2116	-0.0479	0.0076	3.10E-10	0.2143	0.1141	0.01579	4.97E-13	rs62055692:43754909:A:G
17_43754914_C_T	17	43754914	C	0.2344	-0.04	0.0073	4.86E-08	0.2385	0.09286	0.01525	1.14E-09	rs1724402:43754914:C:T
17_43755857_C_A	17	43755857	C	0.2344	-0.0399	0.0073	5.15E-08	0.2385	0.09314	0.01525	1.01E-09	rs1724401:43755857:C:A
17_43755871_A_C	17	43755871	A	0.2344	-0.04	0.0073	4.83E-08	0.2385	0.09314	0.01525	1.01E-09	rs1724400:43755871:A:C
17_43756171_A_AAAAC	17	43756171	AAAAC	0.2117	-0.0469	0.0077	9.68E-10	0.2143	0.1141	0.01579	4.96E-13	17:43756171:A:AAAAC
17_43756340_T_C	17	43756340	C	0.2121	-0.0477	0.0076	3.67E-10	0.2145	0.1129	0.01578	8.32E-13	rs74398257:43756340:T:C
17_43756376_G_C	17	43756376	C	0.2116	-0.0479	0.0076	3.09E-10	0.2143	0.1141	0.01579	5.00E-13	rs17687740:43756376:G:C
17_43756458_G_A	17	43756458	A	0.2116	-0.0479	0.0076	3.10E-10	0.2143	0.1141	0.01579	5.00E-13	rs872972:43756458:G:A
17_43756466_T_C	17	43756466	C	0.2119	-0.0473	0.0076	5.15E-10	0.2146	0.1147	0.01578	3.66E-13	rs757503:43756466:T:C
17_43756506_C_T	17	43756506	T	0.2122	-0.0479	0.0076	3.04E-10	0.2145	0.1138	0.01578	5.55E-13	rs757502:43756506:C:T
17_43756685_A_G	17	43756685	G	0.2121	-0.0477	0.0076	3.54E-10	0.2145	0.1134	0.01578	6.68E-13	rs757501:43756685:A:G
17_43756833_C_A	17	43756833	A	0.2121	-0.0478	0.0076	3.42E-10	0.2145	0.1135	0.01578	6.46E-13	rs757500:43756833:C:A
17_43756910_T_C	17	43756910	C	0.2117	-0.0479	0.0076	3.04E-10	0.2147	0.1138	0.01579	5.70E-13	rs62055693:43756910:T:C
17_43756969_A_G	17	43756969	A	0.2351	-0.04	0.0073	4.91E-08	0.2387	0.09272	0.01523	1.15E-09	rs1635288:43756969:A:G
17_43757161_C_T	17	43757161	T	0.2116	-0.0479	0.0076	3.13E-10	0.2143	0.1141	0.01579	4.93E-13	rs78487840:43757161:C:T
17_43757450_C_A	17	43757450	A	0.206	-0.05	0.0077	1.05E-10	0.21	0.114	0.01608	1.39E-12	rs55974014:43757450:C:A
17_43757776_T_C	17	43757776	C	0.2121	-0.0477	0.0076	3.56E-10	0.2145	0.1137	0.01578	5.86E-13	17:43757776:T:C
17_43757777_C_T	17	43757777	T	0.2116	-0.0479	0.0076	3.17E-10	0.2143	0.1142	0.01579	4.63E-13	17:43757777:C:T
17_43758011_G_C	17	43758011	C	0.2121	-0.0475	0.0076	4.14E-10	0.2146	0.114	0.01577	4.88E-13	rs55651627:43758011:G:C
17_43758078_G_A	17	43758078	A	0.2116	-0.0479	0.0076	3.17E-10	0.2143	0.1142	0.01579	4.63E-13	rs112155389:43758078:G:A
17_43758116_AAAAG_A	17	43758116	A	0.2117	-0.0469	0.0077	9.93E-10	0.2143	0.1143	0.01579	4.49E-13	17:43758116:AAAAG:A
17_43758125_A_G	17	43758125	G	0.2116	-0.0479	0.0076	3.17E-10	0.2143	0.1142	0.01579	4.63E-13	rs62055696:43758125:A:G
17_43758148_C_T	17	43758148	T	0.2116	-0.0479	0.0076	3.07E-10	0.2143	0.1142	0.01579	4.61E-13	rs62055697:43758148:C:T
17_43758238_C_T	17	43758238	T	0.2116	-0.0479	0.0076	3.18E-10	0.2143	0.1142	0.01579	4.63E-13	rs62055698:43758238:C:T
17_43758382_T_C	17	43758382	C	0.2121	-0.0477	0.0076	3.67E-10	0.2145	0.1134	0.01578	6.68E-13	rs17761046:43758382:T:C
17_43758742_T_C	17	43758742	C	0.2116	-0.0479	0.0076	3.18E-10	0.2143	0.1142	0.01579	4.63E-13	rs62055700:43758742:T:C

17_43758787_G_A	17	43758787	A	0.2116	-0.0479	0.0076	3.18E-10	0.2143	0.1142	0.01579	4.63E-13	rs62055701:43758787:G:A
17_43758790_C_T	17	43758790	T	0.2121	-0.0476	0.0076	3.92E-10	0.2145	0.1136	0.01578	6.15E-13	rs62055702:43758790:C:T
17_43758885_A_G	17	43758885	G	0.2121	-0.0477	0.0076	3.67E-10	0.2145	0.1137	0.01578	5.88E-13	rs112431991:43758885:A:G
17_43758887_A_G	17	43758887	G	0.2116	-0.0479	0.0076	3.18E-10	0.2143	0.1142	0.01579	4.63E-13	rs76539714:43758887:A:G
17_43758898_A_G	17	43758898	G	0.2339	-0.0401	0.0073	4.78E-08	0.2383	0.09404	0.01527	7.34E-10	rs57222984:43758898:A:G
17_43759048_T_C	17	43759048	C	0.2121	-0.0477	0.0076	3.70E-10	0.2145	0.1134	0.01578	6.56E-13	rs17687838:43759048:T:C
17_43759426_C_T	17	43759426	T	0.2122	-0.0477	0.0076	3.55E-10	0.2147	0.1134	0.01578	6.64E-13	rs76333921:43759426:C:T
17_43759431_C_T	17	43759431	T	0.2122	-0.0477	0.0076	3.57E-10	0.2147	0.1131	0.01578	7.57E-13	rs76453925:43759431:C:T
17_43759719_A_G	17	43759719	G	0.2121	-0.0477	0.0076	3.78E-10	0.2145	0.1133	0.01578	6.87E-13	rs17687849:43759719:A:G
17_43760080_C_A	17	43760080	A	0.2119	-0.0478	0.0076	3.40E-10	0.2144	0.1124	0.01578	1.07E-12	rs56400821:43760080:C:A
17_43760192_A_G	17	43760192	G	0.2116	-0.0479	0.0076	3.18E-10	0.2144	0.1141	0.01579	5.00E-13	rs112169475:43760192:A:G
17_43760199_C_T	17	43760199	T	0.2116	-0.0477	0.0076	3.56E-10	0.2144	0.1139	0.01579	5.46E-13	rs113728380:43760199:C:T
17_43760374_A_AT	17	43760374	AT	0.2118	-0.047	0.0077	9.40E-10	0.2147	0.1142	0.01579	4.79E-13	17:43760374:A:AT
17_43760389_A_G	17	43760389	G	0.2116	-0.0479	0.0076	3.19E-10	0.2144	0.1141	0.01579	5.00E-13	rs17761100:43760389:A:G
17_43760516_A_T	17	43760516	T	0.2121	-0.0477	0.0076	3.60E-10	0.2145	0.1135	0.01578	6.28E-13	rs17761124:43760516:A:T
17_43760577_G_A	17	43760577	A	0.2116	-0.0479	0.0076	3.19E-10	0.2144	0.1139	0.01579	5.29E-13	rs62055704:43760577:G:A
17_43760599_A_C	17	43760599	C	0.2121	-0.0477	0.0076	3.65E-10	0.2145	0.1133	0.01578	7.12E-13	rs62055705:43760599:A:C
17_43760685_T_C	17	43760685	C	0.2121	-0.0477	0.0076	3.64E-10	0.2145	0.1134	0.01578	6.86E-13	rs62055706:43760685:T:C
17_43760759_AT_A	17	43760759	A	0.2122	-0.0468	0.0077	1.12E-09	0.2145	0.1135	0.01578	6.45E-13	17:43760759:AT:A
17_43761381_A_G	17	43761381	G	0.2116	-0.0478	0.0076	3.24E-10	0.2144	0.1139	0.01579	5.40E-13	rs75115093:43761381:A:G
17_43761482_T_C	17	43761482	C	0.2116	-0.0478	0.0076	3.25E-10	0.2144	0.1139	0.01579	5.40E-13	rs62055707:43761482:T:C
17_43761519_T_G	17	43761519	G	0.234	-0.0402	0.0073	4.54E-08	0.2383	0.09389	0.01527	7.84E-10	rs16941035:43761519:T:G
17_43761565_T_C	17	43761565	C	0.234	-0.0402	0.0073	4.54E-08	0.2383	0.09389	0.01527	7.84E-10	rs16941038:43761565:T:C
17_43761856_C_T	17	43761856	T	0.2121	-0.0477	0.0076	3.55E-10	0.2145	0.1134	0.01578	6.83E-13	rs2049515:43761856:C:T
17_43761939_G_C	17	43761939	C	0.2121	-0.0477	0.0076	3.70E-10	0.2145	0.1132	0.01578	7.29E-13	rs2158474:43761939:G:C
17_43761974_C_A	17	43761974	A	0.2116	-0.0478	0.0076	3.28E-10	0.2144	0.1139	0.01579	5.40E-13	rs62055708:43761974:C:A
17_43761985_A_T	17	43761985	T	0.2121	-0.0478	0.0076	3.45E-10	0.2145	0.1136	0.01578	6.02E-13	rs76927677:43761985:A:T
17_43762255_T_C	17	43762255	C	0.2116	-0.0478	0.0076	3.24E-10	0.2144	0.114	0.01579	5.22E-13	rs17761207:43762255:T:C
17_43762429_C_T	17	43762429	T	0.2117	-0.0479	0.0076	3.12E-10	0.2145	0.1143	0.01579	4.46E-13	rs62055709:43762429:C:T
17_43762537_T_A	17	43762537	A	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.114	0.01579	5.04E-13	rs62055710:43762537:T:A
17_43762554_A_G	17	43762554	G	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.1141	0.01579	5.03E-13	rs62055711:43762554:A:G
17_43762594_A_T	17	43762594	T	0.2121	-0.0478	0.0076	3.39E-10	0.2145	0.1136	0.01578	6.23E-13	rs17688002:43762594:A:T
17_43762846_A_G	17	43762846	G	0.2117	-0.0479	0.0076	3.13E-10	0.2144	0.1142	0.01579	4.66E-13	rs2040846:43762846:A:G
17_43763007_T_C	17	43763007	C	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.1141	0.01579	5.00E-13	rs4486953:43763007:T:C
17_43763202_G_A	17	43763202	A	0.2121	-0.0476	0.0076	3.80E-10	0.2145	0.1136	0.01578	6.03E-13	rs17688032:43763202:G:A
17_43763241_C_T	17	43763241	T	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.1141	0.01579	5.00E-13	rs17688056:43763241:C:T
17_43763935_A_G	17	43763935	G	0.2121	-0.0476	0.0076	3.83E-10	0.2145	0.1137	0.01578	5.82E-13	rs17688068:43763935:A:G
17_43764027_GGCCGAGGT	17	43764027	G	0.2117	-0.0469	0.0077	1.01E-09	0.2144	0.1141	0.01579	5.00E-13	669:43764027:GGCCGAGGTGAGAGGCT:G
17_43764378_G_A	17	43764378	A	0.2121	-0.0476	0.0076	3.83E-10	0.2145	0.1138	0.01578	5.61E-13	rs77220413:43764378:G:A
17_43764565_A_G	17	43764565	G	0.2121	-0.0476	0.0076	3.82E-10	0.2146	0.1132	0.01578	7.32E-13	rs62055712:43764565:A:G
17_43764685_C_T	17	43764685	T	0.2121	-0.0478	0.0076	3.37E-10	0.2146	0.1132	0.01578	7.32E-13	rs62055713:43764685:C:T
17_43764796_G_T	17	43764796	T	0.2124	-0.0479	0.0076	3.11E-10	0.2149	0.1133	0.01578	6.98E-13	rs62055714:43764796:G:T
17_43764847_G_A	17	43764847	A	0.2121	-0.0477	0.0076	3.77E-10	0.2145	0.1137	0.01578	5.97E-13	rs62055715:43764847:G:A
17_43764987_G_A	17	43764987	A	0.2122	-0.0479	0.0076	2.93E-10	0.2146	0.1143	0.01578	4.46E-13	rs17688090:43764987:G:A
17_43765080_A_G	17	43765080	G	0.2121	-0.0477	0.0076	3.60E-10	0.2145	0.1136	0.01578	6.15E-13	rs17688126:43765080:A:G
17_43765381_G_C	17	43765381	C	0.2116	-0.0479	0.0076	3.21E-10	0.2144	0.1141	0.01579	4.96E-13	rs77310586:43765381:G:C
17_43765450_G_A	17	43765450	A	0.2122	-0.0476	0.0076	3.91E-10	0.2146	0.1149	0.01578	3.26E-13	rs17761387:43765450:G:A
17_43765778_C_T	17	43765778	T	0.2121	-0.0476	0.0076	3.91E-10	0.2146	0.1138	0.01578	5.65E-13	rs62055716:43765778:C:T
17_43765881_T_C	17	43765881	C	0.234	-0.0403	0.0073	4.27E-08	0.2384	0.09365	0.01527	8.60E-10	rs6503443:43765881:T:C
17_43766352_G_C	17	43766352	C	0.2121	-0.0475	0.0076	4.13E-10	0.2146	0.114	0.01578	5.12E-13	rs17688205:43766352:G:C
17_43766415_A_G	17	43766415	G	0.2094	-0.049	0.0077	1.66E-10	0.2124	0.114	0.0159	7.52E-13	rs62055717:43766415:A:G
17_43766418_C_T	17	43766418	T	0.2099	-0.0487	0.0077	2.13E-10	0.2127	0.1141	0.0159	7.25E-13	rs62055718:43766418:C:T
17_43766494_A_AC	17	43766494	AC	0.212	-0.0466	0.0077	1.30E-09	0.2147	0.1145	0.01579	4.03E-13	rs180852499:43766494:A:AC
17_43766497_T_C	17	43766497	C	0.2121	-0.0477	0.0076	3.65E-10	0.2146	0.1137	0.01578	5.90E-13	17:43766497:T:C
17_43766754_C_T	17	43766754	T	0.212	-0.0479	0.0076	3.24E-10	0.2142	0.1137	0.01578	5.97E-13	rs17688249:43766754:C:T

17_43767188_G_C	17	43767188	C	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.1142	0.01579	4.65E-13	rs2040845:43767188:G:C
17_43767219_A_C	17	43767219	C	0.2121	-0.0477	0.0076	3.58E-10	0.2146	0.1138	0.01578	5.44E-13	rs2040844:43767219:A:C
17_43767538_A_G	17	43767538	G	0.2119	-0.0478	0.0076	3.48E-10	0.2142	0.1139	0.01578	5.35E-13	rs62055751:43767538:A:G
17_43767628_G_A	17	43767628	A	0.2121	-0.0476	0.0076	3.90E-10	0.2146	0.1134	0.01578	6.58E-13	rs62055752:43767628:G:A
17_43767631_G_A	17	43767631	A	0.2116	-0.0478	0.0076	3.26E-10	0.2144	0.1142	0.01579	4.66E-13	rs62055753:43767631:G:A
17_43767773_T_C	17	43767773	C	0.234	-0.04	0.0073	5.36E-08	0.2384	0.09392	0.01527	7.62E-10	rs7215239:43767773:T:C
17_43767815_C_T	17	43767815	T	0.2116	-0.0478	0.0076	3.27E-10	0.2144	0.1142	0.01579	4.68E-13	rs17688296:43767815:C:T
17_43768230_C_G	17	43768230	G	0.2116	-0.0478	0.0076	3.32E-10	0.2144	0.1141	0.01579	4.83E-13	rs62055754:43768230:C:G
17_43768346_G_A	17	43768346	A	0.2116	-0.0478	0.0076	3.33E-10	0.2144	0.1141	0.01579	4.87E-13	rs78471340:43768346:G:A
17_43768347_C_T	17	43768347	T	0.2116	-0.0478	0.0076	3.34E-10	0.2144	0.1141	0.01579	4.87E-13	rs78052495:43768347:C:T
17_43768467_C_T	17	43768467	T	0.2123	-0.0477	0.0076	3.53E-10	0.2146	0.1129	0.01578	8.23E-13	rs56100013:43768467:C:T
17_43768496_C_T	17	43768496	T	0.2117	-0.0478	0.0076	3.49E-10	0.2146	0.1143	0.01579	4.57E-13	rs55980621:43768496:C:T
17_43768501_C_T	17	43768501	T	0.2116	-0.0478	0.0076	3.35E-10	0.2144	0.1141	0.01579	4.91E-13	rs55669046:43768501:C:T
17_43768621_AG_A	17	43768621	A	0.2117	-0.0468	0.0077	1.05E-09	0.2144	0.1141	0.01579	4.91E-13	17:43768621:AG:A
17_43768633_G_A	17	43768633	A	0.2116	-0.0478	0.0076	3.35E-10	0.2144	0.1141	0.01579	4.91E-13	rs56323832:43768633:G:A
17_43768703_C_T	17	43768703	T	0.2116	-0.0478	0.0076	3.42E-10	0.2144	0.1141	0.01579	4.92E-13	rs55972157:43768703:C:T
17_43768727_G_A	17	43768727	A	0.2121	-0.0476	0.0076	3.98E-10	0.2146	0.1131	0.01578	7.64E-13	rs56110538:43768727:G:A
17_43769088_T_C	17	43769088	C	0.2121	-0.0477	0.0076	3.59E-10	0.2146	0.1134	0.01578	6.61E-13	rs17761581:43769088:T:C
17_43769277_C_G	17	43769277	G	0.212	-0.0478	0.0076	3.27E-10	0.2146	0.1134	0.01578	6.74E-13	rs55840731:43769277:C:G
17_43769321_A_C	17	43769321	C	0.2116	-0.0478	0.0076	3.34E-10	0.2144	0.1141	0.01579	4.92E-13	rs56283089:43769321:A:C
17_43769516_C_A	17	43769516	A	0.2121	-0.0478	0.0076	3.40E-10	0.2145	0.1135	0.01579	6.46E-13	rs56312737:43769516:C:A
17_43769819_AAAATT_A	17	43769819	A	0.2122	-0.0467	0.0077	1.16E-09	0.2146	0.1134	0.01578	6.60E-13	17:43769819:AAAATT:A
17_43770416_T_C	17	43770416	C	0.2116	-0.0478	0.0076	3.30E-10	0.2144	0.1141	0.01579	4.94E-13	rs74765707:43770416:T:C
17_43770443_T_C	17	43770443	C	0.2116	-0.0478	0.0076	3.30E-10	0.2144	0.1141	0.01579	4.94E-13	rs62056861:43770443:T:C
17_43770525_C_T	17	43770525	T	0.2128	-0.0473	0.0076	4.76E-10	0.215	0.1149	0.01577	3.14E-13	rs62056862:43770525:C:T
17_43770595_A_G	17	43770595	G	0.2116	-0.0478	0.0076	3.30E-10	0.2144	0.1141	0.01579	4.94E-13	rs62056863:43770595:A:G
17_43770712_C_T	17	43770712	T	0.2336	-0.04	0.0074	5.16E-08	0.2378	0.09346	0.01528	9.62E-10	rs7207373:43770712:C:T
17_43770995_G_A	17	43770995	A	0.2116	-0.0478	0.0076	3.37E-10	0.2144	0.114	0.01579	5.04E-13	rs62056864:43770995:G:A
17_43771193_T_C	17	43771193	C	0.2116	-0.0478	0.0076	3.29E-10	0.2144	0.1141	0.01579	4.95E-13	rs62056865:43771193:T:C
17_43771493_G_A	17	43771493	A	0.2121	-0.0477	0.0076	3.77E-10	0.2146	0.1134	0.01578	6.79E-13	rs62056866:43771493:G:A
17_43771627_A_G	17	43771627	G	0.2121	-0.0476	0.0076	3.93E-10	0.2146	0.1131	0.01578	7.83E-13	rs62056867:43771627:A:G
17_43772018_G_T	17	43772018	T	0.2121	-0.0477	0.0076	3.50E-10	0.2145	0.1133	0.01578	6.90E-13	rs56200760:43772018:G:T
17_43772109_C_A	17	43772109	A	0.2116	-0.0479	0.0076	3.20E-10	0.2144	0.1141	0.01579	4.96E-13	rs17688391:43772109:C:A
17_43772251_C_T	17	43772251	T	0.2116	-0.0479	0.0076	3.19E-10	0.2144	0.1141	0.01579	4.96E-13	rs17688410:43772251:C:T
17_43772407_C_T	17	43772407	T	0.2121	-0.0477	0.0076	3.52E-10	0.2146	0.1132	0.01578	7.29E-13	rs55927630:43772407:C:T
17_43772540_G_A	17	43772540	A	0.212	-0.0475	0.0076	4.31E-10	0.2145	0.1136	0.01578	6.25E-13	rs17688434:43772540:G:A
17_43773058_GA_G	17	43773058	G	0.2237	-0.0419	0.0076	4.30E-08	0.2284	0.1104	0.01572	2.21E-12	17:43773058:GA:G
17_43773085_G_A	17	43773085	A	0.2116	-0.0479	0.0076	3.18E-10	0.2144	0.1141	0.01579	4.97E-13	rs17688452:43773085:G:A
17_43773124_A_C	17	43773124	C	0.2121	-0.0478	0.0076	3.38E-10	0.2145	0.1136	0.01578	6.14E-13	rs10491144:43773124:A:C
17_43773248_A_T	17	43773248	T	0.2121	-0.0477	0.0076	3.51E-10	0.2145	0.1135	0.01578	6.36E-13	rs10491143:43773248:A:T
17_43773447_T_C	17	43773447	C	0.2121	-0.0478	0.0076	3.36E-10	0.2146	0.1133	0.01578	7.20E-13	rs62056869:43773447:T:C
17_43773514_C_CAAA	17	43773514	CAAA	0.2114	-0.047	0.0077	9.81E-10	0.2141	0.1148	0.01581	3.84E-13	17:43773514:C:CAAA
17_43773525_T_TAAAA	17	43773525	TAAAA	0.2114	-0.047	0.0077	9.81E-10	0.2141	0.1148	0.01581	3.84E-13	s200714673:43773525:T:TAAAA
17_43773607_T_G	17	43773607	G	0.2124	-0.0474	0.0076	4.64E-10	0.2151	0.1131	0.01578	7.73E-13	rs17688511:43773607:T:G
17_43773784_C_A	17	43773784	A	0.2121	-0.0477	0.0076	3.62E-10	0.2146	0.1133	0.01578	7.19E-13	rs62056870:43773784:C:A
17_43773877_A_T	17	43773877	T	0.2121	-0.0477	0.0076	3.70E-10	0.2145	0.1136	0.01578	6.24E-13	rs17688534:43773877:A:T
17_43773943_A_G	17	43773943	G	0.2116	-0.0479	0.0076	3.14E-10	0.2144	0.1141	0.01579	4.98E-13	rs17688558:43773943:A:G
17_43774255_TAGCC_T	17	43774255	T	0.2117	-0.0469	0.0077	9.79E-10	0.2144	0.1141	0.01579	4.99E-13	17:43774255:TAGCC:T
17_43774408_A_AAGAAAG	17	43774408	AAGAAAGAAAGA	0.2117	-0.0469	0.0077	9.74E-10	0.2144	0.1141	0.01579	4.99E-13	25478:43774408:A:AAGAAAGAAAGAG
17_43774497_A_T	17	43774497	T	0.2116	-0.0479	0.0076	3.09E-10	0.2144	0.1141	0.01579	4.99E-13	rs56162163:43774497:A:T
17_43774845_C_T	17	43774845	T	0.2121	-0.0478	0.0076	3.45E-10	0.2145	0.1135	0.01578	6.44E-13	rs56391096:43774845:C:T
17_43774959_T_C	17	43774959	C	0.2121	-0.0478	0.0076	3.29E-10	0.2146	0.1133	0.01578	7.10E-13	rs17761838:43774959:T:C
17_43775015_T_C	17	43775015	C	0.2121	-0.0478	0.0076	3.40E-10	0.2146	0.1134	0.01578	6.86E-13	rs62056872:43775015:T:C
17_43775145_G_A	17	43775145	A	0.2121	-0.0478	0.0076	3.32E-10	0.2146	0.1133	0.01578	6.89E-13	rs12150141:43775145:G:A
17_43775212_CCTT_C	17	43775212	C	0.2117	-0.047	0.0077	9.60E-10	0.2144	0.1141	0.01579	5.00E-13	17:43775212:CCTT:C

17_43775402_T_C	17	43775402	C	0.2121	-0.0477	0.0076	3.50E-10	0.2146	0.1131	0.01578	7.75E-13	rs12150608:43775402:T:C
17_43775479_T_C	17	43775479	C	0.2121	-0.0477	0.0076	3.69E-10	0.2146	0.1131	0.01578	7.68E-13	rs12150610:43775479:T:C
17_43775546_A_G	17	43775546	G	0.2121	-0.0477	0.0076	3.63E-10	0.2146	0.1132	0.01578	7.25E-13	rs12150547:43775546:A:G
17_43775929_C_G	17	43775929	G	0.2116	-0.0479	0.0076	3.03E-10	0.2144	0.1141	0.01579	5.01E-13	rs17688682:43775929:C:G
17_43776061_C_T	17	43776061	T	0.2121	-0.0478	0.0076	3.46E-10	0.2146	0.1133	0.01578	6.95E-13	rs12150454:43776061:C:T
17_43776242_A_G	17	43776242	G	0.2121	-0.0477	0.0076	3.50E-10	0.2146	0.1133	0.01578	6.88E-13	rs12150091:43776242:A:G
17_43776371_C_T	17	43776371	T	0.2116	-0.0479	0.0076	3.03E-10	0.2144	0.1141	0.01579	5.02E-13	rs12150464:43776371:C:T
17_43776391_G_C	17	43776391	C	0.2116	-0.0479	0.0076	3.03E-10	0.2144	0.1141	0.01579	5.02E-13	rs12150435:43776391:G:C
17_43776425_C_T	17	43776425	T	0.2068	-0.0486	0.0077	3.36E-10	0.2075	0.1152	0.01595	5.06E-13	rs112972619:43776425:C:T
17_43776741_T_C	17	43776741	C	0.2116	-0.0479	0.0076	3.02E-10	0.2144	0.1141	0.01579	5.02E-13	rs76761706:43776741:T:C
17_43776742_T_C	17	43776742	C	0.2116	-0.0479	0.0076	3.02E-10	0.2144	0.1141	0.01579	5.02E-13	rs80143279:43776742:T:C
17_43776787_C_T	17	43776787	T	0.2121	-0.0478	0.0076	3.34E-10	0.2146	0.1134	0.01578	6.60E-13	rs17761985:43776787:C:T
17_43776945_T_C	17	43776945	C	0.2121	-0.0477	0.0076	3.62E-10	0.2146	0.1128	0.01578	8.79E-13	rs62056873:43776945:T:C
17_43777542_A_G	17	43777542	G	0.2121	-0.0477	0.0076	3.62E-10	0.2145	0.1133	0.01578	7.00E-13	rs17688767:43777542:A:G
17_43777578_C_T	17	43777578	T	0.2116	-0.0479	0.0076	3.03E-10	0.2144	0.114	0.01579	5.12E-13	rs62056874:43777578:C:T
17_43777710_T_C	17	43777710	C	0.2121	-0.0478	0.0076	3.37E-10	0.2145	0.1134	0.01578	6.70E-13	rs17688773:43777710:T:C
17_43777745_C_A	17	43777745	A	0.2122	-0.0478	0.0076	3.35E-10	0.2146	0.1134	0.01578	6.59E-13	rs17762073:43777745:C:A
17_43777835_TATCCTGCTT	17	43777835	T	0.2117	-0.047	0.0077	9.65E-10	0.2144	0.114	0.01579	5.20E-13	17:43777835:TATCCTGCTTCCC:T
17_43777881_T_G	17	43777881	G	0.2116	-0.0479	0.0076	3.06E-10	0.2144	0.114	0.01579	5.21E-13	rs1724423:43777881:T:G
17_43777957_AATC_A	17	43777957	A	0.214	-0.047	0.0077	8.76E-10	0.2169	0.1121	0.01577	1.18E-12	rs140500355:43777957:AATC:A
17_43778003_T_A	17	43778003	A	0.2121	-0.0476	0.0076	3.93E-10	0.2145	0.1133	0.01578	6.92E-13	rs62056875:43778003:T:A
17_43778315_CA_C	17	43778315	C	0.2122	-0.0469	0.0077	9.62E-10	0.2145	0.1133	0.01578	7.25E-13	17:43778315:CA:C
17_43778406_A_G	17	43778406	G	0.2122	-0.0478	0.0076	3.33E-10	0.2146	0.1128	0.01578	8.69E-13	rs17688875:43778406:A:G
17_43778602_C_T	17	43778602	T	0.212	-0.0476	0.0076	3.85E-10	0.2145	0.1139	0.01579	5.27E-13	rs17762165:43778602:C:T
17_43778680_T_A	17	43778680	A	0.1973	-0.0497	0.0079	3.68E-10	0.1986	0.1095	0.01631	1.91E-11	rs17688916:43778680:T:A
17_43778752_C_T	17	43778752	T	0.212	-0.048	0.0076	2.77E-10	0.2159	0.1134	0.01579	6.95E-13	rs62056876:43778752:C:T
17_43778828_T_G	17	43778828	G	0.2131	-0.0474	0.0076	4.35E-10	0.2164	0.1114	0.01577	1.60E-12	rs62056877:43778828:T:G
17_43779031_C_CCTCCCCA	17	43779031	CCTCCCCA	0.2094	-0.0475	0.0077	8.60E-10	0.2111	0.1143	0.01589	6.36E-13	17:43779031:C:CCTCCCCA
17_43779351_G_A	17	43779351	A	0.212	-0.0479	0.0076	3.01E-10	0.2145	0.1129	0.01578	8.45E-13	rs17688922:43779351:G:A
17_43779419_T_A	17	43779419	A	0.2121	-0.048	0.0076	2.82E-10	0.2145	0.114	0.01578	5.14E-13	rs17688944:43779419:T:A
17_43779624_C_T	17	43779624	T	0.2098	-0.049	0.0077	1.54E-10	0.2103	0.1147	0.01586	4.79E-13	rs1526128:43779624:C:T
17_43779657_T_C	17	43779657	C	0.2116	-0.0479	0.0076	3.07E-10	0.2144	0.1138	0.01579	5.61E-13	rs1526129:43779657:T:C
17_43780561_C_T	17	43780561	T	0.212	-0.0479	0.0076	2.98E-10	0.2145	0.1134	0.01578	6.65E-13	rs62056878:43780561:C:T
17_43780948_T_C	17	43780948	C	0.2121	-0.0486	0.0076	1.72E-10	0.2145	0.1139	0.01579	5.53E-13	rs17762308:43780948:T:C
17_43781105_A_G	17	43781105	G	0.212	-0.0484	0.0076	2.06E-10	0.2145	0.113	0.01578	7.98E-13	rs968028:43781105:A:G
17_43781250_C_T	17	43781250	T	0.2119	-0.0481	0.0076	2.65E-10	0.2145	0.1136	0.01579	6.36E-13	rs968027:43781250:C:T
17_43781426_T_C	17	43781426	C	0.2121	-0.0482	0.0076	2.36E-10	0.2145	0.1136	0.01578	6.09E-13	rs62056879:43781426:T:C
17_43781505_C_T	17	43781505	T	0.2124	-0.0485	0.0076	1.80E-10	0.2146	0.1135	0.01578	6.28E-13	rs79892630:43781505:C:T
17_43781720_T_TAAAAAA	17	43781720	TAAAAAAAAGAG	0.2114	-0.0472	0.0077	8.18E-10	0.2134	0.1141	0.0158	5.21E-13	17:43781720:T:TAAAAAAAAGAG
17_43781778_A_G	17	43781778	G	0.212	-0.0481	0.0076	2.66E-10	0.2145	0.1135	0.01578	6.36E-13	rs17762361:43781778:A:G
17_43782304_T_C	17	43782304	C	0.212	-0.0481	0.0076	2.70E-10	0.2145	0.113	0.01578	8.20E-13	rs62056880:43782304:T:C
17_43782455_G_T	17	43782455	T	0.212	-0.048	0.0076	2.78E-10	0.2145	0.1135	0.01578	6.51E-13	rs62056881:43782455:G:T
17_43782492_A_G	17	43782492	G	0.212	-0.0481	0.0076	2.69E-10	0.2145	0.1136	0.01578	6.16E-13	rs17689104:43782492:A:G
17_43782558_T_C	17	43782558	C	0.2115	-0.0481	0.0076	2.71E-10	0.2143	0.1137	0.01579	5.85E-13	rs17689116:43782558:T:C
17_43782693_A_G	17	43782693	G	0.2125	-0.0483	0.0076	2.19E-10	0.2155	0.1124	0.01577	1.03E-12	rs62056905:43782693:A:G
17_43782708_T_C	17	43782708	C	0.2121	-0.048	0.0076	2.78E-10	0.2145	0.1138	0.01578	5.60E-13	rs62056906:43782708:T:C
17_43783573_C_T	17	43783573	T	0.2106	-0.0474	0.0076	5.35E-10	0.2125	0.1133	0.01583	8.22E-13	rs17689182:43783573:C:T
17_43783590_G_A	17	43783590	A	0.2102	-0.048	0.0076	3.48E-10	0.2124	0.1116	0.01584	1.78E-12	rs62056908:43783590:G:A
17_43783803_A_G	17	43783803	G	0.2107	-0.048	0.0076	3.50E-10	0.2127	0.1153	0.01581	3.03E-13	rs62056909:43783803:A:G
17_43784222_T_C	17	43784222	C	0.2122	-0.0482	0.0076	2.27E-10	0.2144	0.1133	0.01577	6.85E-13	rs62056910:43784222:T:C
17_43784228_T_C	***17***	***43784228***	***T***	***0.3484***	***0.0168***	***0.0065***	***0.009801***	***0.3634***	***-0.08791***	***0.01399***	***3.30E-10***	***rs9912362:43784228:T:C***
17_43784624_T_C	17	43784624	C	0.212	-0.0481	0.0076	2.52E-10	0.2143	0.1137	0.01578	5.80E-13	rs62056911:43784624:T:C
17_43784935_C_G	17	43784935	G	0.2119	-0.0482	0.0076	2.43E-10	0.2139	0.1136	0.01579	6.18E-13	rs78568882:43784935:C:G
17_43784948_G_T	17	43784948	T	0.2114	-0.0481	0.0076	2.70E-10	0.2138	0.1141	0.01579	5.00E-13	rs62056912:43784948:G:T
17_43784994_C_T	17	43784994	T	0.2115	-0.0479	0.0076	3.18E-10	0.2142	0.1145	0.01581	4.43E-13	rs62056913:43784994:C:T

17_43785096_G_A	17	43785096	A	0.2114	-0.048	0.0076	3.05E-10	0.2135	0.1138	0.01579	5.86E-13	rs78454137:43785096:G:A
17_43785098_C_T	17	43785098	T	0.2109	-0.0479	0.0076	3.35E-10	0.2133	0.1141	0.0158	5.19E-13	rs112123127:43785098:C:T
17_43785104_C_CTTA	17	43785104	CTTA	0.2117	-0.0471	0.0077	8.55E-10	0.2141	0.1137	0.01579	5.89E-13	17:43785104:C:CTTA
17_43785349_T_C	17	43785349	C	0.2118	-0.048	0.0076	2.89E-10	0.2145	0.112	0.01578	1.26E-12	rs61667602:43785349:T:C
17_43785627_A_T	17	43785627	T	0.212	-0.0482	0.0076	2.34E-10	0.2143	0.1132	0.01578	7.44E-13	rs62056915:43785627:A:T
17_43785808_T_C	17	43785808	C	0.212	-0.0483	0.0076	2.12E-10	0.2143	0.1127	0.01578	9.19E-13	rs17689218:43785808:T:C
17_43785938_C_T	17	43785938	T	0.212	-0.0483	0.0076	2.25E-10	0.2143	0.1132	0.01578	7.23E-13	rs62056916:43785938:C:T
17_43786013_G_T	17	43786013	T	0.212	-0.0485	0.0076	1.87E-10	0.2144	0.1138	0.01578	5.57E-13	rs62056917:43786013:G:T
17_43786676_T_G	17	43786676	G	0.2115	-0.0481	0.0076	2.66E-10	0.2141	0.1137	0.01579	5.85E-13	rs62056918:43786676:T:G
17_43786698_C_T	17	43786698	T	0.212	-0.0482	0.0076	2.37E-10	0.2143	0.113	0.01578	8.10E-13	rs62056919:43786698:C:T
17_43787130_T_C	17	43787130	C	0.212	-0.0482	0.0076	2.35E-10	0.2143	0.1133	0.01578	7.16E-13	rs17762535:43787130:T:C
17_43787226_G_A	17	43787226	A	0.212	-0.0483	0.0076	2.16E-10	0.2143	0.113	0.01578	8.05E-13	rs62056920:43787226:G:A
17_43787306_T_C	17	43787306	C	0.2115	-0.0481	0.0076	2.66E-10	0.2141	0.1137	0.01579	5.82E-13	rs62056921:43787306:T:C
17_43787563_C_G	17	43787563	G	0.2122	-0.0483	0.0076	2.29E-10	0.215	0.1128	0.01578	8.95E-13	rs62056922:43787563:C:G
17_43788371_C_T	17	43788371	T	0.2123	-0.0484	0.0076	2.02E-10	0.2145	0.1134	0.01578	6.81E-13	rs56290582:43788371:C:T
17_43788419_C_A	17	43788419	A	0.2115	-0.0481	0.0076	2.67E-10	0.2141	0.1137	0.01579	5.81E-13	rs56397077:43788419:C:A
17_43788649_T_C	17	43788649	C	0.212	-0.0483	0.0076	2.22E-10	0.2143	0.1129	0.01578	8.29E-13	rs62056925:43788649:T:C
17_43788666_C_G	17	43788666	G	0.2115	-0.0481	0.0076	2.67E-10	0.2141	0.1137	0.01579	5.80E-13	rs62056926:43788666:C:G
17_43788767_G_A	17	43788767	A	0.2115	-0.0481	0.0076	2.67E-10	0.2141	0.1137	0.01579	5.80E-13	rs62056927:43788767:G:A
17_43788782_C_T	17	43788782	T	0.2115	-0.0481	0.0076	2.67E-10	0.2141	0.1137	0.01579	5.80E-13	rs62056928:43788782:C:T
17_43789144_G_A	17	43789144	A	0.212	-0.0483	0.0076	2.17E-10	0.2143	0.1132	0.01578	7.27E-13	rs62056929:43789144:G:A
17_43789413_CT_C	17	43789413	C	0.2123	-0.0471	0.0077	8.15E-10	0.2145	0.1118	0.01578	1.40E-12	17:43789413:CT:C
17_43789640_A_C	17	43789640	C	0.2133	-0.0474	0.0076	4.76E-10	0.2159	0.1118	0.01579	1.40E-12	rs62056930:43789640:A:C
17_43789698_G_A	17	43789698	A	0.2103	-0.0483	0.0076	2.56E-10	0.2132	0.1135	0.01583	7.44E-13	rs62056931:43789698:G:A
17_43789971_G_C	17	43789971	C	0.2114	-0.0483	0.0076	2.30E-10	0.2136	0.1142	0.0158	4.98E-13	rs62056932:43789971:G:C
17_43789978_G_A	17	43789978	A	0.2111	-0.0484	0.0076	2.23E-10	0.2135	0.1139	0.0158	5.64E-13	rs62056933:43789978:G:A
17_43790005_A_G	17	43790005	G	0.2115	-0.0486	0.0076	1.86E-10	0.2136	0.1134	0.0158	6.89E-13	rs62056934:43790005:A:G
17_43790401_A_G	17	43790401	G	0.2121	-0.0482	0.0076	2.30E-10	0.2143	0.113	0.01577	7.85E-13	rs79322350:43790401:A:G
17_43790446_A_G	17	43790446	G	0.212	-0.0483	0.0076	2.27E-10	0.2143	0.1136	0.01578	5.94E-13	rs62056935:43790446:A:G
17_43790598_G_GAA	17	43790598	GAA	0.2126	-0.0485	0.0077	2.92E-10	0.2151	0.111	0.0158	2.15E-12	17:43790598:G:GAA
17_43790649_C_A	17	43790649	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs75076131:43790649:C:A
17_43790770_A_G	17	43790770	G	0.2117	-0.048	0.0076	2.97E-10	0.214	0.114	0.01579	5.15E-13	rs77727624:43790770:A:G
17_43790911_A_T	17	43790911	T	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs62056936:43790911:A:T
17_43791181_A_C	17	43791181	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs62056937:43791181:A:C
17_43791332_T_C	17	43791332	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs62056939:43791332:T:C
17_43791344_T_A	17	43791344	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs62056940:43791344:T:A
17_43791405_C_A	17	43791405	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs78803763:43791405:C:A
17_43791429_G_A	17	43791429	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs77387379:43791429:G:A
17_43791468_T_C	17	43791468	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs75990322:43791468:T:C
17_43791610_T_C	17	43791610	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs113661667:43791610:T:C
17_43791652_G_A	17	43791652	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.16E-13	rs74579538:43791652:G:A
17_43792090_G_C	17	43792090	C	0.2114	-0.0486	0.0076	1.94E-10	0.2134	0.1136	0.01581	6.59E-13	17:43792090:G:C
17_43792091_C_T	17	43792091	T	0.2114	-0.0486	0.0076	1.94E-10	0.2134	0.1136	0.01581	6.59E-13	17:43792091:C:T
17_43792099_T_C	17	43792099	C	0.2114	-0.0486	0.0076	1.83E-10	0.2134	0.1136	0.0158	6.74E-13	rs56406407:43792099:T:C
17_43792252_C_A	17	43792252	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.15E-13	rs55973918:43792252:C:A
17_43792326_C_T	17	43792326	T	0.212	-0.0483	0.0076	2.22E-10	0.2143	0.1131	0.01578	7.74E-13	rs56220242:43792326:C:T
17_43792358_A_G	17	43792358	G	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.15E-13	rs56160448:43792358:A:G
17_43792411_A_G	17	43792411	G	0.2115	-0.0481	0.0076	2.70E-10	0.2141	0.1137	0.01579	5.88E-13	rs56167560:43792411:A:G
17_43792418_T_C	17	43792418	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.15E-13	rs55849973:43792418:T:C
17_43792493_T_TAAAC	17	43792493	TAAAC	0.2121	-0.0472	0.0077	7.60E-10	0.2143	0.1133	0.01578	7.15E-13	17:43792493:T:TAAAC
17_43792586_A_C	17	43792586	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.15E-13	rs1880749:43792586:A:C
17_43792895_T_G	17	43792895	G	0.212	-0.0483	0.0076	2.29E-10	0.2143	0.1133	0.01578	7.07E-13	rs1568951:43792895:T:G
17_43792896_T_C	17	43792896	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.15E-13	rs1568950:43792896:T:C
17_43792975_G_A	17	43792975	A	0.2121	-0.0482	0.0076	2.42E-10	0.2143	0.1131	0.01578	7.60E-13	rs1568949:43792975:G:A
17_43793200_A_T	17	43793200	T	0.212	-0.0482	0.0076	2.31E-10	0.2143	0.1131	0.01578	7.79E-13	rs1105571:43793200:A:T

17_43793342_A_G	17	43793342	G	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs1105570:43793342:A:G
17_43793388_C_T	17	43793388	T	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs1105569:43793388:C:T
17_43793651_G_A	17	43793651	A	0.2121	-0.0484	0.0076	1.95E-10	0.2145	0.1127	0.01578	9.33E-13	rs7502718:43793651:G:A
17_43793665_A_G	17	43793665	G	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs7502937:43793665:A:G
17_43793828_G_A	17	43793828	A	0.2135	-0.0487	0.0076	1.52E-10	0.2171	0.1119	0.01578	1.32E-12	rs4479288:43793828:G:A
17_43793951_G_A	17	43793951	A	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs4479289:43793951:G:A
17_43794182_G_A	17	43794182	A	0.2115	-0.048	0.0076	2.75E-10	0.2141	0.1137	0.01579	5.97E-13	rs4609898:43794182:G:A
17_43794209_G_C	17	43794209	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs4605208:43794209:G:C
17_43794286_C_T	17	43794286	T	0.2121	-0.0482	0.0076	2.28E-10	0.2143	0.1126	0.01578	9.47E-13	rs75310534:43794286:C:T
17_43794828_T_C	17	43794828	C	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs111511018:43794828:T:C
17_43794899_C_T	17	43794899	T	0.212	-0.0482	0.0076	2.30E-10	0.2143	0.1133	0.01578	7.14E-13	rs113173628:43794899:C:T
17_43795238_G_A	17	43795238	A	0.212	-0.0485	0.0076	1.85E-10	0.2143	0.1135	0.01578	6.51E-13	rs76007856:43795238:G:A
17_43795573_C_T	17	43795573	T	0.212	-0.0482	0.0076	2.31E-10	0.2143	0.1133	0.01578	7.13E-13	rs111415173:43795573:C:T
17_43795634_C_T	17	43795634	T	0.2118	-0.0484	0.0076	2.15E-10	0.214	0.1136	0.01579	6.24E-13	rs113991678:43795634:C:T
17_43795676_CCTTCTT_C	17	43795676	C	0.2121	-0.0472	0.0077	7.66E-10	0.2143	0.1133	0.01578	7.13E-13	s147863707:43795676:CCTTCTT:C
17_43795715_C_CT	17	43795715	C	0.4313	-0.0237	0.007	0.0007317	0.4318	0.0928	0.01464	2.33E-10	rs66696505:43795715:C:CT
17_43795768_T_C	17	43795768	C	0.212	-0.0482	0.0076	2.33E-10	0.2143	0.1133	0.01578	7.13E-13	rs112995313:43795768:T:C
17_43795859_A_G	17	43795859	G	0.212	-0.0482	0.0076	2.33E-10	0.2143	0.1133	0.01578	7.13E-13	rs111985258:43795859:A:G
17_43796396_TG_T	17	43796396	T	0.2122	-0.0473	0.0077	7.35E-10	0.2143	0.1132	0.01578	7.49E-13	17:43796396:TG:T
17_43796541_T_A	17	43796541	A	0.2118	-0.048	0.0076	3.03E-10	0.2139	0.1127	0.01579	9.68E-13	rs1880750:43796541:T:A
17_43797087_A_T	17	43797087	T	0.2115	-0.048	0.0076	2.83E-10	0.214	0.1137	0.01579	5.97E-13	rs56167344:43797087:A:T
17_43797157_TA_T	17	43797157	T	0.2121	-0.0472	0.0077	7.81E-10	0.2143	0.1132	0.01578	7.48E-13	17:43797157:TA:T
17_43797246_C_T	17	43797246	T	0.212	-0.0483	0.0076	2.26E-10	0.2142	0.1131	0.01578	7.78E-13	rs56046792:43797246:C:T
17_43798015_A_C	17	43798015	C	0.212	-0.0481	0.0076	2.64E-10	0.2143	0.113	0.01578	8.14E-13	rs56323722:43798015:A:C
17_43798160_G_A	17	43798160	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.49E-13	rs55989971:43798160:G:A
17_43798348_T_TTTG	17	43798348	T	0.2147	-0.0465	0.0077	1.36E-09	0.2164	0.1128	0.01576	8.07E-13	rs3072094:43798348:T:TTTG
17_43798401_G_A	17	43798401	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.49E-13	rs62056946:43798401:G:A
17_43798546_A_G	17	43798546	G	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.49E-13	rs75403953:43798546:A:G
17_43798584_CA_C	17	43798584	C	0.2121	-0.0472	0.0077	7.82E-10	0.2142	0.1132	0.01578	7.49E-13	rs71917787:43798584:CA:C
17_43798775_G_C	17	43798775	C	0.2106	-0.0493	0.0077	1.13E-10	0.2131	0.1122	0.01586	1.54E-12	rs62054372:43798775:G:C
17_43798784_A_AGAG	17	43798784	AGAG	0.2121	-0.0472	0.0077	7.82E-10	0.2143	0.1133	0.01578	7.14E-13	17:43798784:A:AGAG
17_43798787_G_T	17	43798787	G	0.2554	-0.0395	0.0071	3.19E-08	0.2525	0.07198	0.01489	1.33E-06	17:43798787:G:T
17_43798790_TTTC_T	17	43798790	T	0.2107	-0.0484	0.0077	3.71E-10	0.2131	0.1122	0.01586	1.54E-12	rs201758601:43798790:TTTC:T
17_43798902_C_T	17	43798902	T	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.49E-13	rs55838058:43798902:C:T
17_43798903_A_G	17	43798903	G	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.49E-13	rs56062621:43798903:A:G
17_43799033_C_T	17	43799033	T	0.212	-0.0482	0.0076	2.29E-10	0.2142	0.1132	0.01578	7.48E-13	rs55962674:43799033:C:T
17_43799048_G_A	17	43799048	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.48E-13	rs55896111:43799048:G:A
17_43799052_A_G	17	43799052	G	0.212	-0.0482	0.0076	2.39E-10	0.2142	0.1129	0.01578	8.54E-13	rs55787734:43799052:A:G
17_43799509_A_C	17	43799509	C	0.212	-0.0483	0.0076	2.16E-10	0.2142	0.1133	0.01578	6.93E-13	rs55653963:43799509:A:C
17_43799667_C_A	17	43799667	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.48E-13	rs62054378:43799667:C:A
17_43799804_C_A	17	43799804	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.48E-13	rs77819001:43799804:C:A
17_43799810_G_C	17	43799810	C	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1133	0.01578	7.13E-13	rs76667867:43799810:G:C
17_43800351_A_C	17	43800351	C	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.48E-13	rs17563433:43800351:A:C
17_43800404_T_G	17	43800404	G	0.212	-0.0483	0.0076	2.22E-10	0.2142	0.1131	0.01578	7.86E-13	rs77370070:43800404:T:G
17_43800987_C_A	17	43800987	A	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1132	0.01578	7.48E-13	rs62054380:43800987:C:A
17_43801092_T_C	17	43801092	C	0.212	-0.0483	0.0076	2.25E-10	0.2142	0.1127	0.01578	9.24E-13	rs112570965:43801092:T:C
17_43801185_A_G	17	43801185	G	0.2121	-0.0482	0.0076	2.40E-10	0.2144	0.1124	0.01578	1.08E-12	rs62054381:43801185:A:G
17_43801593_G_A	17	43801593	A	0.212	-0.0483	0.0076	2.25E-10	0.2142	0.1132	0.01578	7.41E-13	rs17649019:43801593:G:A
17_43801695_C_T	17	43801695	T	0.212	-0.0482	0.0076	2.30E-10	0.2142	0.1133	0.01578	7.06E-13	rs17563501:43801695:C:T
17_43802525_C_T	17	43802525	T	0.212	-0.0481	0.0076	2.51E-10	0.2142	0.1131	0.01578	7.84E-13	rs62054382:43802525:C:T
17_43802907_T_C	17	43802907	C	0.212	-0.0483	0.0076	2.14E-10	0.2143	0.1128	0.01578	8.66E-13	rs62054383:43802907:T:C
17_43802971_C_T	17	43802971	T	0.212	-0.0483	0.0076	2.26E-10	0.2142	0.1132	0.01578	7.47E-13	rs10514879:43802971:C:T
17_43803189_C_A	17	43803189	C	0.2562	-0.0389	0.0071	4.44E-08	0.2528	0.07355	0.01483	7.00E-07	rs1358071:43803189:C:A
17_43803773_A_AG	17	43803773	AG	0.2121	-0.0472	0.0077	7.79E-10	0.2142	0.1133	0.01578	7.08E-13	17:43803773:A:AG
17_43803788_T_C	17	43803788	C	0.212	-0.0482	0.0076	2.37E-10	0.2142	0.1133	0.01578	7.08E-13	rs56280222:43803788:T:C

17_43804306_T_C	17	43804306	C	0.212	-0.0482	0.0076	2.31E-10	0.2142	0.1133	0.01578	7.05E-13	rs62054384:43804306:T:C
17_43804317_A_G	17	43804317	A	0.2123	-0.0477	0.0076	3.55E-10	0.2147	0.1133	0.01577	6.69E-13	rs9897399:43804317:A:G
17_43804389_T_A	17	43804389	A	0.212	-0.0482	0.0076	2.31E-10	0.2142	0.1133	0.01578	7.04E-13	rs56205560:43804389:T:A
17_43804619_C_T	17	43804619	T	0.212	-0.0482	0.0076	2.31E-10	0.2142	0.1131	0.01578	7.67E-13	rs56380663:43804619:C:T
17_43805525_A_C	17	43805525	C	0.212	-0.0483	0.0076	2.13E-10	0.2142	0.1131	0.01578	7.56E-13	rs62054387:43805525:A:C
17_43805590_C_T	17	43805590	T	0.2121	-0.0483	0.0076	2.22E-10	0.2143	0.1131	0.01578	7.69E-13	rs62054388:43805590:C:T
17_43806015_G_A	17	43806015	A	0.2121	-0.0482	0.0076	2.30E-10	0.2143	0.113	0.01578	8.24E-13	rs4401083:43806015:G:A
17_43806264_C_T	17	43806264	T	0.2121	-0.0483	0.0076	2.27E-10	0.2143	0.1134	0.01578	6.81E-13	rs1880752:43806264:C:T
17_43806451_C_T	17	43806451	T	0.2121	-0.0483	0.0076	2.21E-10	0.2143	0.1135	0.01578	6.46E-13	rs4617909:43806451:C:T
17_43806925_G_A	17	43806925	A	0.2121	-0.0483	0.0076	2.23E-10	0.2143	0.1131	0.01578	7.75E-13	rs2902662:43806925:G:A
17_43807063_C_T	17	43807063	T	0.2121	-0.0482	0.0076	2.32E-10	0.2143	0.113	0.01578	8.28E-13	rs2864087:43807063:C:T
17_43807099_G_A	17	43807099	A	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.1131	0.01578	7.77E-13	rs2902661:43807099:G:A
17_43807113_C_T	17	43807113	T	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.1131	0.01578	7.77E-13	rs4609899:43807113:C:T
17_43807134_T_C	17	43807134	C	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.113	0.01578	8.16E-13	rs4471726:43807134:T:C
17_43807485_T_C	17	43807485	C	0.2121	-0.0482	0.0076	2.31E-10	0.2142	0.1129	0.01578	8.58E-13	rs79226879:43807485:T:C
17_43807642_T_G	17	43807642	G	0.212	-0.0483	0.0076	2.23E-10	0.2141	0.1132	0.01578	7.47E-13	rs76493835:43807642:T:G
17_43807911_A_G	17	43807911	G	0.2116	-0.0478	0.0076	3.41E-10	0.2141	0.1133	0.01579	7.10E-13	rs192006062:43807911:A:G
17_43807955_A_C	17	43807955	C	0.2121	-0.0482	0.0076	2.29E-10	0.2143	0.1131	0.01578	7.91E-13	rs17563599:43807955:A:C
17_43808067_G_A	17	43808067	A	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.1132	0.01578	7.57E-13	rs17649138:43808067:G:A
17_43808321_G_A	17	43808321	A	0.2121	-0.0482	0.0076	2.29E-10	0.2142	0.1131	0.01578	7.89E-13	rs62054389:43808321:G:A
17_43808443_A_C	17	43808443	C	0.2121	-0.0482	0.0076	2.35E-10	0.2143	0.1129	0.01578	8.39E-13	rs62054390:43808443:A:C
17_43808763_A_G	17	43808763	G	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.113	0.01578	7.94E-13	rs55947210:43808763:A:G
17_43808945_C_T	17	43808945	T	0.2126	-0.0479	0.0076	2.78E-10	0.2143	0.1124	0.01572	8.64E-13	rs62054392:43808945:C:T
17_43809016_C_T	17	43809016	T	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.113	0.01578	7.97E-13	rs4390635:43809016:C:T
17_43809096_C_G	17	43809096	G	0.4004	-0.0285	0.0063	6.29E-06	0.4011	0.09142	0.01338	8.43E-12	rs7225384:43809096:C:G
17_43809264_T_G	17	43809264	G	0.2121	-0.0483	0.0076	2.27E-10	0.2142	0.1128	0.01578	8.87E-13	rs62054393:43809264:T:G
17_43809328_A_G	17	43809328	G	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.1129	0.01578	8.42E-13	rs75986348:43809328:A:G
17_43809559_GT_G	17	43809559	G	0.2135	-0.0472	0.0077	7.96E-10	0.2153	0.1129	0.01579	8.42E-13	rs66763181:43809559:GT:G
17_43810371_G_C	17	43810371	C	0.2121	-0.0482	0.0076	2.36E-10	0.2142	0.1129	0.01578	8.55E-13	rs17649162:43810371:G:C
17_43810608_T_A	17	43810608	A	0.2121	-0.0482	0.0076	2.35E-10	0.2142	0.1129	0.01578	8.61E-13	rs62054394:43810608:T:A
17_43810782_G_C	17	43810782	C	0.2121	-0.0483	0.0076	2.19E-10	0.2142	0.1124	0.01578	1.06E-12	rs113790915:43810782:G:C
17_43810851_G_C	17	43810851	C	0.2113	-0.048	0.0076	3.07E-10	0.2133	0.114	0.01583	5.93E-13	rs77807457:43810851:G:C
17_43810873_A_T	17	43810873	T	0.2121	-0.0483	0.0076	2.23E-10	0.2142	0.1129	0.01578	8.57E-13	rs75022332:43810873:A:T
17_43810896_C_T	17	43810896	T	0.2188	-0.0461	0.0075	9.12E-10	0.2214	0.1067	0.01567	9.61E-12	rs77804065:43810896:C:T
17_43810902_A_G	17	43810902	G	0.2121	-0.0482	0.0076	2.29E-10	0.2142	0.1129	0.01578	8.58E-13	rs77301847:43810902:A:G
17_43811060_T_G	17	43811060	G	0.2121	-0.0482	0.0076	2.29E-10	0.2142	0.1129	0.01578	8.58E-13	rs62054395:43811060:T:G
17_43811072_A_G	17	43811072	G	0.2121	-0.0483	0.0076	2.26E-10	0.2142	0.1123	0.01578	1.11E-12	rs17563683:43811072:A:G
17_43811510_T_C	17	43811510	C	0.2121	-0.0482	0.0076	2.37E-10	0.2142	0.1129	0.01578	8.44E-13	rs62054396:43811510:T:C
17_43811673_C_T	17	43811673	T	0.2121	-0.0482	0.0076	2.33E-10	0.2143	0.1126	0.01578	9.62E-13	rs17563718:43811673:C:T
17_43811792_C_T	17	43811792	T	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.60E-13	rs62054397:43811792:C:T
17_43811950_A_C	17	43811950	C	0.2121	-0.0482	0.0076	2.37E-10	0.2142	0.1128	0.01578	8.87E-13	rs4569335:43811950:A:C
17_43811990_CTTAG_C	17	43811990	C	0.2122	-0.0472	0.0077	7.76E-10	0.2142	0.1129	0.01578	8.61E-13	17:43811990:CTTAG:C
17_43812177_C_T	17	43812177	T	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.62E-13	rs1526125:43812177:C:T
17_43812218_C_T	17	43812218	T	0.2121	-0.0483	0.0076	2.27E-10	0.2142	0.1129	0.01578	8.62E-13	rs1526126:43812218:C:T
17_43812398_C_G	17	43812398	G	0.2124	-0.0481	0.0076	2.66E-10	0.2147	0.1125	0.01579	1.05E-12	rs1526127:43812398:C:G
17_43812599_A_G	17	43812599	G	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.64E-13	rs62054398:43812599:A:G
17_43812624_G_A	17	43812624	A	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.64E-13	rs62054399:43812624:G:A
17_43812649_T_C	17	43812649	C	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.64E-13	rs62054400:43812649:T:C
17_43812684_A_G	17	43812684	G	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.65E-13	rs62054411:43812684:A:G
17_43812897_T_C	17	43812897	C	0.4049	-0.0295	0.0063	2.70E-06	0.4086	0.08657	0.01338	9.67E-11	rs12938476:43812897:T:C
17_43813002_G_A	17	43813002	A	0.2121	-0.0482	0.0076	2.40E-10	0.2142	0.1131	0.01578	7.69E-13	rs62054412:43813002:G:A
17_43813186_G_A	17	43813186	A	0.4053	-0.0298	0.0063	2.23E-06	0.4086	0.088	0.01337	4.68E-11	rs8067527:43813186:G:A
17_43813252_C_G	17	43813252	G	0.2121	-0.0482	0.0076	2.29E-10	0.2142	0.1126	0.01578	9.72E-13	rs17563787:43813252:C:G
17_43813370_G_C	17	43813370	C	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.66E-13	rs62054413:43813370:G:C
17_43813415_G_A	17	43813415	A	0.2121	-0.0482	0.0076	2.42E-10	0.2142	0.1129	0.01578	8.66E-13	rs62054414:43813415:G:A

17_43814020_T_C	17	43814020	C	0.2119	-0.0473	0.0076	5.26E-10	0.2143	0.1128	0.01578	8.63E-13	rs10451283:43814020:T:C
17_43814370_AC_A	17	43814370	A	0.2122	-0.0472	0.0077	7.77E-10	0.2142	0.1129	0.01578	8.66E-13	rs370719108:43814370:AC:A
17_43814427_T_C	17	43814427	C	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.66E-13	rs76421814:43814427:T:C
17_43814930_GCGTA_G	17	43814930	G	0.2122	-0.0472	0.0077	7.77E-10	0.2142	0.1129	0.01578	8.66E-13	17:43814930:GCGTA:G
17_43815141_A_G	17	43815141	G	0.2121	-0.0483	0.0076	2.27E-10	0.2142	0.1127	0.01578	9.34E-13	rs56006248:43815141:A:G
17_43815336_A_G	17	43815336	G	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs56298110:43815336:A:G
17_43815713_C_T	17	43815713	T	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs1608955:43815713:C:T
17_43815820_T_A	17	43815820	A	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs1608956:43815820:T:A
17_43815859_A_C	17	43815859	C	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs62054417:43815859:A:C
17_43816052_C_T	17	43816052	T	0.2124	-0.0477	0.0076	3.76E-10	0.2145	0.1119	0.01578	1.31E-12	rs78440279:43816052:C:T
17_43816106_C_A	17	43816106	A	0.2121	-0.0483	0.0076	2.22E-10	0.2142	0.1129	0.01578	8.39E-13	rs75500942:43816106:C:A
17_43816306_G_A	17	43816306	A	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs62054418:43816306:G:A
17_43816605_A_C	17	43816605	C	0.2121	-0.0482	0.0076	2.33E-10	0.2142	0.1129	0.01578	8.66E-13	rs62054419:43816605:A:C
17_43816655_C_G	17	43816655	G	0.2131	-0.049	0.0076	1.19E-10	0.2151	0.114	0.01576	4.79E-13	rs62054420:43816655:C:G
17_43816657_G_A	17	43816657	A	0.2132	-0.049	0.0076	1.19E-10	0.2151	0.1139	0.01576	4.94E-13	rs62054421:43816657:G:A
17_43817459_C_T	17	43817459	T	0.2121	-0.0482	0.0076	2.49E-10	0.2143	0.1128	0.01578	8.70E-13	rs17563800:43817459:C:T
17_43817557_C_T	17	43817557	T	0.2121	-0.0483	0.0076	2.17E-10	0.2142	0.1126	0.01578	9.53E-13	rs56295996:43817557:C:T
17_43817608_G_A	17	43817608	A	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.1129	0.01578	8.66E-13	rs56384960:43817608:G:A
17_43817832_G_A	17	43817832	A	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.1129	0.01578	8.66E-13	rs56178230:43817832:G:A
17_43817898_G_A	17	43817898	A	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1129	0.01578	8.66E-13	rs80157557:43817898:G:A
17_43818160_A_C	17	43818160	C	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.1129	0.01578	8.66E-13	rs76728632:43818160:A:C
17_43818222_C_A	17	43818222	A	0.2121	-0.0483	0.0076	2.21E-10	0.2142	0.1129	0.01578	8.66E-13	rs17563827:43818222:C:A
17_43818611_G_A	17	43818611	A	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1129	0.01578	8.66E-13	rs80072429:43818611:G:A
17_43818657_T_C	17	43818657	C	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1129	0.01578	8.66E-13	rs77114624:43818657:T:C
17_43818690_G_T	17	43818690	T	0.2121	-0.0482	0.0076	2.34E-10	0.2142	0.1126	0.01578	9.60E-13	rs76311426:43818690:G:T
17_43818906_A_G	17	43818906	G	0.2119	-0.0482	0.0076	2.54E-10	0.2139	0.1124	0.01579	1.07E-12	rs17563861:43818906:A:G
17_43818946_A_T	17	43818946	T	0.2122	-0.0483	0.0076	2.23E-10	0.2142	0.1125	0.01577	9.53E-13	rs17563889:43818946:A:T
17_43819384_G_A	17	43819384	A	0.2121	-0.0483	0.0076	2.14E-10	0.2142	0.1129	0.01578	8.65E-13	rs62054424:43819384:G:A
17_43819450_G_A	17	43819450	A	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1129	0.01578	8.65E-13	rs17563923:43819450:G:A
17_43819480_C_T	17	43819480	T	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1129	0.01578	8.65E-13	rs62054425:43819480:C:T
17_43819597_AC_A	17	43819597	A	0.2122	-0.0473	0.0077	6.93E-10	0.2142	0.1126	0.01578	9.50E-13	17:43819597:AC:A
17_43820669_G_T	17	43820669	G	0.4042	-0.0294	0.0063	3.20E-06	0.4076	0.08765	0.01338	5.81E-11	rs8075654:43820669:G:T
17_43820741_A_T	17	43820741	T	0.2114	-0.048	0.0076	3.19E-10	0.2131	0.1119	0.01581	1.47E-12	rs62054426:43820741:A:T
17_43821062_A_G	17	43821062	G	0.2121	-0.0482	0.0076	2.35E-10	0.2142	0.1129	0.01578	8.62E-13	rs62054427:43821062:A:G
17_43821685_C_A	17	43821685	A	0.2121	-0.0483	0.0076	2.22E-10	0.2142	0.1129	0.01578	8.46E-13	rs74464991:43821685:C:A
17_43822398_T_C	17	43822398	C	0.2121	-0.0483	0.0076	2.24E-10	0.2142	0.1129	0.01578	8.30E-13	rs2004260:43822398:T:C
17_43822511_G_A	17	43822511	A	0.212	-0.0487	0.0076	1.62E-10	0.2142	0.1132	0.01578	7.22E-13	rs62054428:43822511:G:A
17_43822769_C_T	17	43822769	T	0.2119	-0.0479	0.0076	3.12E-10	0.2141	0.1131	0.01578	7.88E-13	rs75788861:43822769:C:T
17_43822772_T_C	17	43822772	C	0.2124	-0.0475	0.0076	4.34E-10	0.2145	0.1125	0.01577	1.01E-12	rs9906974:43822772:T:C
17_43823125_G_A	17	43823125	A	0.2121	-0.0484	0.0076	2.04E-10	0.2142	0.1133	0.01578	6.98E-13	rs62054429:43823125:G:A
17_43823229_T_C	17	43823229	C	0.2121	-0.0484	0.0076	1.94E-10	0.2142	0.1134	0.01578	6.57E-13	rs76171147:43823229:T:C
17_43823326_A_G	17	43823326	G	0.2122	-0.0485	0.0076	1.87E-10	0.2143	0.1132	0.01578	7.33E-13	rs75643244:43823326:A:G
17_43823880_C_T	17	43823880	T	0.2121	-0.0482	0.0076	2.38E-10	0.2142	0.113	0.01578	8.10E-13	rs62054431:43823880:C:T
17_43823889_C_A	17	43823889	A	0.2121	-0.0483	0.0076	2.26E-10	0.2142	0.1129	0.01578	8.59E-13	rs62054432:43823889:C:A
17_43824201_G_A	17	43824201	A	0.2121	-0.0484	0.0076	2.03E-10	0.2142	0.1129	0.01578	8.59E-13	rs111497072:43824201:G:A
17_43824348_T_C	17	43824348	C	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1127	0.01578	9.20E-13	rs62054433:43824348:T:C
17_43824382_T_G	17	43824382	G	0.2121	-0.0483	0.0076	2.20E-10	0.2142	0.1127	0.01578	9.20E-13	rs62054434:43824382:T:G
17_43824848_A_G	17	43824848	G	0.2121	-0.0483	0.0076	2.14E-10	0.2142	0.1129	0.01578	8.58E-13	rs12150683:43824848:A:G
17_43824908_C_T	17	43824908	T	0.2121	-0.0483	0.0076	2.11E-10	0.2142	0.1129	0.01578	8.64E-13	rs12150332:43824908:C:T
17_43825339_C_G	17	43825339	G	0.2121	-0.0484	0.0076	2.06E-10	0.2142	0.1132	0.01578	7.27E-13	rs62054435:43825339:C:G
17_43825478_G_A	17	43825478	A	0.2121	-0.0485	0.0076	1.89E-10	0.2142	0.1129	0.01578	8.58E-13	rs75715199:43825478:G:A
17_43825568_C_T	17	43825568	T	0.2121	-0.0483	0.0076	2.16E-10	0.2142	0.1129	0.01578	8.58E-13	rs62054436:43825568:C:T
17_43825576_T_C	17	43825576	C	0.2137	-0.0477	0.0076	3.62E-10	0.2154	0.1136	0.01577	5.82E-13	rs62054437:43825576:T:C
17_43825711_A_C	17	43825711	C	0.2121	-0.0484	0.0076	2.08E-10	0.2142	0.1129	0.01578	8.58E-13	rs62054438:43825711:A:C
17_43825725_G_T	17	43825725	T	0.2121	-0.0484	0.0076	2.07E-10	0.2142	0.1129	0.01578	8.58E-13	rs62054439:43825725:G:T

17_43825912_A_G	17	43825912	G	0.2122	-0.0484	0.0076	2.07E-10	0.2143	0.1129	0.01578	8.34E-13	rs17334797:43825912:A:G
17_43826305_G_A	17	43826305	A	0.2121	-0.0484	0.0076	2.08E-10	0.2142	0.113	0.01578	8.14E-13	rs12150658:43826305:G:A
17_43826351_A_G	17	43826351	G	0.2121	-0.0482	0.0076	2.29E-10	0.2142	0.1129	0.01578	8.43E-13	rs12150363:43826351:A:G
17_43826637_G_A	17	43826637	A	0.2121	-0.0483	0.0076	2.25E-10	0.2142	0.1119	0.01578	1.31E-12	rs12150672:43826637:G:A
17_43827156_GA_G	17	43827156	G	0.2122	-0.0472	0.0077	7.81E-10	0.2142	0.1129	0.01578	8.47E-13	17:43827156:GA:G
17_43827209_G_A	17	43827209	A	0.2122	-0.0482	0.0076	2.40E-10	0.2145	0.1131	0.01578	7.77E-13	rs17334894:43827209:G:A
17_43827244_C_T	17	43827244	T	0.2125	-0.048	0.0076	2.85E-10	0.2147	0.1123	0.01579	1.14E-12	rs17334923:43827244:C:T
17_43827391_G_C	17	43827391	C	0.2121	-0.0482	0.0076	2.30E-10	0.2142	0.1129	0.01578	8.38E-13	rs62054440:43827391:G:C
17_43827431_A_G	17	43827431	G	0.2121	-0.0482	0.0076	2.36E-10	0.2142	0.1129	0.01578	8.47E-13	rs12150451:43827431:A:G
17_43827471_G_C	17	43827471	C	0.2117	-0.0485	0.0076	2.00E-10	0.2138	0.113	0.01579	8.33E-13	rs12150048:43827471:G:C
17_43827508_A_G	17	43827508	G	0.2121	-0.0482	0.0076	2.36E-10	0.2142	0.1129	0.01578	8.47E-13	rs12150455:43827508:A:G
17_43828221_T_A	17	43828221	A	0.2121	-0.0483	0.0076	2.24E-10	0.2142	0.1128	0.01578	8.94E-13	rs12150604:43828221:T:A
17_43828617_G_A	17	43828617	A	0.2125	-0.0485	0.0076	1.87E-10	0.2145	0.1127	0.01579	9.61E-13	rs17334944:43828617:G:A
17_43828698_C_T	17	43828698	T	0.2121	-0.0484	0.0076	1.95E-10	0.2142	0.1128	0.01578	9.08E-13	rs17426064:43828698:C:T
17_43828764_G_A	17	43828764	A	0.1897	-0.0477	0.0081	3.66E-09	0.1891	0.1201	0.01684	9.82E-13	rs79172804:43828764:G:A
17_43828935_G_C	17	43828935	C	0.2125	-0.0485	0.0076	1.77E-10	0.2149	0.1125	0.01578	1.01E-12	rs17426106:43828935:G:C
17_43829353_A_G	17	43829353	G	0.2124	-0.0482	0.0076	2.38E-10	0.2145	0.1124	0.01577	1.04E-12	rs62054442:43829353:A:G
17_43830382_G_A	17	43830382	A	0.212	-0.0481	0.0076	2.69E-10	0.2141	0.1133	0.01578	7.05E-13	rs35879086:43830382:G:A
17_43830640_C_T	17	43830640	T	0.2122	-0.0483	0.0076	2.29E-10	0.2143	0.1129	0.01578	8.31E-13	rs62055868:43830640:C:T
17_43830685_G_A	17	43830685	A	0.212	-0.0482	0.0076	2.46E-10	0.2141	0.1131	0.01578	7.81E-13	rs62055869:43830685:G:A
17_43830938_G_C	17	43830938	C	0.212	-0.0482	0.0076	2.46E-10	0.2141	0.1131	0.01578	7.81E-13	rs17426174:43830938:G:C
17_43831112_G_A	17	43831112	A	0.212	-0.0482	0.0076	2.46E-10	0.2141	0.1131	0.01578	7.81E-13	rs62055871:43831112:G:A
17_43832115_A_G	17	43832115	G	0.212	-0.0482	0.0076	2.43E-10	0.2141	0.1132	0.01578	7.33E-13	rs55645418:43832115:A:G
17_43832139_C_CAA	17	43832139	CAA	0.2117	-0.047	0.0077	9.46E-10	0.2139	0.1135	0.01579	6.62E-13	rs11657611:43832139:C:CAA
17_43832337_A_G	17	43832337	G	0.212	-0.0481	0.0076	2.50E-10	0.2141	0.1131	0.01578	7.81E-13	rs35631660:43832337:A:G
17_43832367_G_A	17	43832367	A	0.2121	-0.0482	0.0076	2.44E-10	0.2142	0.1132	0.01579	7.36E-13	rs17426195:43832367:G:A
17_43832618_G_A	17	43832618	A	0.212	-0.0482	0.0076	2.46E-10	0.2141	0.1131	0.01578	7.80E-13	rs35282504:43832618:G:A
17_43832864_T_C	17	43832864	C	0.212	-0.0482	0.0076	2.47E-10	0.2141	0.1132	0.01578	7.33E-13	rs62055875:43832864:T:C
17_43832940_A_G	17	43832940	G	0.2118	-0.0479	0.0076	3.17E-10	0.2145	0.1139	0.0158	5.60E-13	rs62055876:43832940:A:G
17_43833824_G_C	17	43833824	C	0.212	-0.0483	0.0076	2.21E-10	0.2141	0.1139	0.01578	5.39E-13	rs36047693:43833824:G:C
17_43833921_G_A	17	43833921	A	0.212	-0.0482	0.0076	2.42E-10	0.2141	0.1131	0.01578	7.80E-13	rs34195569:43833921:G:A
17_43833981_A_G	17	43833981	G	0.212	-0.0483	0.0076	2.29E-10	0.2141	0.1128	0.01578	8.88E-13	rs34579278:43833981:A:G
17_43834074_C_G	17	43834074	G	0.212	-0.0482	0.0076	2.41E-10	0.2141	0.1131	0.01578	7.81E-13	rs34211253:43834074:C:G
17_43834314_A_G	17	43834314	G	0.212	-0.0482	0.0076	2.38E-10	0.2141	0.1131	0.01578	7.79E-13	rs34008514:43834314:A:G
17_43834482_G_A	17	43834482	A	0.212	-0.0484	0.0076	2.01E-10	0.2141	0.1132	0.01579	7.30E-13	rs12943085:43834482:G:A
17_43834671_A_AC	17	43834671	AC	0.2123	-0.0472	0.0077	7.62E-10	0.2142	0.1132	0.01578	7.45E-13	rs71363552:43834671:A:AC
17_43834873_G_A	17	43834873	A	0.2149	-0.0491	0.0076	1.06E-10	0.2177	0.1097	0.01574	3.24E-12	17:43834873:G:A
17_43834970_C_T	17	43834970	T	0.212	-0.0483	0.0076	2.12E-10	0.2141	0.1133	0.01578	6.99E-13	rs7350923:43834970:C:T
17_43835351_T_C	17	43835351	C	0.212	-0.0482	0.0076	2.36E-10	0.2141	0.1125	0.01578	1.00E-12	rs11079717:43835351:T:C
17_43835854_C_A	17	43835854	A	0.212	-0.0483	0.0076	2.29E-10	0.2141	0.113	0.01578	7.95E-13	rs62055878:43835854:C:A
17_43836051_T_A	17	43836051	A	0.2121	-0.0483	0.0076	2.24E-10	0.2143	0.1129	0.01578	8.13E-13	rs76669427:43836051:T:A
17_43836109_A_AATT	17	43836109	AATT	0.2121	-0.0472	0.0077	7.61E-10	0.2141	0.1128	0.01578	8.83E-13	rs143196316:43836109:A:AATT
17_43836191_G_A	17	43836191	A	0.212	-0.0483	0.0076	2.30E-10	0.2141	0.1128	0.01578	8.88E-13	rs74514268:43836191:G:A
17_43836578_G_A	17	43836578	A	0.212	-0.0483	0.0076	2.29E-10	0.2142	0.1128	0.01578	9.09E-13	rs62055879:43836578:G:A
17_43836673_C_T	17	43836673	T	0.212	-0.0483	0.0076	2.29E-10	0.2142	0.1128	0.01578	9.08E-13	rs12948216:43836673:C:T
17_43836920_T_C	17	43836920	C	0.212	-0.0483	0.0076	2.29E-10	0.2142	0.1128	0.01578	9.05E-13	rs56013908:43836920:T:C
17_43836953_A_C	17	43836953	C	0.1821	-0.0435	0.0082	1.20E-07	0.1868	0.1116	0.01684	3.46E-11	rs56214516:43836953:A:C
17_43837091_T_C	17	43837091	C	0.212	-0.0483	0.0076	2.28E-10	0.2142	0.1129	0.01578	8.32E-13	rs56168907:43837091:T:C
17_43837115_A_G	17	43837115	G	0.212	-0.0483	0.0076	2.29E-10	0.2142	0.1128	0.01578	9.03E-13	rs55747440:43837115:A:G
17_43837237_A_G	17	43837237	G	0.212	-0.0483	0.0076	2.28E-10	0.2142	0.1128	0.01578	9.03E-13	rs55801356:43837237:A:G
17_43837446_C_G	17	43837446	G	0.212	-0.0483	0.0076	2.26E-10	0.2142	0.1128	0.01578	9.03E-13	rs62055883:43837446:C:G
17_43837567_C_T	17	43837567	T	0.2137	-0.0491	0.0076	1.13E-10	0.2153	0.1128	0.01579	9.24E-13	rs62055884:43837567:C:T
17_43837782_A_G	17	43837782	G	0.212	-0.0483	0.0076	2.27E-10	0.2143	0.1128	0.01578	8.85E-13	rs79882507:43837782:A:G
17_43837868_T_TTTATGTT	17	43837868	TTTATGTTATG	0.2108	-0.0472	0.0077	8.72E-10	0.2135	0.1127	0.01586	1.19E-12	17:43837868:T:TTTATGTTATG
17_43838014_A_G	17	43838014	G	0.212	-0.0483	0.0076	2.28E-10	0.2143	0.1128	0.01578	8.90E-13	rs62055885:43838014:A:G

17_43838071_C_T	17	43838071	T	0.212	-0.0483	0.0076	2.29E-10	0.2143	0.1128	0.01579	8.86E-13	rs28439278:43838071:C:T
17_43838482_G_T	17	43838482	T	0.2119	-0.0482	0.0076	2.36E-10	0.2143	0.1129	0.01579	8.64E-13	rs12150621:43838482:G:T
17_43838678_G_A	17	43838678	A	0.2119	-0.0482	0.0076	2.38E-10	0.2143	0.1129	0.01579	8.55E-13	rs62055886:43838678:G:A
17_43838710_T_C	17	43838710	C	0.2119	-0.0482	0.0076	2.40E-10	0.2143	0.1129	0.01579	8.52E-13	rs62055887:43838710:T:C
17_43838720_C_T	17	43838720	T	0.2103	-0.0489	0.0077	1.76E-10	0.2131	0.1133	0.01588	9.45E-13	rs62055888:43838720:C:T
17_43838919_G_A	17	43838919	A	0.2119	-0.0482	0.0076	2.43E-10	0.2143	0.113	0.01579	8.43E-13	rs62055889:43838919:G:A
17_43839150_AT_A	17	43839150	A	0.2141	-0.047	0.0077	9.41E-10	0.2168	0.1112	0.01579	1.87E-12	rs66470052:43839150:AT:A
17_43839253_G_A	17	43839253	A	0.2118	-0.0482	0.0076	2.49E-10	0.2143	0.113	0.01579	8.28E-13	rs71375313:43839253:G:A
17_43839951_A_T	17	43839951	T	0.2125	-0.0481	0.0076	2.55E-10	0.2158	0.1131	0.01577	7.59E-13	rs11079718:43839951:A:T
17_43840006_T_G	17	43840006	G	0.2132	-0.0475	0.0076	4.01E-10	0.2161	0.113	0.01576	7.48E-13	rs11079719:43840006:T:G
17_43840016_G_A	17	43840016	A	0.2106	-0.0476	0.0076	4.39E-10	0.2122	0.1116	0.01585	1.97E-12	rs11079720:43840016:G:A
17_43840107_C_A	17	43840107	A	0.2121	-0.0481	0.0076	2.68E-10	0.2145	0.1118	0.01577	1.37E-12	rs11079721:43840107:C:A
17_43840681_C_T	17	43840681	T	0.2115	-0.0481	0.0076	2.59E-10	0.2143	0.1133	0.01579	7.18E-13	rs62055890:43840681:C:T
17_43840726_C_CTT	17	43840726	CTT	0.2126	-0.0465	0.0077	1.43E-09	0.2157	0.113	0.01579	8.20E-13	17:43840726:C:CTT
17_43840864_G_A	17	43840864	A	0.212	-0.0484	0.0076	2.00E-10	0.2144	0.1124	0.01578	1.06E-12	rs77849344:43840864:G:A
17_43840899_G_C	17	43840899	C	0.2115	-0.0482	0.0076	2.51E-10	0.2143	0.1132	0.01579	7.36E-13	rs74918686:43840899:G:C
17_43840935_T_C	17	43840935	C	0.212	-0.0484	0.0076	1.97E-10	0.2144	0.112	0.01578	1.27E-12	rs79545140:43840935:T:C
17_43841356_CTT_C	17	43841356	C	0.216	-0.0478	0.0077	4.54E-10	0.2198	0.1146	0.01576	3.45E-13	rs371083624:43841356:CTT:C
17_43841571_T_A	17	43841571	A	0.212	-0.0485	0.0076	1.82E-10	0.2145	0.1121	0.01578	1.22E-12	rs56369036:43841571:T:A
17_43841624_G_GATGGAT	17	43841624	GATGGATGA	0.211	-0.0473	0.0077	8.18E-10	0.2135	0.1128	0.01581	9.51E-13	17:43841624:G:GATGGATGA
17_43841729_T_C	17	43841729	C	0.2121	-0.0481	0.0076	2.66E-10	0.2145	0.1139	0.01579	5.42E-13	rs11079723:43841729:T:C
17_43841912_C_T	17	43841912	T	0.212	-0.0485	0.0076	1.88E-10	0.2145	0.1121	0.01578	1.19E-12	rs11079724:43841912:C:T
17_43842462_T_C	17	43842462	C	0.2121	-0.0486	0.0076	1.73E-10	0.2145	0.1122	0.01578	1.17E-12	rs55707339:43842462:T:C
17_43842494_A_G	17	43842494	G	0.2121	-0.0485	0.0076	1.80E-10	0.2146	0.1121	0.01578	1.19E-12	rs62055893:43842494:A:G
17_43843395_C_T	17	43843395	T	0.2126	-0.0483	0.0076	2.15E-10	0.2152	0.1116	0.01578	1.56E-12	rs75257002:43843395:C:T
17_43843943_G_A	17	43843943	A	0.212	-0.0484	0.0076	2.01E-10	0.2146	0.112	0.01578	1.26E-12	rs62055894:43843943:G:A
17_43844044_A_G	17	43844044	G	0.212	-0.0483	0.0076	2.15E-10	0.2146	0.1125	0.01578	1.03E-12	rs62055895:43844044:A:G
17_43844201_C_T	17	43844201	T	0.212	-0.0483	0.0076	2.26E-10	0.2146	0.1122	0.01578	1.15E-12	rs62055896:43844201:C:T
17_43844486_T_A	17	43844486	A	0.212	-0.0483	0.0076	2.14E-10	0.2146	0.1121	0.01578	1.21E-12	rs55725840:43844486:T:A
17_43844559_T_G	17	43844559	G	0.212	-0.0483	0.0076	2.24E-10	0.2146	0.1123	0.01578	1.13E-12	rs56194509:43844559:T:G
17_43844560_T_G	17	43844560	G	0.212	-0.0483	0.0076	2.26E-10	0.2146	0.1119	0.01578	1.30E-12	rs55657917:43844560:T:G
17_43844798_G_A	17	43844798	A	0.2128	-0.048	0.0076	2.84E-10	0.2153	0.1123	0.01577	1.08E-12	rs56082319:43844798:G:A
17_43844859_A_G	17	43844859	G	0.212	-0.0483	0.0076	2.18E-10	0.2146	0.1121	0.01578	1.22E-12	rs56109643:43844859:A:G
17_43844977_T_A	17	43844977	A	0.212	-0.0483	0.0076	2.23E-10	0.2146	0.1121	0.01578	1.21E-12	rs62055899:43844977:T:A
17_43845002_C_G	17	43845002	G	0.2115	-0.0481	0.0076	2.66E-10	0.2144	0.1132	0.01578	7.32E-13	rs62055900:43845002:C:G
17_43845041_G_A	17	43845041	A	0.2116	-0.0481	0.0076	2.69E-10	0.2144	0.1133	0.01578	7.21E-13	rs62055901:43845041:G:A
17_43845480_T_C	17	43845480	T	0.2593	-0.0388	0.0071	4.83E-08	0.2542	0.07439	0.01481	5.12E-07	rs58089049:43845480:T:C
17_43846668_C_A	17	43846668	A	0.2115	-0.0481	0.0076	2.59E-10	0.2144	0.1132	0.01578	7.30E-13	rs62055903:43846668:C:A
17_43846820_G_A	17	43846820	A	0.212	-0.0484	0.0076	2.10E-10	0.2146	0.1123	0.01578	1.13E-12	rs111374028:43846820:G:A
17_43847039_C_T	17	43847039	T	0.2115	-0.0481	0.0076	2.58E-10	0.2144	0.1132	0.01578	7.30E-13	rs113934115:43847039:C:T
17_43847095_C_T	17	43847095	T	0.2116	-0.0481	0.0076	2.61E-10	0.2145	0.1134	0.01578	6.80E-13	rs113762994:43847095:C:T
17_43847374_G_A	17	43847374	A	0.212	-0.0484	0.0076	2.11E-10	0.2146	0.1122	0.01578	1.17E-12	rs62055928:43847374:G:A
17_43847741_T_C	17	43847741	C	0.2115	-0.0481	0.0076	2.57E-10	0.2144	0.1132	0.01578	7.29E-13	rs56268325:43847741:T:C
17_43847868_T_C	17	43847868	C	0.2115	-0.0481	0.0076	2.57E-10	0.2144	0.1132	0.01578	7.28E-13	rs56070245:43847868:T:C
17_43847912_T_C	17	43847912	C	0.212	-0.0483	0.0076	2.18E-10	0.2146	0.1119	0.01578	1.31E-12	rs56387266:43847912:T:C
17_43848181_C_T	17	43848181	T	0.212	-0.0487	0.0076	1.55E-10	0.2146	0.1127	0.01578	9.36E-13	rs34303488:43848181:C:T
17_43848412_A_G	17	43848412	G	0.2115	-0.0479	0.0076	3.29E-10	0.2145	0.1141	0.01581	5.37E-13	rs62055932:43848412:A:G
17_43848461_G_A	17	43848461	A	0.2112	-0.0483	0.0076	2.27E-10	0.2138	0.1135	0.01579	6.54E-13	rs62055933:43848461:G:A
17_43848495_G_T	***17***	***43848495***	***G***	***0.3549***	***0.0153***	***0.0065***	***0.01801***	***0.3592***	***-0.08039***	***0.01385***	***6.53E-09***	***rs7225082:43848495:G:T***
17_43848638_G_A	17	43848638	A	0.2117	-0.0483	0.0076	2.28E-10	0.2145	0.1095	0.0158	4.14E-12	rs62055934:43848638:G:A
17_43848646_AG_A	17	43848646	A	0.2117	-0.0471	0.0077	8.75E-10	0.2144	0.1132	0.01579	7.28E-13	rs66516551:43848646:AG:A
17_43848750_T_C	17	43848750	C	0.2115	-0.0481	0.0076	2.60E-10	0.2144	0.1133	0.01579	7.22E-13	rs62055935:43848750:T:C
17_43848761_T_A	17	43848761	A	0.2125	-0.0483	0.0076	2.13E-10	0.2152	0.1127	0.01578	9.06E-13	rs62055936:43848761:T:A
17_43848968_G_T	17	43848968	T	0.2115	-0.0481	0.0076	2.54E-10	0.2144	0.1133	0.01579	7.08E-13	rs62055937:43848968:G:T
17_43849327_G_A	17	43849327	A	0.2115	-0.0482	0.0076	2.45E-10	0.2144	0.1134	0.01579	6.88E-13	rs76294809:43849327:G:A

17_43849366_T_C	17	43849366	C	0.2115	-0.0482	0.0076	2.44E-10	0.2144	0.1134	0.01579	6.85E-13	rs75916678:43849366:T:C
17_43849415_T_C	17	43849415	C	0.2164	-0.0475	0.0076	3.97E-10	0.2208	0.1166	0.01572	1.20E-13	rs79730878:43849415:T:C
17_43849572_AT_A	17	43849572	A	0.2127	-0.0471	0.0077	8.72E-10	0.2153	0.1135	0.01579	6.37E-13	17:43849572:AT:A
17_43849656_C_A	17	43849656	A	0.2119	-0.0484	0.0076	2.00E-10	0.2146	0.1124	0.01578	1.04E-12	rs62055938:43849656:C:A
17_43849787_A_T	17	43849787	T	0.212	-0.0484	0.0076	2.06E-10	0.2146	0.1121	0.01578	1.23E-12	rs62055939:43849787:A:T
17_43849896_A_G	17	43849896	G	0.2115	-0.0482	0.0076	2.36E-10	0.2144	0.1134	0.01579	6.69E-13	rs62055940:43849896:A:G
17_43850037_C_CTT	17	43850037	CTT	0.2117	-0.0472	0.0077	8.01E-10	0.2144	0.1134	0.01579	6.71E-13	rs66499916:43850037:C:CTT
17_43850519_C_T	17	43850519	T	0.212	-0.0484	0.0076	2.10E-10	0.2146	0.1122	0.01578	1.17E-12	rs76885724:43850519:C:T
17_43850645_C_T	17	43850645	T	0.2149	-0.0484	0.0076	1.84E-10	0.2165	0.1116	0.01573	1.33E-12	rs60814418:43850645:C:T
17_43850932_C_T	17	43850932	T	0.2115	-0.0482	0.0076	2.35E-10	0.2144	0.1134	0.01579	6.67E-13	rs113518470:43850932:C:T
17_43850935_CA_C	17	43850935	C	0.2119	-0.047	0.0077	9.31E-10	0.2148	0.114	0.01579	5.26E-13	rs66488378:43850935:CA:C
17_43850966_A_G	17	43850966	G	0.2116	-0.0482	0.0076	2.39E-10	0.2145	0.1135	0.01579	6.58E-13	rs62055942:43850966:A:G
17_43851018_T_C	17	43851018	C	0.2115	-0.0482	0.0076	2.35E-10	0.2144	0.1134	0.01579	6.67E-13	rs62055943:43851018:T:C
17_43851209_A_AT	17	43851209	AT	0.2118	-0.0471	0.0077	8.31E-10	0.2161	0.1133	0.01579	7.21E-13	17:43851209:A:AT
17_43851851_G_A	17	43851851	A	0.212	-0.0485	0.0076	1.89E-10	0.2146	0.1124	0.01578	1.08E-12	rs62055945:43851851:G:A
17_43851971_C_A	17	43851971	A	0.2115	-0.0482	0.0076	2.35E-10	0.2144	0.1134	0.01579	6.76E-13	rs62055946:43851971:C:A
17_43852605_C_T	17	43852605	T	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1115	0.01578	1.59E-12	rs62055947:43852605:C:T
17_43852621_T_C	17	43852621	C	0.212	-0.0484	0.0076	1.97E-10	0.2146	0.1125	0.01578	1.03E-12	rs62055948:43852621:T:C
17_43852733_G_A	17	43852733	A	0.2115	-0.0482	0.0076	2.47E-10	0.2144	0.1133	0.01579	7.26E-13	rs113871181:43852733:G:A
17_43852742_T_C	17	43852742	C	0.2115	-0.0482	0.0076	2.47E-10	0.2144	0.1133	0.01579	7.25E-13	rs111370985:43852742:T:C
17_43853109_G_A	17	43853109	A	0.2115	-0.0482	0.0076	2.38E-10	0.2144	0.1134	0.01579	6.93E-13	rs55787105:43853109:G:A
17_43853133_T_C	17	43853133	C	0.2115	-0.0482	0.0076	2.38E-10	0.2144	0.1134	0.01579	6.91E-13	rs62055950:43853133:T:C
17_43853235_T_G	17	43853235	G	0.2115	-0.0482	0.0076	2.38E-10	0.2144	0.1134	0.01579	6.83E-13	rs56043078:43853235:T:G
17_43853457_A_G	17	43853457	G	0.212	-0.0485	0.0076	1.86E-10	0.2146	0.1123	0.01578	1.13E-12	rs77965652:43853457:A:G
17_43853526_A_G	17	43853526	G	0.212	-0.0485	0.0076	1.88E-10	0.2146	0.1122	0.01578	1.16E-12	rs55849949:43853526:A:G
17_43853922_G_A	17	43853922	A	0.2116	-0.0483	0.0076	2.16E-10	0.2145	0.1134	0.01578	6.63E-13	rs56303031:43853922:G:A
17_43854267_C_T	17	43854267	T	0.2115	-0.0482	0.0076	2.37E-10	0.2144	0.1134	0.01579	6.81E-13	rs55991914:43854267:C:T
17_43854340_A_G	17	43854340	G	0.2121	-0.0484	0.0076	1.94E-10	0.2148	0.1127	0.01578	9.00E-13	rs62055955:43854340:A:G
17_43854449_C_T	17	43854449	T	0.2121	-0.0485	0.0076	1.81E-10	0.2146	0.1119	0.01578	1.34E-12	rs62055956:43854449:C:T
17_43854536_C_A	17	43854536	A	0.212	-0.0484	0.0076	2.10E-10	0.2146	0.1126	0.01578	9.74E-13	rs62055957:43854536:C:A
17_43855228_G_T	17	43855228	T	0.2122	-0.0485	0.0076	1.82E-10	0.2148	0.1123	0.01578	1.12E-12	rs4074462:43855228:G:T
17_43855501_AC_A	17	43855501	A	0.2117	-0.0472	0.0077	8.21E-10	0.2144	0.1134	0.01578	6.89E-13	rs368284065:43855501:AC:A
17_43855503_C_T	17	43855503	T	0.2115	-0.0482	0.0076	2.42E-10	0.2144	0.1134	0.01578	6.86E-13	17:43855503:C:T
17_43856293_G_GCCCCTCC	17	43856293	GCCCCTCCCCTGCA	0.0664	-0.0546	0.0164	0.0008504	0.06901	0.2093	0.03376	5.62E-10	TGCAACCCCCAGCCTCATCCCATCTCCTGTTCCCATCAGACCAGC
17_43856341_C_T	17	43856341	T	0.2112	-0.0482	0.0076	2.65E-10	0.2142	0.1137	0.01582	6.41E-13	rs111878933:43856341:C:T
17_43856372_G_A	17	43856372	A	0.2112	-0.0481	0.0076	2.66E-10	0.2142	0.1137	0.01582	6.38E-13	rs111735741:43856372:G:A
17_43856639_C_G	17	43856639	G	0.2118	-0.0483	0.0076	2.15E-10	0.2145	0.1119	0.01578	1.36E-12	rs62057061:43856639:C:G
17_43856710_G_A	17	43856710	A	0.2115	-0.0482	0.0076	2.47E-10	0.2144	0.1135	0.01578	6.54E-13	rs62057062:43856710:G:A
17_43856730_C_T	17	43856730	T	0.2115	-0.0482	0.0076	2.47E-10	0.2144	0.1135	0.01578	6.52E-13	rs62057063:43856730:C:T
17_43857033_C_T	17	43857033	T	0.212	-0.0484	0.0076	2.06E-10	0.2146	0.1124	0.01578	1.05E-12	rs62057064:43857033:C:T
17_43857129_A_C	17	43857129	C	0.212	-0.0485	0.0076	1.94E-10	0.2146	0.1127	0.01578	9.22E-13	rs76830096:43857129:A:C
17_43857989_T_G	17	43857989	G	0.2099	-0.0483	0.0077	2.78E-10	0.211	0.1153	0.01587	3.84E-13	rs111433752:43857989:T:G
17_43857990_T_C	17	43857990	C	0.2099	-0.0483	0.0077	2.78E-10	0.211	0.1153	0.01587	3.84E-13	rs111664122:43857990:T:C
17_43858187_G_T	17	43858187	T	0.2115	-0.0481	0.0076	2.54E-10	0.2144	0.1134	0.01578	6.70E-13	rs62057065:43858187:G:T
17_43858307_T_C	17	43858307	C	0.2118	-0.0476	0.0076	4.06E-10	0.2147	0.1127	0.01578	9.35E-13	rs62057066:43858307:T:C
17_43858326_C_T	17	43858326	T	0.2115	-0.0481	0.0076	2.53E-10	0.2144	0.1134	0.01578	6.76E-13	rs62057067:43858326:C:T
17_43858482_C_T	17	43858482	T	0.2116	-0.0482	0.0076	2.46E-10	0.2144	0.1135	0.01578	6.41E-13	rs78917495:43858482:C:T
17_43858629_A_G	17	43858629	G	0.212	-0.0484	0.0076	2.10E-10	0.2146	0.1118	0.01578	1.43E-12	rs62057068:43858629:A:G
17_43859065_T_C	17	43859065	C	0.212	-0.0483	0.0076	2.12E-10	0.2146	0.1125	0.01578	9.90E-13	rs62057069:43859065:T:C
17_43859640_A_G	17	43859640	G	0.212	-0.0483	0.0076	2.15E-10	0.2146	0.1121	0.01578	1.23E-12	rs62057070:43859640:A:G
17_43859691_C_G	17	43859691	G	0.212	-0.0484	0.0076	2.06E-10	0.2146	0.112	0.01578	1.25E-12	rs62057071:43859691:C:G
17_43859929_C_CACG	17	43859929	CACG	0.2117	-0.0471	0.0077	8.50E-10	0.2144	0.1133	0.01578	7.18E-13	rs145503157:43859929:C:CACG
17_43861117_C_T	17	43861117	T	0.2115	-0.0482	0.0076	2.47E-10	0.2144	0.1132	0.01579	7.49E-13	rs62057073:43861117:C:T
17_43871982_C_T	17	43871982	T	0.2116	-0.0488	0.0076	1.54E-10	0.2145	0.1115	0.01579	1.66E-12	rs56319902:43871982:C:T
17_43872228_G_A	17	43872228	A	0.2112	-0.0484	0.0076	2.07E-10	0.2144	0.1121	0.0158	1.30E-12	rs55943044:43872228:G:A

17_43879308_A_G	17	43879308	G	0.212	-0.0482	0.0076	2.39E-10	0.2146	0.1118	0.01578	1.41E-12	rs80184151:43879308:A:G
17_43881790_C_T	17	43881790	T	0.2102	-0.0479	0.0076	3.28E-10	0.2136	0.1114	0.01583	1.93E-12	rs17689378:43881790:C:T
17_43885291_G_A	17	43885291	A	0.2103	-0.0481	0.0076	2.65E-10	0.2139	0.1116	0.01582	1.72E-12	rs62057101:43885291:G:A
17_43887480_T_C	17	43887480	C	0.2106	-0.0484	0.0076	2.14E-10	0.214	0.1122	0.01584	1.38E-12	rs62057103:43887480:T:C
17_43892784_T_G	17	43892784	G	0.2061	-0.0473	0.0078	1.23E-09	0.2052	0.109	0.0159	6.98E-12	rs55915917:43892784:T:G
17_43892788_G_A	17	43892788	A	0.2055	-0.0479	0.0078	7.61E-10	0.205	0.1108	0.01592	3.41E-12	rs55668363:43892788:G:A
17_43892973_T_C	17	43892973	C	0.2122	-0.0481	0.0076	2.62E-10	0.2145	0.1117	0.01578	1.41E-12	rs17689471:43892973:T:C
17_43893146_CCCAGTTCA	17	43893146	C	0.2115	-0.0474	0.0077	6.69E-10	0.2143	0.1114	0.01578	1.69E-12	82197:43893146:CCCAGTTCAGTGTGT:C
17_43893259_G_A	17	43893259	A	0.2122	-0.0481	0.0076	2.67E-10	0.2145	0.1122	0.01577	1.15E-12	rs117365970:43893259:G:A
17_43893260_T_C	17	43893260	C	0.2122	-0.0481	0.0076	2.69E-10	0.2145	0.112	0.01578	1.25E-12	rs117646503:43893260:T:C
17_43893403_G_A	17	43893403	A	0.2122	-0.0481	0.0076	2.54E-10	0.2145	0.112	0.01578	1.23E-12	rs17762769:43893403:G:A
17_43893716_C_T	17	43893716	T	0.2122	-0.0482	0.0076	2.38E-10	0.2146	0.1115	0.01577	1.53E-12	rs8072451:43893716:C:T
17_43893751_A_G	17	43893751	G	0.2117	-0.0482	0.0076	2.30E-10	0.2144	0.1112	0.01578	1.83E-12	rs8073146:43893751:A:G
17_43894102_T_C	17	43894102	C	0.2122	-0.0478	0.0076	3.43E-10	0.2146	0.1114	0.01578	1.66E-12	rs28364025:43894102:T:C
17_43894159_C_T	17	43894159	T	0.2114	-0.0484	0.0076	1.99E-10	0.2143	0.1114	0.01578	1.72E-12	rs28364023:43894159:C:T
17_43894485_G_GA	17	43894485	GA	0.2115	-0.0473	0.0077	7.02E-10	0.2143	0.1114	0.01578	1.71E-12	17:43894485:G:GA
17_43894510_G_A	17	43894510	A	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1114	0.01578	1.71E-12	rs55779147:43894510:G:A
17_43894547_C_T	17	43894547	T	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1114	0.01578	1.71E-12	rs56357543:43894547:C:T
17_43894609_A_G	17	43894609	G	0.2122	-0.048	0.0076	2.74E-10	0.2145	0.1119	0.01578	1.33E-12	rs56099546:43894609:A:G
17_43894990_T_G	17	43894990	G	0.2122	-0.048	0.0076	2.80E-10	0.2145	0.1117	0.01577	1.46E-12	rs739645:43894990:T:G
17_43895008_C_G	17	43895008	G	0.2114	-0.0484	0.0076	2.03E-10	0.2143	0.1113	0.01578	1.75E-12	rs739644:43895008:C:G
17_43895168_T_TG	17	43895168	TG	0.2115	-0.0473	0.0077	7.06E-10	0.2143	0.1114	0.01578	1.72E-12	17:43895168:T:TG
17_43895501_G_C	17	43895501	C	0.2121	-0.0479	0.0076	2.94E-10	0.2145	0.1121	0.01578	1.21E-12	rs4564621:43895501:G:C
17_43895530_C_T	17	43895530	T	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1115	0.01578	1.65E-12	rs2316763:43895530:C:T
17_43895602_T_G	17	43895602	G	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1115	0.01578	1.65E-12	rs2316764:43895602:T:G
17_43895653_A_G	17	43895653	G	0.2114	-0.0484	0.0076	2.01E-10	0.2143	0.1115	0.01578	1.64E-12	rs4277389:43895653:A:G
17_43895696_G_A	17	43895696	A	0.2122	-0.0481	0.0076	2.61E-10	0.2145	0.1123	0.01578	1.07E-12	rs4566211:43895696:G:A
17_43895751_G_A	17	43895751	A	0.2122	-0.0481	0.0076	2.57E-10	0.2145	0.1125	0.01578	9.78E-13	rs4566212:43895751:G:A
17_43895797_T_C	17	43895797	C	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1116	0.01578	1.54E-12	rs4309444:43895797:T:C
17_43896032_C_T	17	43896032	T	0.2114	-0.0484	0.0076	2.02E-10	0.2143	0.1116	0.01578	1.51E-12	rs62057107:43896032:C:T
17_43896228_T_C	17	43896228	C	0.2114	-0.0484	0.0076	2.01E-10	0.2143	0.1117	0.01578	1.49E-12	rs12150390:43896228:T:C
17_43896528_C_G	17	43896528	G	0.2122	-0.048	0.0076	2.77E-10	0.2145	0.1122	0.01577	1.15E-12	rs17689608:43896528:C:G
17_43896616_T_C	17	43896616	C	0.2114	-0.0484	0.0076	1.97E-10	0.2143	0.1117	0.01578	1.45E-12	rs62057108:43896616:T:C
17_43896637_T_C	17	43896637	C	0.2122	-0.0481	0.0076	2.61E-10	0.2145	0.112	0.01578	1.25E-12	rs62057109:43896637:T:C
17_43896690_T_C	17	43896690	C	0.2123	-0.0482	0.0076	2.29E-10	0.2146	0.1124	0.01577	1.03E-12	rs78074121:43896690:T:C
17_43896734_T_C	17	43896734	C	0.2114	-0.0484	0.0076	1.95E-10	0.2143	0.1119	0.01578	1.32E-12	rs62057110:43896734:T:C
17_43896862_CT_C	17	43896862	C	0.183	-0.0433	0.0082	1.43E-07	0.1888	0.1099	0.01676	5.56E-11	17:43896862:CT:C
17_43897026_TGGAG_T	17	43897026	T	0.2116	-0.0474	0.0077	6.75E-10	0.2143	0.112	0.01578	1.24E-12	17:43897026:TGGAG:T
17_43897130_A_G	17	43897130	G	0.2122	-0.048	0.0076	2.68E-10	0.2145	0.1122	0.01576	1.10E-12	rs62057111:43897130:A:G
17_43897202_T_A	17	43897202	A	0.2114	-0.0484	0.0076	1.98E-10	0.2143	0.112	0.01578	1.24E-12	rs62057112:43897202:T:A
17_43897246_A_G	17	43897246	G	0.2114	-0.0485	0.0076	1.90E-10	0.2143	0.1121	0.01578	1.22E-12	rs78587102:43897246:A:G
17_43897449_A_T	17	43897449	T	0.2114	-0.0485	0.0076	1.90E-10	0.2143	0.1121	0.01578	1.22E-12	rs62057113:43897449:A:T
17_43897480_A_G	17	43897480	G	0.2114	-0.0485	0.0076	1.90E-10	0.2143	0.1121	0.01578	1.22E-12	rs78506181:43897480:A:G
17_43897722_T_C	17	43897722	C	0.2122	-0.048	0.0076	2.83E-10	0.2145	0.112	0.01577	1.25E-12	rs79600142:43897722:T:C
17_43898362_AAGG_A	17	43898362	A	0.2116	-0.0474	0.0077	6.69E-10	0.2143	0.1121	0.01578	1.22E-12	17:43898362:AAGG:A
17_43898459_C_T	17	43898459	T	0.2114	-0.0485	0.0076	1.88E-10	0.2143	0.1121	0.01578	1.22E-12	rs111739681:43898459:C:T
17_43898887_T_C	17	43898887	C	0.2114	-0.0485	0.0076	1.88E-10	0.2143	0.1121	0.01578	1.22E-12	rs17762882:43898887:T:C
17_43898963_A_T	17	43898963	T	0.2114	-0.0485	0.0076	1.88E-10	0.2143	0.1121	0.01578	1.22E-12	rs17689653:43898963:A:T
17_43899161_A_C	17	43899161	C	0.2114	-0.0485	0.0076	1.88E-10	0.2143	0.112	0.01578	1.22E-12	rs17762912:43899161:A:C
17_43899401_C_T	17	43899401	T	0.2122	-0.0482	0.0076	2.43E-10	0.2145	0.1125	0.01577	9.86E-13	rs62057114:43899401:C:T
17_43899417_G_C	17	43899417	C	0.2122	-0.0481	0.0076	2.61E-10	0.2145	0.1129	0.01573	7.08E-13	rs62057115:43899417:G:C
17_43899611_C_T	17	43899611	T	0.2122	-0.0481	0.0076	2.63E-10	0.2145	0.113	0.01573	6.83E-13	rs78917479:43899611:C:T
17_43899655_T_C	17	43899655	C	0.2114	-0.0485	0.0076	1.90E-10	0.2143	0.1127	0.01576	8.49E-13	rs62057116:43899655:T:C
17_43899657_C_G	17	43899657	G	0.2122	-0.048	0.0076	2.81E-10	0.2145	0.1135	0.01573	5.50E-13	rs62057117:43899657:C:G
17_43899727_A_G	17	43899727	G	0.2122	-0.0481	0.0076	2.48E-10	0.2145	0.1129	0.01573	7.02E-13	rs62057118:43899727:A:G

17_43899736_G_A	17	43899736	A	0.2115	-0.0485	0.0076	1.84E-10	0.2143	0.1126	0.01576	9.15E-13	rs62057119:43899736:G:A
17_43899786_C_T	17	43899786	T	0.2123	-0.0478	0.0076	3.20E-10	0.2147	0.1103	0.01576	2.55E-12	rs17762954:43899786:C:T
17_43900081_C_T	17	43900081	T	0.2115	-0.0485	0.0076	1.92E-10	0.2143	0.1123	0.01576	1.05E-12	rs55979424:43900081:C:T
17_43900215_T_TAA	17	43900215	TAA	0.2108	-0.0479	0.0077	5.09E-10	0.2129	0.1119	0.01581	1.50E-12	rs56284150:43900215:T:TAA
17_43900434_A_G	17	43900434	G	0.2115	-0.0485	0.0076	1.84E-10	0.2143	0.1124	0.01576	9.96E-13	rs55638417:43900434:A:G
17_43900697_C_T	17	43900697	T	0.2122	-0.0481	0.0076	2.47E-10	0.2145	0.1127	0.01573	7.84E-13	rs79501144:43900697:C:T
17_43900760_G_A	17	43900760	A	0.2115	-0.0485	0.0076	1.83E-10	0.2143	0.1124	0.01576	9.74E-13	rs62057121:43900760:G:A
17_43900817_A_G	17	43900817	G	0.2115	-0.0485	0.0076	1.82E-10	0.2143	0.1125	0.01576	9.55E-13	rs112137135:43900817:A:G
17_43901001_C_T	17	43901001	T	0.2129	-0.0492	0.0076	1.00E-10	0.216	0.1121	0.01575	1.10E-12	rs62057122:43901001:C:T
17_43901238_A_G	17	43901238	G	0.2122	-0.0481	0.0076	2.60E-10	0.2145	0.1128	0.01577	8.62E-13	rs62057123:43901238:A:G
17_43901528_T_C	17	43901528	C	0.2115	-0.0486	0.0076	1.74E-10	0.2143	0.1127	0.01576	8.67E-13	rs62057143:43901528:T:C
17_43901558_A_G	17	43901558	G	0.2115	-0.0486	0.0076	1.74E-10	0.2143	0.1127	0.01576	8.68E-13	rs62057144:43901558:A:G
17_43902216_C_T	17	43902216	T	0.2123	-0.0481	0.0076	2.48E-10	0.2146	0.1128	0.01574	7.67E-13	rs4335809:43902216:C:T
17_43902505_C_T	17	43902505	T	0.2123	-0.0483	0.0076	2.23E-10	0.2143	0.1127	0.01577	8.73E-13	rs4341787:43902505:C:T
17_43902522_G_A	17	43902522	A	0.2115	-0.0486	0.0076	1.76E-10	0.2143	0.1125	0.01577	9.45E-13	rs4523962:43902522:G:A
17_43902541_A_G	17	43902541	G	0.1835	-0.0449	0.0082	3.68E-08	0.19	0.1131	0.0167	1.29E-11	rs4327090:43902541:A:G
17_43902738_C_A	17	43902738	A	0.2115	-0.0485	0.0076	1.78E-10	0.2143	0.1126	0.01577	9.51E-13	rs3885074:43902738:C:A
17_43902799_A_G	17	43902799	G	0.2115	-0.0485	0.0076	1.78E-10	0.2143	0.1126	0.01577	9.54E-13	rs3885075:43902799:A:G
17_43902842_C_T	17	43902842	T	0.2115	-0.0485	0.0076	1.79E-10	0.2143	0.1126	0.01577	9.57E-13	rs41280116:43902842:C:T
17_43902861_C_A	17	43902861	A	0.2114	-0.0485	0.0076	1.82E-10	0.2142	0.1125	0.01577	9.83E-13	rs34283254:43902861:C:A
17_43902944_C_T	17	43902944	T	0.2115	-0.0485	0.0076	1.80E-10	0.2143	0.1125	0.01577	9.65E-13	rs1912151:43902944:C:T
17_43902997_G_A	17	43902997	A	0.2122	-0.048	0.0076	2.72E-10	0.2145	0.1122	0.01577	1.11E-12	rs1396862:43902997:G:A
17_43903089_C_T	17	43903089	T	0.2115	-0.0485	0.0076	1.81E-10	0.2143	0.1126	0.01577	9.60E-13	rs41280118:43903089:C:T
17_43903106_A_G	17	43903106	G	0.2115	-0.0485	0.0076	1.80E-10	0.2143	0.1126	0.01577	9.59E-13	rs62057146:43903106:A:G
17_43903298_G_A	17	43903298	A	0.2116	-0.0484	0.0076	2.03E-10	0.2144	0.1125	0.01577	9.80E-13	rs62057147:43903298:G:A
17_43903336_G_A	17	43903336	A	0.2115	-0.0485	0.0076	1.80E-10	0.2143	0.1126	0.01577	9.38E-13	rs17763050:43903336:G:A
17_43903485_G_C	17	43903485	C	0.2123	-0.048	0.0076	2.88E-10	0.2146	0.1121	0.01577	1.17E-12	rs62057148:43903485:G:C
17_43903546_A_G	17	43903546	G	0.2123	-0.048	0.0076	2.70E-10	0.2145	0.1126	0.01574	8.23E-13	rs62057149:43903546:A:G
17_43903548_C_T	17	43903548	T	0.2115	-0.0485	0.0076	1.80E-10	0.2143	0.1124	0.01577	1.02E-12	rs62057150:43903548:C:T
17_43903842_C_T	17	43903842	T	0.2183	-0.0485	0.0075	1.28E-10	0.2245	0.1082	0.01558	3.85E-12	rs62057151:43903842:C:T
17_43904110_G_C	17	43904110	C	0.2115	-0.0485	0.0076	1.78E-10	0.2143	0.1124	0.01577	1.01E-12	rs62057152:43904110:G:C
17_43904397_C_T	17	43904397	T	0.2123	-0.0481	0.0076	2.60E-10	0.2146	0.1125	0.01577	9.79E-13	rs17689824:43904397:C:T
17_43904528_T_C	17	43904528	C	0.2118	-0.0488	0.0076	1.46E-10	0.2148	0.1118	0.01577	1.35E-12	rs62057153:43904528:T:C
17_43904610_C_T	17	43904610	T	0.2115	-0.0486	0.0076	1.70E-10	0.2143	0.1127	0.01577	8.71E-13	rs62057154:43904610:C:T
17_43904673_C_T	17	43904673	T	0.2115	-0.0486	0.0076	1.74E-10	0.2143	0.1129	0.01576	7.83E-13	rs62057155:43904673:C:T
17_43904948_G_C	17	43904948	C	0.2122	-0.0482	0.0076	2.41E-10	0.2145	0.1146	0.01574	3.35E-13	rs62057156:43904948:G:C
17_43905134_G_A	17	43905134	A	0.2115	-0.0486	0.0076	1.76E-10	0.2143	0.1134	0.01576	6.07E-13	rs78872653:43905134:G:A
17_43905313_G_C	17	43905313	C	0.2122	-0.0479	0.0076	3.09E-10	0.2146	0.114	0.01572	4.10E-13	rs62057157:43905313:G:C
17_43905481_T_G	17	43905481	G	0.2115	-0.0485	0.0076	1.77E-10	0.2143	0.1134	0.01576	6.24E-13	rs17763086:43905481:T:G
17_43906726_A_C	17	43906726	C	0.2112	-0.0485	0.0076	1.97E-10	0.2141	0.1126	0.01577	9.17E-13	rs17425752:43906726:A:C
17_43906828_G_A	17	43906828	A	0.2121	-0.0482	0.0076	2.46E-10	0.2144	0.1121	0.01578	1.20E-12	rs17689882:43906828:G:A
17_43907143_G_A	17	43907143	A	0.2115	-0.0485	0.0076	1.80E-10	0.2143	0.113	0.01576	7.52E-13	rs62057158:43907143:G:A
17_43907641_C_CAGGTGG	17	43907641	CAGGTGG	0.2116	-0.0475	0.0077	6.28E-10	0.2143	0.113	0.01575	7.44E-13	17:43907641:C:CAGGTGG
17_43907745_C_T	17	43907745	T	0.2115	-0.0485	0.0076	1.78E-10	0.2143	0.113	0.01575	7.43E-13	rs1876831:43907745:C:T
17_43907896_T_C	17	43907896	C	0.2123	-0.048	0.0076	2.68E-10	0.2145	0.1152	0.01572	2.31E-13	rs16940665:43907896:T:C
17_43907966_G_A	17	43907966	A	0.2115	-0.0485	0.0076	1.82E-10	0.2143	0.1131	0.01575	7.15E-13	rs16940668:43907966:G:A
17_43908151_C_T	17	43908151	T	0.2123	-0.048	0.0076	2.81E-10	0.2145	0.1141	0.01571	3.76E-13	rs16940671:43908151:C:T
17_43908152_C_T	17	43908152	T	0.2115	-0.0484	0.0076	1.92E-10	0.2143	0.1133	0.01575	6.49E-13	rs16940672:43908152:C:T
17_43908476_GT_G	17	43908476	G	0.2115	-0.0474	0.0077	6.44E-10	0.214	0.1133	0.01575	6.24E-13	17:43908476:GT:G
17_43908773_G_C	17	43908773	C	0.2123	-0.0479	0.0076	2.99E-10	0.2145	0.1149	0.01571	2.62E-13	rs55763795:43908773:G:C
17_43908826_T_G	17	43908826	G	0.2122	-0.048	0.0076	2.79E-10	0.2145	0.1144	0.01572	3.49E-13	rs55865707:43908826:T:G
17_43908989_C_T	17	43908989	T	0.2101	-0.0479	0.0076	3.85E-10	0.2121	0.1139	0.01583	6.23E-13	rs62054760:43908989:C:T
17_43909008_C_T	17	43909008	T	0.2101	-0.0479	0.0076	3.85E-10	0.2121	0.1139	0.01583	6.23E-13	rs62054761:43909008:C:T
17_43909022_G_T	17	43909022	T	0.2101	-0.0479	0.0076	3.85E-10	0.2121	0.1139	0.01583	6.23E-13	rs62054762:43909022:G:T
17_43909435_C_CAAAAAA	17	43909435	CAAAAAAACAAAA	0.2112	-0.0473	0.0077	7.63E-10	0.2139	0.1126	0.01577	9.25E-13	.7:43909435:C:CAAAAAAACAAAA

17_43910088_G_A	17	43910088	A	0.2116	-0.0475	0.0076	4.32E-10	0.2145	0.1155	0.01573	2.05E-13	rs17689918:43910088:G:A
17_43910183_G_A	17	43910183	A	0.2114	-0.0483	0.0076	2.13E-10	0.2141	0.1132	0.01576	6.65E-13	rs17763199:43910183:G:A
17_43910262_C_G	17	43910262	G	0.2114	-0.0483	0.0076	2.26E-10	0.2143	0.1134	0.01575	6.21E-13	rs62054763:43910262:C:G
17_43910507_C_T	17	43910507	T	0.2121	-0.0477	0.0076	3.46E-10	0.2145	0.114	0.01573	4.15E-13	rs16940674:43910507:C:T
17_43911036_G_A	17	43911036	A	0.2113	-0.0481	0.0076	2.65E-10	0.2142	0.1132	0.01576	6.72E-13	rs16940676:43911036:G:A
17_43911352_C_T	17	43911352	T	0.2114	-0.0482	0.0076	2.30E-10	0.2143	0.1134	0.01575	6.04E-13	rs1876830:43911352:C:T
17_43911424_C_T	17	43911424	T	0.2123	-0.0479	0.0076	3.05E-10	0.2145	0.115	0.01571	2.52E-13	rs41457044:43911424:C:T
17_43911443_T_C	17	43911443	C	0.2123	-0.0476	0.0076	3.79E-10	0.2151	0.1104	0.01576	2.54E-12	rs1876829:43911443:T:C
17_43911525_C_T	17	43911525	T	0.2123	-0.0484	0.0076	2.01E-10	0.2147	0.113	0.01576	7.52E-13	rs1876828:43911525:C:T
17_43911832_T_C	17	43911832	C	0.2122	-0.0481	0.0076	2.52E-10	0.2145	0.1122	0.01577	1.11E-12	rs1876827:43911832:T:C
17_43911898_C_T	17	43911898	T	0.2119	-0.0482	0.0076	2.29E-10	0.2154	0.1128	0.01576	8.20E-13	rs16940677:43911898:C:T
17_43912159_G_C	17	43912159	C	0.2114	-0.0483	0.0076	2.11E-10	0.2143	0.1132	0.01575	6.63E-13	rs16940681:43912159:G:C
17_43912267_T_TG	17	43912267	TG	0.2054	-0.0502	0.0077	7.25E-11	0.2118	0.1139	0.01585	6.65E-13	rs66808254:43912267:T:TG
17_43912282_C_T	17	43912282	T	0.2114	-0.0484	0.0076	2.08E-10	0.2142	0.1131	0.01575	6.96E-13	rs28364021:43912282:C:T
17_43912454_T_C	17	43912454	C	0.2115	-0.0484	0.0076	1.94E-10	0.2143	0.1131	0.01575	6.93E-13	rs2316765:43912454:T:C
17_43912490_C_G	17	43912490	G	0.2117	-0.0484	0.0076	1.94E-10	0.2145	0.1129	0.01575	7.78E-13	rs878886:43912490:C:G
17_43912582_C_T	17	43912582	T	0.2123	-0.048	0.0076	2.77E-10	0.2146	0.1147	0.01572	2.93E-13	rs878887:43912582:C:T
17_43912635_A_G	17	43912635	G	0.2124	-0.0482	0.0076	2.25E-10	0.2146	0.1146	0.01572	3.11E-13	rs878888:43912635:A:G
17_43912723_T_C	17	43912723	C	0.2115	-0.0485	0.0076	1.87E-10	0.2143	0.1132	0.01575	6.48E-13	rs4525537:43912723:T:C
17_43912786_G_C	17	43912786	C	0.2124	-0.0482	0.0076	2.20E-10	0.2152	0.1146	0.01571	3.08E-13	rs4640231:43912786:G:C
17_43912830_T_C	17	43912830	C	0.2123	-0.0482	0.0076	2.19E-10	0.2145	0.1148	0.01572	2.78E-13	rs4482334:43912830:T:C
17_43913315_C_T	17	43913315	T	0.2126	-0.0481	0.0076	2.23E-10	0.2146	0.1155	0.01569	1.77E-13	rs56127111:43913315:C:T
17_43913360_TGAGGGCAG	17	43913360	T	0.2116	-0.0474	0.0077	6.52E-10	0.2143	0.1137	0.01575	5.37E-13	7:43913360:TGAGGGCAGGAGG:T
17_43913557_T_G	17	43913557	G	0.2116	-0.0487	0.0076	1.59E-10	0.2144	0.114	0.01575	4.67E-13	rs75104593:43913557:T:G
17_43913558_T_G	17	43913558	G	0.2125	-0.0482	0.0076	2.27E-10	0.2146	0.1163	0.01572	1.39E-13	rs74998289:43913558:T:G
17_43914554_C_A	17	43914554	A	0.2114	-0.0484	0.0076	1.99E-10	0.2143	0.1119	0.01577	1.29E-12	rs10445362:43914554:C:A
17_43914558_G_A	17	43914558	A	0.2114	-0.0484	0.0076	2.03E-10	0.2142	0.1117	0.01577	1.41E-12	rs10445363:43914558:G:A
17_43914598_G_C	17	43914598	C	0.2122	-0.0481	0.0076	2.59E-10	0.2145	0.1123	0.01577	1.07E-12	rs62054802:43914598:G:C
17_43914728_G_T	17	43914728	T	0.2122	-0.0479	0.0076	2.92E-10	0.2145	0.113	0.01575	7.28E-13	rs62054803:43914728:G:T
17_43914809_C_T	17	43914809	T	0.2114	-0.0484	0.0076	1.99E-10	0.2143	0.1118	0.01577	1.34E-12	rs62054804:43914809:C:T
17_43914979_AC_A	17	43914979	A	0.2121	-0.0472	0.0077	7.96E-10	0.2149	0.1124	0.01577	9.98E-13	rs201128097:43914979:AC:A
17_43914981_C_G	17	43914981	G	0.212	-0.0482	0.0076	2.33E-10	0.2149	0.1124	0.01577	9.98E-13	17:43914981:C:G
17_43914990_AAC_A	17	43914990	A	0.2115	-0.0473	0.0077	7.21E-10	0.2143	0.1116	0.01577	1.49E-12	17:43914990:AAC:A
17_43915054_A_G	17	43915054	G	0.2122	-0.0481	0.0076	2.47E-10	0.2146	0.1119	0.01576	1.24E-12	rs62054805:43915054:A:G
17_43915312_C_T	17	43915312	T	0.2122	-0.0481	0.0076	2.57E-10	0.2145	0.1118	0.01577	1.33E-12	rs62054806:43915312:C:T
17_43915497_C_T	17	43915497	T	0.2815	-0.0306	0.0069	8.95E-06	0.2857	0.09038	0.01447	4.18E-10	rs62054807:43915497:C:T
17_43916356_G_A	17	43916356	A	0.2122	-0.0481	0.0076	2.57E-10	0.2145	0.112	0.01576	1.18E-12	rs10445364:43916356:G:A
17_43916509_A_G	17	43916509	G	0.2122	-0.0482	0.0076	2.34E-10	0.2145	0.1119	0.01577	1.27E-12	rs10445333:43916509:A:G
17_43916773_A_C	17	43916773	C	0.2123	-0.0481	0.0076	2.62E-10	0.2146	0.1122	0.01575	1.05E-12	rs17690176:43916773:A:C
17_43916932_G_A	17	43916932	A	0.2114	-0.0485	0.0076	1.88E-10	0.2143	0.1111	0.01578	1.93E-12	rs78328427:43916932:G:A
17_43917086_A_G	17	43917086	G	0.2114	-0.0485	0.0076	1.87E-10	0.2143	0.1111	0.01578	1.90E-12	rs77692262:43917086:A:G
17_43917776_G_T	17	43917776	T	0.2122	-0.0482	0.0076	2.34E-10	0.2145	0.1123	0.01576	1.05E-12	rs56023973:43917776:G:T
17_43917818_G_A	17	43917818	A	0.2114	-0.0485	0.0076	1.80E-10	0.2143	0.1113	0.01578	1.77E-12	rs17763515:43917818:G:A
17_43918190_T_C	17	43918190	C	0.2122	-0.048	0.0076	2.82E-10	0.2145	0.1116	0.01577	1.46E-12	rs17763533:43918190:T:C
17_43918239_C_T	17	43918239	T	0.2114	-0.0485	0.0076	1.82E-10	0.2143	0.111	0.01578	1.96E-12	rs62054809:43918239:C:T
17_43918301_GCCAGGAGT	17	43918301	G	0.2115	-0.0475	0.0077	6.33E-10	0.2143	0.111	0.01578	1.95E-12	'9950:43918301:GCCAGGAGTTCGAGA:G
17_43918418_A_G	17	43918418	G	0.2114	-0.0485	0.0076	1.83E-10	0.2143	0.1111	0.01578	1.93E-12	rs112583797:43918418:A:G
17_43918524_A_G	17	43918524	G	0.2114	-0.0485	0.0076	1.84E-10	0.2143	0.1111	0.01578	1.91E-12	rs74922289:43918524:A:G
17_43918613_T_C	17	43918613	C	0.2123	-0.0482	0.0076	2.30E-10	0.2147	0.1116	0.01577	1.46E-12	rs56971664:43918613:T:C
17_43918651_C_G	17	43918651	G	0.2114	-0.0485	0.0076	1.85E-10	0.2143	0.1111	0.01578	1.90E-12	rs62054811:43918651:C:G
17_43919068_G_T	17	43919068	T	0.2096	-0.0483	0.0077	2.92E-10	0.212	0.1116	0.01588	2.12E-12	rs2316766:43919068:G:T
17_43919070_T_C	17	43919070	C	0.2096	-0.0483	0.0077	2.92E-10	0.212	0.1116	0.01588	2.12E-12	rs2316767:43919070:T:C
17_43919073_G_T	17	43919073	T	0.2096	-0.0483	0.0077	2.92E-10	0.212	0.1116	0.01588	2.12E-12	rs2316768:43919073:G:T
17_43919096_A_G	17	43919096	G	0.2109	-0.0486	0.0076	1.77E-10	0.2135	0.1114	0.0158	1.77E-12	rs2106786:43919096:A:G
17_43919105_C_T	17	43919105	T	0.2117	-0.0483	0.0076	2.34E-10	0.2138	0.1123	0.01578	1.11E-12	rs2106785:43919105:C:T

17_43919301_T_C	17	43919301	C	0.2122	-0.0482	0.0076	2.34E-10	0.2145	0.1122	0.01577	1.12E-12	rs56150806:43919301:T:C
17_43919884_T_G	17	43919884	G	0.2122	-0.0481	0.0076	2.55E-10	0.2146	0.1129	0.01575	7.51E-13	rs17690314:43919884:T:G
17_43920219_AAAG_A	17	43920219	A	0.2115	-0.0474	0.0077	6.43E-10	0.2142	0.1112	0.01577	1.77E-12	rs56166546:43920219:AAAG:A
17_43920300_T_C	17	43920300	C	0.2114	-0.0485	0.0076	1.82E-10	0.2143	0.1112	0.01577	1.75E-12	rs56233672:43920300:T:C
17_43920378_C_T	17	43920378	T	0.2114	-0.0485	0.0076	1.81E-10	0.2143	0.1112	0.01577	1.77E-12	rs56354807:43920378:C:T
17_43920411_T_C	17	43920411	C	0.2114	-0.0485	0.0076	1.81E-10	0.2143	0.1112	0.01577	1.78E-12	rs55718212:43920411:T:C
17_43920974_T_C	17	43920974	C	0.2122	-0.0482	0.0076	2.46E-10	0.2146	0.1118	0.01576	1.34E-12	rs17690326:43920974:T:C
17_43921210_G_T	17	43921210	T	0.2122	-0.048	0.0076	2.75E-10	0.2146	0.1122	0.01577	1.12E-12	rs17763596:43921210:G:T
17_43921572_T_A	17	43921572	A	0.2122	-0.0483	0.0076	2.24E-10	0.2146	0.1126	0.01575	8.89E-13	rs62054814:43921572:T:A
17_43921754_T_C	17	43921754	C	0.2122	-0.0482	0.0076	2.26E-10	0.2146	0.1142	0.01574	4.02E-13	rs17763634:43921754:T:C
17_43922942_T_C	17	43922942	C	0.2114	-0.0485	0.0076	1.83E-10	0.2143	0.1127	0.01576	8.51E-13	rs62621252:43922942:T:C
17_43923266_G_A	17	43923266	A	0.2122	-0.0482	0.0076	2.36E-10	0.2146	0.1148	0.01574	2.97E-13	rs62054815:43923266:G:A
17_43923654_G_C	17	43923654	C	0.2123	-0.048	0.0076	2.74E-10	0.2147	0.1144	0.01574	3.59E-13	rs12185233:43923654:G:C
17_43923683_A_G	17	43923683	G	0.2124	-0.0482	0.0076	2.32E-10	0.2147	0.1152	0.01574	2.51E-13	rs12185268:43923683:A:G
17_43923703_C_T	17	43923703	T	0.2118	-0.0481	0.0076	2.70E-10	0.2143	0.1155	0.01574	2.16E-13	rs12185235:43923703:C:T
17_43923934_T_C	17	43923934	C	0.2114	-0.0486	0.0076	1.77E-10	0.2144	0.1121	0.01578	1.18E-12	rs11079725:43923934:T:C
17_43924073_T_C	17	43924073	C	0.2122	-0.0483	0.0076	2.25E-10	0.2146	0.1121	0.01577	1.17E-12	rs12373123:43924073:T:C
17_43924130_G_A	17	43924130	A	0.2122	-0.0483	0.0076	2.22E-10	0.2146	0.1125	0.01577	9.76E-13	rs12373139:43924130:G:A
17_43924200_C_G	17	43924200	G	0.2122	-0.0482	0.0076	2.33E-10	0.2146	0.1129	0.01577	8.22E-13	rs12373142:43924200:C:G
17_43924219_T_C	17	43924219	C	0.2114	-0.0486	0.0076	1.74E-10	0.2144	0.1114	0.01578	1.64E-12	rs12373124:43924219:T:C
17_43924231_G_A	17	43924231	A	0.2114	-0.0486	0.0076	1.74E-10	0.2143	0.1114	0.01578	1.63E-12	rs12373140:43924231:G:A
17_43924337_A_C	17	43924337	C	0.2136	-0.0479	0.0076	2.67E-10	0.2155	0.1142	0.01574	4.07E-13	rs12373168:43924337:A:C
17_43924521_G_A	17	43924521	A	0.2122	-0.0483	0.0076	2.14E-10	0.2146	0.1122	0.01577	1.13E-12	rs17690661:43924521:G:A
17_43924776_C_T	17	43924776	T	0.2114	-0.0486	0.0076	1.70E-10	0.2143	0.1119	0.01578	1.34E-12	rs55943825:43924776:C:T
17_43924803_A_G	17	43924803	G	0.2121	-0.0482	0.0076	2.40E-10	0.2145	0.1118	0.01577	1.37E-12	rs17690679:43924803:A:G
17_43925297_C_T	17	43925297	T	0.2486	-0.042	0.0072	4.88E-09	0.2447	0.07938	0.01496	1.12E-07	rs17690703:43925297:C:T
17_43925605_G_A	17	43925605	A	0.2125	-0.0472	0.0076	5.06E-10	0.2148	0.1128	0.01574	7.83E-13	rs17769490:43925605:G:A
17_43925729_A_G	17	43925729	G	0.2122	-0.0478	0.0076	3.06E-10	0.2147	0.1123	0.01574	9.63E-13	rs77063768:43925729:A:G
17_43925966_G_A	17	43925966	A	0.2126	-0.0475	0.0076	3.95E-10	0.2149	0.1131	0.01574	6.63E-13	rs62054817:43925966:G:A
17_43926056_A_C	17	43926056	C	0.2126	-0.0474	0.0076	4.11E-10	0.2148	0.1128	0.01574	7.53E-13	rs62054818:43926056:A:C
17_43926149_A_G	17	43926149	G	0.2122	-0.0478	0.0076	3.05E-10	0.2147	0.1123	0.01574	9.64E-13	rs62054819:43926149:A:G
17_43926755_A_G	17	43926755	G	0.2122	-0.0478	0.0076	3.05E-10	0.2147	0.1124	0.01574	9.40E-13	rs62054820:43926755:A:G
17_43926948_A_G	17	43926948	G	0.2122	-0.0478	0.0076	3.06E-10	0.2147	0.1124	0.01574	9.35E-13	rs56113217:43926948:A:G
17_43926992_C_T	17	43926992	T	0.2122	-0.0478	0.0076	3.06E-10	0.2147	0.1124	0.01574	9.34E-13	rs56269136:43926992:C:T
17_43927255_G_T	17	43927255	T	0.2122	-0.0478	0.0076	3.07E-10	0.2147	0.1124	0.01574	9.26E-13	rs56385754:43927255:G:T
17_43927290_G_A	17	43927290	A	0.2082	-0.0465	0.0077	1.36E-09	0.2094	0.1103	0.01589	3.91E-12	rs17769552:43927290:G:A
17_43927708_A_G	17	43927708	G	0.2128	-0.0474	0.0076	4.33E-10	0.215	0.1122	0.01573	9.74E-13	rs62054822:43927708:A:G
17_43928614_T_G	17	43928614	G	0.2126	-0.0478	0.0076	3.14E-10	0.215	0.1117	0.01574	1.29E-12	rs885639:43928614:T:G
17_43928629_GCACA_G	17	43928629	G	0.2122	-0.0473	0.0077	7.59E-10	0.2148	0.1113	0.01577	1.69E-12	s143247888:43928629:GCACA:G
17_43929029_A_G	17	43929029	G	0.212	-0.0473	0.0076	5.12E-10	0.215	0.1129	0.01579	8.77E-13	rs62054823:43929029:A:G
17_43929992_C_T	17	43929992	T	0.2115	-0.0484	0.0076	2.07E-10	0.2143	0.1124	0.01578	1.08E-12	rs62054824:43929992:C:T
17_43930033_G_A	17	43930033	A	0.2115	-0.0482	0.0076	2.49E-10	0.2144	0.1125	0.01578	1.02E-12	rs62054825:43930033:G:A
17_43930238_C_A	17	43930238	A	0.2122	-0.0481	0.0076	2.53E-10	0.2145	0.1122	0.01577	1.13E-12	rs79589869:43930238:C:A
17_43930798_A_G	17	43930798	G	0.2115	-0.0483	0.0076	2.13E-10	0.2143	0.1122	0.01578	1.14E-12	rs2316769:43930798:A:G
17_43930955_G_A	17	43930955	A	0.2115	-0.0484	0.0076	2.09E-10	0.2143	0.1123	0.01578	1.13E-12	rs2873268:43930955:G:A
17_43930980_C_T	17	43930980	T	0.2115	-0.0484	0.0076	2.09E-10	0.2143	0.1123	0.01578	1.13E-12	rs4340365:43930980:C:T
17_43931122_C_T	17	43931122	T	0.2122	-0.0481	0.0076	2.63E-10	0.2146	0.1124	0.01577	1.04E-12	rs2873269:43931122:C:T
17_43931244_G_C	17	43931244	C	0.2115	-0.0484	0.0076	2.01E-10	0.2144	0.1122	0.01578	1.15E-12	rs56026128:43931244:G:C
17_43931245_G_A	17	43931245	A	0.2123	-0.0481	0.0076	2.48E-10	0.2146	0.1124	0.01577	1.04E-12	rs56329743:43931245:G:A
17_43931380_A_G	17	43931380	G	0.2122	-0.0481	0.0076	2.57E-10	0.2146	0.1126	0.01577	9.33E-13	rs56288604:43931380:A:G
17_43931626_T_C	17	43931626	C	0.2123	-0.0481	0.0076	2.49E-10	0.2147	0.1127	0.01577	8.90E-13	rs17690987:43931626:T:C
17_43931855_GAGAGAGAC	17	43931855	G	0.2141	-0.0472	0.0077	8.42E-10	0.2172	0.1115	0.01581	1.73E-12	17:43931855:GAGAGAGAC:G
17_43931907_C_A	17	43931907	A	0.2114	-0.0483	0.0076	2.33E-10	0.2142	0.1126	0.0158	1.04E-12	rs56146262:43931907:C:A
17_43932028_A_G	17	43932028	G	0.2115	-0.0484	0.0076	2.10E-10	0.2144	0.1119	0.0158	1.43E-12	rs55942528:43932028:A:G
17_43932049_C_T	17	43932049	T	0.2114	-0.0483	0.0076	2.28E-10	0.2143	0.1127	0.0158	9.95E-13	rs56254732:43932049:C:T

17_43932129_C_T	17	43932129	T	0.2121	-0.048	0.0076	2.96E-10	0.2145	0.1135	0.01579	6.56E-13	rs56323304:43932129:C:T
17_43932155_A_G	17	43932155	G	0.2115	-0.0483	0.0076	2.30E-10	0.2143	0.1127	0.0158	9.97E-13	rs55751924:43932155:A:G
17_43932173_A_G	17	43932173	G	0.2002	-0.0508	0.0079	1.39E-10	0.1976	0.1136	0.0163	3.15E-12	rs55660209:43932173:A:G
17_43932277_G_A	17	43932277	A	0.2115	-0.0483	0.0076	2.34E-10	0.2143	0.1127	0.0158	1.00E-12	rs113856644:43932277:G:A
17_43932381_C_T	17	43932381	T	0.2115	-0.0483	0.0076	2.37E-10	0.2143	0.1127	0.0158	1.01E-12	rs62054831:43932381:C:T
17_43932741_C_T	17	43932741	T	0.2081	-0.0463	0.0077	1.53E-09	0.2125	0.1112	0.01593	2.90E-12	rs4627402:43932741:C:T
17_43932789_C_T	17	43932789	T	0.1793	-0.0472	0.0084	1.62E-08	0.1781	0.1192	0.01743	8.15E-12	rs10445365:43932789:C:T
17_43932797_G_C	17	43932797	C	0.1793	-0.0472	0.0084	1.66E-08	0.1781	0.1192	0.01743	8.14E-12	rs10445366:43932797:G:C
17_43932798_G_T	17	43932798	T	0.1792	-0.0472	0.0084	1.63E-08	0.1781	0.1192	0.01743	8.15E-12	rs10445367:43932798:G:T
17_43933171_C_T	17	43933171	T	0.2086	-0.0476	0.0077	5.28E-10	0.2124	0.1077	0.01585	1.10E-11	rs10445368:43933171:C:T
17_43933190_GTTTTTA_G	17	43933190	G	0.2082	-0.0453	0.0077	4.66E-09	0.2126	0.1103	0.0159	4.09E-12	17:43933190:GTTTTTA:G
17_43933579_C_A	17	43933579	A	0.2087	-0.0477	0.0077	5.42E-10	0.2121	0.1138	0.01598	1.06E-12	rs62054832:43933579:C:A
17_43933673_T_C	17	43933673	C	0.2113	-0.0479	0.0076	3.16E-10	0.2147	0.1105	0.01582	2.86E-12	rs62054833:43933673:T:C
17_43933790_G_T	17	43933790	T	0.2087	-0.048	0.0077	4.03E-10	0.212	0.1119	0.01595	2.23E-12	rs142955985:43933790:G:T
17_43933802_G_T	17	43933802	T	0.2119	-0.0395	0.0082	1.45E-06	0.2159	0.09892	0.01712	7.64E-09	17:43933802:G:T
17_43933830_G_T	17	43933830	T	0.2075	-0.0483	0.0077	4.03E-10	0.211	0.1129	0.01601	1.76E-12	rs80209523:43933830:G:T
17_43933834_G_T	17	43933834	T	0.2075	-0.0483	0.0077	4.03E-10	0.211	0.1129	0.01601	1.76E-12	rs78993847:43933834:G:T
17_43933879_C_G	17	43933879	G	0.2109	-0.0478	0.0076	3.55E-10	0.2143	0.1112	0.01582	2.11E-12	rs76563578:43933879:C:G
17_43933956_G_GTGTTTGT	17	43933956	GTGTTTGTTTGTT	0.211	-0.0467	0.0077	1.20E-09	0.2144	0.1112	0.01582	2.11E-12	17:43933956:G:GTGTTTGTTTGTT
17_43934016_G_C	17	43934016	C	0.2109	-0.0478	0.0076	3.56E-10	0.2144	0.1112	0.01582	2.11E-12	rs111962225:43934016:G:C
17_43934116_T_G	17	43934116	G	0.2108	-0.0479	0.0076	3.31E-10	0.214	0.1113	0.01582	1.99E-12	rs113093579:43934116:T:G
17_43934314_T_C	17	43934314	C	0.2108	-0.0479	0.0076	3.34E-10	0.214	0.1113	0.01582	1.99E-12	rs62054834:43934314:T:C
17_43934587_GT_G	17	43934587	G	0.2111	-0.0467	0.0077	1.23E-09	0.2144	0.1111	0.01581	2.12E-12	rs112588484:43934587:GT:G
17_43934672_A_C	17	43934672	C	0.211	-0.0477	0.0076	3.67E-10	0.2144	0.1111	0.01581	2.12E-12	rs62054835:43934672:A:C
17_43934776_A_G	17	43934776	G	0.211	-0.0477	0.0076	3.68E-10	0.2144	0.1111	0.01581	2.13E-12	rs10445369:43934776:A:G
17_43934826_T_G	17	43934826	G	0.2111	-0.0477	0.0076	3.69E-10	0.2144	0.1111	0.01581	2.13E-12	rs10445334:43934826:T:G
17_43934896_T_A	17	43934896	A	0.2111	-0.0477	0.0076	3.70E-10	0.2144	0.1111	0.01581	2.13E-12	rs10445335:43934896:T:A
17_43934948_A_G	17	43934948	G	0.2111	-0.0477	0.0076	3.71E-10	0.2144	0.1111	0.01581	2.14E-12	rs10445336:43934948:A:G
17_43935118_G_A	17	43935118	A	0.2123	-0.0482	0.0076	2.30E-10	0.2148	0.112	0.01577	1.25E-12	rs10445370:43935118:G:A
17_43935888_C_T	17	43935888	T	0.2112	-0.0478	0.0076	3.55E-10	0.2145	0.1114	0.01581	1.87E-12	rs55996632:43935888:C:T
17_43936011_A_G	17	43936011	G	0.2123	-0.0483	0.0076	2.18E-10	0.2148	0.1122	0.01577	1.12E-12	rs55886302:43936011:A:G
17_43936298_C_A	17	43936298	A	0.2119	-0.0481	0.0076	2.61E-10	0.2147	0.1128	0.01577	8.62E-13	rs56136075:43936298:C:A
17_43936804_A_G	17	43936804	G	0.2119	-0.0481	0.0076	2.61E-10	0.2147	0.1128	0.01577	8.65E-13	rs62054839:43936804:A:G
17_43936812_G_A	17	43936812	A	0.2119	-0.0481	0.0076	2.61E-10	0.2147	0.1128	0.01577	8.65E-13	rs62054840:43936812:G:A
17_43937104_G_A	17	43937104	A	0.2119	-0.0481	0.0076	2.56E-10	0.2147	0.1128	0.01577	8.66E-13	rs62054841:43937104:G:A
17_43937162_C_T	17	43937162	T	0.2119	-0.0481	0.0076	2.55E-10	0.2147	0.1128	0.01577	8.67E-13	rs62054842:43937162:C:T
17_43937184_T_C	17	43937184	C	0.2124	-0.0482	0.0076	2.33E-10	0.2148	0.1115	0.01577	1.54E-12	rs62054843:43937184:T:C
17_43937333_T_G	17	43937333	G	0.2123	-0.0482	0.0076	2.25E-10	0.2148	0.1119	0.01577	1.32E-12	rs62054844:43937333:T:G
17_43937460_G_A	17	43937460	A	0.212	-0.0481	0.0076	2.46E-10	0.2147	0.1128	0.01578	8.68E-13	rs76627340:43937460:G:A
17_43937505_C_T	17	43937505	T	0.2124	-0.0482	0.0076	2.38E-10	0.2148	0.1121	0.01577	1.17E-12	rs75945623:43937505:C:T
17_43937633_A_G	17	43937633	G	0.2119	-0.0481	0.0076	2.55E-10	0.2147	0.1128	0.01578	8.69E-13	rs79889833:43937633:A:G
17_43937671_C_T	17	43937671	T	0.2123	-0.0482	0.0076	2.37E-10	0.2148	0.1119	0.01577	1.32E-12	rs77625338:43937671:C:T
17_43937736_C_T	17	43937736	T	0.2124	-0.0484	0.0076	1.97E-10	0.2148	0.1122	0.01577	1.10E-12	rs77489223:43937736:C:T
17_43938107_A_G	17	43938107	G	0.2123	-0.0483	0.0076	2.09E-10	0.2148	0.1116	0.01578	1.51E-12	rs55888391:43938107:A:G
17_43938394_A_G	17	43938394	G	0.2119	-0.0481	0.0076	2.55E-10	0.2147	0.1128	0.01578	8.73E-13	rs74872829:43938394:A:G
17_43938499_G_A	17	43938499	A	0.2119	-0.0481	0.0076	2.55E-10	0.2147	0.1128	0.01578	8.74E-13	rs76329216:43938499:G:A
17_43938634_A_G	17	43938634	G	0.2123	-0.0482	0.0076	2.34E-10	0.2148	0.1118	0.01577	1.33E-12	rs62054846:43938634:A:G
17_43938796_A_G	17	43938796	G	0.2124	-0.0484	0.0076	1.86E-10	0.2148	0.1121	0.01576	1.13E-12	rs55646970:43938796:A:G
17_43938882_G_A	17	43938882	A	0.2123	-0.0482	0.0076	2.26E-10	0.2148	0.1115	0.01577	1.54E-12	rs55673092:43938882:G:A
17_43939255_T_C	17	43939255	C	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.77E-13	rs56347602:43939255:T:C
17_43939389_C_T	17	43939389	T	0.212	-0.0481	0.0076	2.65E-10	0.2148	0.1121	0.01577	1.17E-12	rs56026524:43939389:C:T
17_43939395_A_T	17	43939395	T	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.78E-13	rs56100710:43939395:A:T
17_43939399_A_C	17	43939399	C	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.78E-13	rs56026232:43939399:A:C
17_43939432_G_T	17	43939432	T	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.78E-13	rs56249080:43939432:G:T
17_43939609_A_T	17	43939609	T	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.79E-13	rs56227067:43939609:A:T

17_43939638_G_A	17	43939638	A	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.79E-13	rs55719714:43939638:G:A
17_43939659_G_A	17	43939659	A	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.80E-13	rs56299858:43939659:G:A
17_43939936_G_A	17	43939936	A	0.2123	-0.0481	0.0076	2.46E-10	0.2148	0.1125	0.01577	9.73E-13	rs62054857:43939936:G:A
17_43940012_T_C	17	43940012	C	0.2115	-0.0487	0.0076	1.64E-10	0.2144	0.113	0.01579	8.20E-13	rs75210307:43940012:T:C
17_43940020_T_C	17	43940020	C	0.2115	-0.0487	0.0076	1.64E-10	0.2144	0.113	0.01579	8.20E-13	rs74944644:43940020:T:C
17_43940021_G_A	17	43940021	A	0.2115	-0.0487	0.0076	1.64E-10	0.2144	0.113	0.01579	8.20E-13	rs79412431:43940021:G:A
17_43940188_T_C	17	43940188	C	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.81E-13	rs62054858:43940188:T:C
17_43940497_C_T	17	43940497	T	0.2123	-0.0482	0.0076	2.28E-10	0.2148	0.1119	0.01577	1.31E-12	rs79406732:43940497:C:T
17_43940685_G_A	17	43940685	A	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.83E-13	rs62054859:43940685:G:A
17_43940825_G_C	17	43940825	C	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1128	0.01578	8.84E-13	rs62055460:43940825:G:C
17_43941350_C_T	17	43941350	T	0.2123	-0.0483	0.0076	2.08E-10	0.2148	0.1117	0.01577	1.44E-12	rs62055461:43941350:C:T
17_43941476_A_C	17	43941476	C	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1127	0.01578	8.88E-13	rs62055462:43941476:A:C
17_43941491_A_G	17	43941491	G	0.2123	-0.0483	0.0076	2.18E-10	0.2148	0.1115	0.01577	1.58E-12	rs62055463:43941491:A:G
17_43941608_C_G	17	43941608	G	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1127	0.01578	8.88E-13	rs77652965:43941608:C:G
17_43941710_C_T	17	43941710	T	0.2123	-0.0483	0.0076	2.20E-10	0.2148	0.1118	0.01577	1.35E-12	rs75690239:43941710:C:T
17_43941858_T_G	17	43941858	G	0.2123	-0.0483	0.0076	2.20E-10	0.2148	0.1118	0.01577	1.35E-12	rs62055464:43941858:T:G
17_43942046_T_A	17	43942046	A	0.2123	-0.0482	0.0076	2.23E-10	0.2148	0.1116	0.01577	1.49E-12	rs62055465:43942046:T:A
17_43942656_G_A	17	43942656	A	0.2123	-0.0483	0.0076	2.12E-10	0.2148	0.1116	0.01577	1.47E-12	rs62055466:43942656:G:A
17_43942820_T_C	17	43942820	C	0.2119	-0.0481	0.0076	2.53E-10	0.2147	0.1127	0.01578	9.01E-13	rs62055467:43942820:T:C
17_43943000_A_C	17	43943000	C	0.2119	-0.0481	0.0076	2.53E-10	0.2147	0.1127	0.01578	9.10E-13	rs62055468:43943000:A:C
17_43943655_A_C	17	43943655	C	0.2123	-0.0482	0.0076	2.23E-10	0.2148	0.1116	0.01577	1.47E-12	rs62055469:43943655:A:C
17_43943657_A_G	17	43943657	G	0.2123	-0.0482	0.0076	2.39E-10	0.2148	0.1113	0.01577	1.66E-12	rs62055470:43943657:A:G
17_43943755_T_C	17	43943755	C	0.2125	-0.0484	0.0076	1.86E-10	0.2154	0.1119	0.01577	1.24E-12	rs62055471:43943755:T:C
17_43943957_G_C	17	43943957	C	0.2123	-0.0482	0.0076	2.41E-10	0.2148	0.1118	0.01577	1.34E-12	rs56327054:43943957:G:C
17_43943974_C_T	17	43943974	T	0.2123	-0.0482	0.0076	2.33E-10	0.2148	0.1118	0.01577	1.35E-12	rs56036719:43943974:C:T
17_43944158_C_T	17	43944158	T	0.2119	-0.0481	0.0076	2.53E-10	0.2147	0.1127	0.01578	9.27E-13	rs55781174:43944158:C:T
17_43944204_T_C	17	43944204	C	0.2119	-0.0481	0.0076	2.53E-10	0.2147	0.1127	0.01578	9.26E-13	rs12150223:43944204:T:C
17_43944519_C_T	17	43944519	T	0.2123	-0.0483	0.0076	2.21E-10	0.2148	0.1119	0.01577	1.30E-12	rs12150516:43944519:C:T
17_43945106_T_C	17	43945106	C	0.2123	-0.0482	0.0076	2.27E-10	0.2148	0.1115	0.01577	1.54E-12	rs62055475:43945106:T:C
17_43945495_A_G	17	43945495	G	0.2119	-0.0481	0.0076	2.53E-10	0.2147	0.1127	0.01578	8.95E-13	rs62055476:43945495:A:G
17_43945687_C_A	17	43945687	A	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1127	0.01578	8.96E-13	rs62055477:43945687:C:A
17_43945855_G_A	17	43945855	A	0.2119	-0.0481	0.0076	2.54E-10	0.2147	0.1127	0.01578	8.98E-13	rs78637438:43945855:G:A
17_43945931_T_C	17	43945931	C	0.2125	-0.0478	0.0076	3.10E-10	0.2148	0.1133	0.01576	6.49E-13	rs2316771:43945931:T:C
17_43945938_C_T	17	43945938	T	0.2118	-0.0483	0.0076	2.17E-10	0.2142	0.1126	0.01578	9.67E-13	rs62055478:43945938:C:T
17_43946112_T_C	17	43946112	C	0.2123	-0.0484	0.0076	2.04E-10	0.2143	0.1125	0.01578	1.01E-12	rs1078830:43946112:T:C
17_43946223_G_A	17	43946223	A	0.2143	-0.0477	0.0076	3.02E-10	0.216	0.1156	0.01573	1.98E-13	rs753235:43946223:G:A
17_43946291_A_G	17	43946291	G	0.1955	-0.0501	0.008	3.42E-10	0.1963	0.1115	0.0166	1.83E-11	rs886249:43946291:A:G
17_43946318_T_C	17	43946318	C	0.212	-0.0483	0.0076	2.28E-10	0.2144	0.113	0.0158	8.63E-13	rs753236:43946318:T:C
17_43946423_A_C	17	43946423	C	0.2127	-0.047	0.0076	6.57E-10	0.2149	0.1132	0.01578	7.14E-13	rs2316772:43946423:A:C
17_43946536_C_T	17	43946536	T	0.212	-0.0482	0.0076	2.37E-10	0.2147	0.1128	0.01578	8.76E-13	rs2316773:43946536:C:T
17_43946642_T_C	17	43946642	C	0.2119	-0.0482	0.0076	2.45E-10	0.2147	0.1127	0.01578	8.98E-13	rs2316774:43946642:T:C
17_43946707_T_C	17	43946707	C	0.212	-0.0481	0.0076	2.52E-10	0.2147	0.1121	0.01578	1.22E-12	rs739643:43946707:T:C
17_43946838_C_A	17	43946838	A	0.2119	-0.0482	0.0076	2.40E-10	0.2146	0.1127	0.01578	8.99E-13	rs739642:43946838:C:A
17_43946875_C_T	17	43946875	T	0.2119	-0.0482	0.0076	2.40E-10	0.2146	0.1127	0.01578	8.99E-13	rs757055:43946875:C:T
17_43947171_G_A	17	43947171	A	0.2121	-0.0483	0.0076	2.13E-10	0.2148	0.1122	0.01578	1.13E-12	rs75676226:43947171:G:A
17_43947176_AC_A	17	43947176	A	0.2124	-0.0473	0.0077	7.30E-10	0.2147	0.1117	0.01577	1.41E-12	rs67983220:43947176:AC:A
17_43947488_A_G	17	43947488	G	0.2123	-0.0484	0.0076	2.04E-10	0.2147	0.1116	0.01577	1.48E-12	rs56398500:43947488:A:G
17_43947883_T_G	17	43947883	G	0.1959	-0.0484	0.008	1.81E-09	0.1993	0.1114	0.01678	3.13E-11	17:43947883:T:G
17_43947928_A_G	17	43947928	G	0.2119	-0.0482	0.0076	2.32E-10	0.2146	0.1128	0.01578	8.76E-13	rs56289364:43947928:A:G
17_43948040_C_T	17	43948040	T	0.212	-0.0482	0.0076	2.38E-10	0.2146	0.1128	0.01578	8.60E-13	rs62055483:43948040:C:T
17_43948159_G_A	17	43948159	A	0.2123	-0.0484	0.0076	2.00E-10	0.2147	0.1117	0.01577	1.45E-12	rs78238042:43948159:G:A
17_43948733_C_T	17	43948733	T	0.2119	-0.0483	0.0076	2.22E-10	0.2146	0.1126	0.01578	9.39E-13	rs55673340:43948733:C:T
17_43948977_G_A	17	43948977	A	0.2115	-0.0484	0.0076	2.08E-10	0.214	0.1123	0.01579	1.11E-12	rs55967721:43948977:G:A
17_43949008_C_T	17	43949008	T	0.2119	-0.0483	0.0076	2.21E-10	0.2146	0.1126	0.01578	9.41E-13	rs111644193:43949008:C:T
17_43949092_T_G	17	43949092	G	0.2119	-0.0483	0.0076	2.21E-10	0.2146	0.1126	0.01578	9.41E-13	rs62055486:43949092:T:G

17_43949342_G_A	17	43949342	A	0.2121	-0.0481	0.0076	2.60E-10	0.2149	0.112	0.01579	1.29E-12	rs34739559:43949342:G:A
17_43949448_C_A	17	43949448	A	0.2098	-0.0473	0.0076	6.02E-10	0.2142	0.1067	0.01585	1.69E-11	rs34097347:43949448:C:A
17_43949892_C_T	17	43949892	T	0.2119	-0.0483	0.0076	2.21E-10	0.2146	0.1127	0.01578	9.27E-13	rs2106784:43949892:C:T
17_43950195_T_C	17	43950195	C	0.2119	-0.0483	0.0076	2.22E-10	0.2146	0.1127	0.01578	9.17E-13	rs2158072:43950195:T:C
17_43950394_C_T	17	43950394	T	0.2119	-0.0483	0.0076	2.23E-10	0.2146	0.1127	0.01578	9.10E-13	rs62055488:43950394:C:T
17_43950441_C_A	17	43950441	A	0.2121	-0.0482	0.0076	2.40E-10	0.2147	0.1124	0.01578	1.06E-12	rs62055489:43950441:C:A
17_43950444_CA_C	17	43950444	C	0.2121	-0.0472	0.0077	7.47E-10	0.2146	0.1127	0.01578	9.09E-13	17:43950444:CA:C
17_43950533_A_G	17	43950533	G	0.2119	-0.0483	0.0076	2.23E-10	0.2146	0.1127	0.01578	9.06E-13	rs62055490:43950533:A:G
17_43950976_G_T	17	43950976	T	0.214	-0.0481	0.0076	2.19E-10	0.2152	0.1096	0.0157	2.89E-12	rs10491140:43950976:G:T
17_43951120_T_C	17	43951120	C	0.2123	-0.0485	0.0076	1.86E-10	0.2147	0.1117	0.01577	1.45E-12	rs62055491:43951120:T:C
17_43951220_T_G	17	43951220	G	0.2123	-0.0483	0.0076	2.08E-10	0.2147	0.1118	0.01577	1.38E-12	rs34416056:43951220:T:G
17_43951345_C_A	17	43951345	A	0.2123	-0.0483	0.0076	2.08E-10	0.2147	0.1114	0.01577	1.63E-12	rs62055492:43951345:C:A
17_43951599_CAGAT_C	17	43951599	C	0.2124	-0.0476	0.0077	5.29E-10	0.2147	0.1123	0.01577	1.10E-12	17:43951599:CAGAT:C
17_43951717_G_A	17	43951717	A	0.2123	-0.0483	0.0076	2.19E-10	0.2147	0.1122	0.01577	1.13E-12	rs2055794:43951717:G:A
17_43951995_C_T	17	43951995	T	0.212	-0.0482	0.0076	2.28E-10	0.2146	0.1127	0.01578	9.32E-13	rs2055795:43951995:C:T
17_43952191_A_T	17	43952191	T	0.2119	-0.0482	0.0076	2.28E-10	0.2146	0.1127	0.01578	9.13E-13	rs2055796:43952191:A:T
17_43952634_A_T	17	43952634	T	0.212	-0.0482	0.0076	2.32E-10	0.2146	0.1127	0.01578	9.13E-13	rs80348388:43952634:A:T
17_43952944_T_C	17	43952944	C	0.2123	-0.0482	0.0076	2.36E-10	0.2149	0.1116	0.01578	1.50E-12	rs62055493:43952944:T:C
17_43953016_C_T	17	43953016	T	0.2123	-0.0482	0.0076	2.36E-10	0.2149	0.1116	0.01578	1.50E-12	rs62055494:43953016:C:T
17_43953043_A_C	17	43953043	C	0.2123	-0.0482	0.0076	2.36E-10	0.2149	0.1116	0.01578	1.50E-12	rs62055495:43953043:A:C
17_43953170_C_T	17	43953170	T	0.2119	-0.0482	0.0076	2.34E-10	0.2146	0.1127	0.01578	9.13E-13	rs111321973:43953170:C:T
17_43953179_A_G	17	43953179	G	0.2121	-0.0482	0.0076	2.37E-10	0.2146	0.1128	0.01578	8.71E-13	rs140713557:43953179:A:G
17_43953240_CTATATA_C	17	43953240	C	0.2121	-0.0472	0.0077	7.81E-10	0.2146	0.1127	0.01578	9.13E-13	17:43953240:CTATATA:C
17_43953307_C_T	17	43953307	T	0.2123	-0.0483	0.0076	2.16E-10	0.2146	0.1116	0.01577	1.47E-12	rs62055496:43953307:C:T
17_43953529_A_G	17	43953529	G	0.2119	-0.0482	0.0076	2.35E-10	0.2145	0.1127	0.01578	9.13E-13	rs62055497:43953529:A:G
17_43953695_T_C	17	43953695	C	0.2119	-0.0482	0.0076	2.35E-10	0.2145	0.1127	0.01578	9.13E-13	rs2188888:43953695:T:C
17_43953707_C_T	17	43953707	T	0.2119	-0.0482	0.0076	2.35E-10	0.2145	0.1127	0.01578	9.13E-13	rs3919455:43953707:C:T
17_43953719_G_C	17	43953719	C	0.2119	-0.0482	0.0076	2.35E-10	0.2145	0.1127	0.01578	9.13E-13	rs2214258:43953719:G:C
17_43953814_G_A	17	43953814	A	0.2119	-0.0482	0.0076	2.35E-10	0.2145	0.1127	0.01578	9.12E-13	rs62055498:43953814:G:A
17_43953991_C_G	17	43953991	G	0.2123	-0.0483	0.0076	2.13E-10	0.2146	0.1115	0.01577	1.60E-12	rs62055499:43953991:C:G
17_43954134_G_A	17	43954134	A	0.2123	-0.0483	0.0076	2.16E-10	0.2146	0.1115	0.01577	1.57E-12	rs62055500:43954134:G:A
17_43954227_G_A	17	43954227	A	0.2123	-0.0483	0.0076	2.12E-10	0.2146	0.1116	0.01577	1.51E-12	rs62055501:43954227:G:A
17_43954284_G_A	17	43954284	A	0.2123	-0.0483	0.0076	2.14E-10	0.2146	0.1114	0.01577	1.60E-12	rs62055502:43954284:G:A
17_43954416_A_AC	17	43954416	AC	0.213	-0.0468	0.0077	1.00E-09	0.2158	0.1103	0.01575	2.42E-12	17:43954416:A:AC
17_43954686_G_A	17	43954686	A	0.2124	-0.0485	0.0076	1.80E-10	0.2146	0.1113	0.01577	1.68E-12	rs916793:43954686:G:A
17_43954982_TTCTCTTCCT	17	43954982	T	0.2121	-0.0472	0.0077	7.83E-10	0.2145	0.1127	0.01578	9.12E-13	17:43954982:TTCTCTTCCTCA:T
17_43955030_A_G	17	43955030	G	0.2123	-0.0481	0.0076	2.43E-10	0.2146	0.1117	0.01577	1.44E-12	rs4441322:43955030:A:G
17_43955093_T_C	17	43955093	C	0.2123	-0.0483	0.0076	2.17E-10	0.2146	0.1114	0.01577	1.66E-12	rs113414067:43955093:T:C
17_43955365_C_A	17	43955365	A	0.2123	-0.0483	0.0076	2.14E-10	0.2146	0.1117	0.01577	1.46E-12	rs55905252:43955365:C:A
17_43955487_C_T	17	43955487	T	0.2121	-0.0482	0.0076	2.27E-10	0.2148	0.1123	0.01578	1.11E-12	rs17691328:43955487:C:T
17_43956139_AAAAAT_AA	17	43956139	AAAAATAAAAT	0.213	-0.0475	0.0077	6.03E-10	0.2155	0.1113	0.01578	1.74E-12	:43956139:AAAAAT:AAAAATAAAAT
17_43956305_CTT_C	17	43956305	C	0.213	-0.0473	0.0077	7.28E-10	0.2156	0.1131	0.01578	7.56E-13	17:43956305:CTT:C
17_43956370_G_T	17	43956370	T	0.2118	-0.0481	0.0076	2.67E-10	0.2141	0.113	0.01579	8.02E-13	rs62055515:43956370:G:T
17_43956390_T_C	17	43956390	C	0.2118	-0.0481	0.0076	2.67E-10	0.2141	0.113	0.01579	8.02E-13	rs62055516:43956390:T:C
17_43956425_C_T	17	43956425	T	0.2118	-0.0481	0.0076	2.67E-10	0.2141	0.113	0.01579	8.02E-13	rs62055517:43956425:C:T
17_43956505_A_C	17	43956505	C	0.2119	-0.0482	0.0076	2.37E-10	0.2145	0.1127	0.01578	9.12E-13	rs62055518:43956505:A:C
17_43956642_T_C	17	43956642	C	0.2119	-0.0482	0.0076	2.38E-10	0.2145	0.1127	0.01578	9.12E-13	rs56364632:43956642:T:C
17_43956734_C_A	17	43956734	A	0.212	-0.0482	0.0076	2.36E-10	0.2146	0.112	0.01578	1.25E-12	rs55768605:43956734:C:A
17_43956778_A_G	17	43956778	G	0.2119	-0.0482	0.0076	2.38E-10	0.2145	0.1127	0.01578	9.11E-13	rs55653657:43956778:A:G
17_43957221_C_T	17	43957221	T	0.2119	-0.0482	0.0076	2.38E-10	0.2145	0.1127	0.01578	9.11E-13	rs55894109:43957221:C:T
17_43957269_T_C	17	43957269	C	0.2119	-0.0482	0.0076	2.38E-10	0.2145	0.1127	0.01578	9.11E-13	rs56101773:43957269:T:C
17_43957328_C_T	17	43957328	T	0.2119	-0.0482	0.0076	2.38E-10	0.2145	0.1127	0.01578	9.11E-13	rs56249780:43957328:C:T
17_43958079_C_T	17	43958079	T	0.2128	-0.0478	0.0076	3.07E-10	0.2158	0.1101	0.01574	2.63E-12	rs56040418:43958079:C:T
17_43958099_T_C	17	43958099	C	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.11E-13	rs55721252:43958099:T:C
17_43958139_A_C	17	43958139	C	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.11E-13	rs55876817:43958139:A:C

17_43958172_A_G	17	43958172	G	0.2121	-0.0481	0.0076	2.61E-10	0.2146	0.1123	0.01577	1.07E-12	rs55944735:43958172:A:G
17_43958207_C_CAAAAAA	17	43958207	CAAAAAAAT	0.2121	-0.0472	0.0077	7.86E-10	0.2145	0.1127	0.01578	9.11E-13	17:43958207:C:CAAAAAAAT
17_43958362_T_G	17	43958362	G	0.2163	-0.0462	0.0076	9.84E-10	0.2183	0.112	0.0157	9.68E-13	rs56356641:43958362:T:G
17_43958431_T_C	17	43958431	C	0.2123	-0.0482	0.0076	2.27E-10	0.2146	0.1116	0.01577	1.48E-12	rs55711631:43958431:T:C
17_43958736_G_A	17	43958736	A	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.11E-13	rs62055525:43958736:G:A
17_43958744_A_G	17	43958744	G	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.11E-13	rs112915466:43958744:A:G
17_43959092_G_T	17	43959092	T	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.10E-13	rs56343551:43959092:G:T
17_43959113_A_G	17	43959113	G	0.2119	-0.0482	0.0076	2.39E-10	0.2145	0.1127	0.01578	9.10E-13	rs55975673:43959113:A:G
17_43959261_G_A	17	43959261	A	0.2123	-0.0483	0.0076	2.07E-10	0.2146	0.1118	0.01577	1.36E-12	rs56387391:43959261:G:A
17_43959596_CT_C	17	43959596	C	0.2203	-0.0442	0.0076	7.31E-09	0.2281	0.1102	0.01566	1.97E-12	17:43959596:CT:C
17_43959661_G_A	17	43959661	A	0.2119	-0.0482	0.0076	2.40E-10	0.2145	0.1127	0.01578	9.10E-13	rs2019816:43959661:G:A
17_43959752_A_T	17	43959752	T	0.2119	-0.0482	0.0076	2.40E-10	0.2145	0.1127	0.01578	9.10E-13	rs2006305:43959752:A:T
17_43959918_T_A	17	43959918	A	0.2123	-0.0483	0.0076	2.22E-10	0.2145	0.1117	0.01577	1.45E-12	rs2019822:43959918:T:A
17_43960020_A_G	17	43960020	G	0.2123	-0.0483	0.0076	2.21E-10	0.2145	0.1116	0.01577	1.48E-12	rs62055529:43960020:A:G
17_43960172_C_T	17	43960172	T	0.2123	-0.0483	0.0076	2.07E-10	0.2145	0.1116	0.01577	1.51E-12	rs79580365:43960172:C:T
17_43960283_A_G	17	43960283	G	0.2123	-0.0483	0.0076	2.11E-10	0.2145	0.1117	0.01577	1.45E-12	rs55937610:43960283:A:G
17_43960323_A_G	17	43960323	G	0.2119	-0.0482	0.0076	2.40E-10	0.2144	0.1127	0.01578	9.10E-13	rs56365901:43960323:A:G
17_43960325_T_C	17	43960325	C	0.2119	-0.0482	0.0076	2.40E-10	0.2144	0.1127	0.01578	9.10E-13	rs55767267:43960325:T:C
17_43960341_G_A	17	43960341	A	0.2123	-0.0482	0.0076	2.39E-10	0.2148	0.1116	0.01578	1.51E-12	rs56127309:43960341:G:A
17_43960600_T_C	17	43960600	C	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.10E-13	rs56194412:43960600:T:C
17_43960812_A_T	17	43960812	T	0.2123	-0.0482	0.0076	2.29E-10	0.2145	0.1115	0.01577	1.53E-12	rs56338487:43960812:A:T
17_43960911_A_G	17	43960911	G	0.2123	-0.0481	0.0076	2.60E-10	0.215	0.1118	0.01577	1.35E-12	rs56180212:43960911:A:G
17_43960918_T_C	17	43960918	C	0.2123	-0.0484	0.0076	1.98E-10	0.2145	0.1114	0.01578	1.69E-12	rs56301449:43960918:T:C
17_43960997_T_C	17	43960997	C	0.2123	-0.0483	0.0076	2.05E-10	0.2145	0.1113	0.01578	1.75E-12	rs62055538:43960997:T:C
17_43961044_A_G	17	43961044	G	0.2123	-0.0482	0.0076	2.25E-10	0.2145	0.112	0.01577	1.24E-12	rs62055539:43961044:A:G
17_43961142_T_C	17	43961142	C	0.2123	-0.0481	0.0076	2.44E-10	0.2145	0.1116	0.01577	1.51E-12	rs62055540:43961142:T:C
17_43961292_G_T	17	43961292	T	0.2123	-0.0483	0.0076	2.12E-10	0.2145	0.1115	0.01577	1.57E-12	rs17770108:43961292:G:T
17_43961694_C_CT	17	43961694	CT	0.1361	-0.0536	0.0104	2.80E-07	0.1327	0.1344	0.02177	6.62E-10	17:43961694:C:CT
17_43961699_C_CT	17	43961699	CT	0.1361	-0.0536	0.0104	2.80E-07	0.1327	0.1344	0.02177	6.62E-10	17:43961699:C:CT
17_43961712_C_T	17	43961712	T	0.136	-0.0552	0.0104	1.04E-07	0.1327	0.1344	0.02177	6.61E-10	rs374039905:43961712:C:T
17_43961719_CTTTT_C	17	43961719	C	0.1361	-0.0536	0.0104	2.80E-07	0.1327	0.1344	0.02177	6.61E-10	17:43961719:CTTTT:C
17_43962017_G_C	17	43962017	C	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.09E-13	rs62055541:43962017:G:C
17_43962982_G_A	17	43962982	A	0.212	-0.0482	0.0076	2.42E-10	0.2144	0.1098	0.01577	3.35E-12	rs77426526:43962982:G:A
17_43963046_G_A	17	43963046	A	0.2123	-0.0483	0.0076	2.19E-10	0.2145	0.1117	0.01577	1.45E-12	rs77129180:43963046:G:A
17_43963120_C_T	17	43963120	T	0.2123	-0.0483	0.0076	2.06E-10	0.2145	0.1117	0.01577	1.45E-12	rs74863825:43963120:C:T
17_43963282_C_G	17	43963282	G	0.2123	-0.0483	0.0076	2.18E-10	0.2145	0.1119	0.01577	1.31E-12	rs80254317:43963282:C:G
17_43963416_C_G	17	43963416	G	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.09E-13	rs112425426:43963416:C:G
17_43963844_C_T	17	43963844	T	0.2123	-0.0482	0.0076	2.23E-10	0.2145	0.1117	0.01577	1.45E-12	rs62055542:43963844:C:T
17_43963943_C_A	17	43963943	A	0.2123	-0.0483	0.0076	2.05E-10	0.2145	0.1117	0.01577	1.45E-12	rs17770120:43963943:C:A
17_43964163_G_A	17	43964163	A	0.2123	-0.0483	0.0076	2.21E-10	0.2146	0.1116	0.01577	1.48E-12	rs17770150:43964163:G:A
17_43964191_C_A	17	43964191	A	0.2121	-0.0481	0.0076	2.53E-10	0.2144	0.1117	0.01578	1.49E-12	rs17770186:43964191:C:A
17_43964283_G_C	17	43964283	C	0.2122	-0.048	0.0076	2.79E-10	0.2145	0.1119	0.01577	1.33E-12	rs17691449:43964283:G:C
17_43964539_A_G	17	43964539	G	0.2124	-0.0479	0.0076	3.18E-10	0.2147	0.1129	0.01578	8.55E-13	rs62055544:43964539:A:G
17_43964561_C_T	17	43964561	T	0.2118	-0.0482	0.0076	2.49E-10	0.2143	0.1127	0.01579	9.47E-13	rs62055545:43964561:C:T
17_43964567_A_C	17	43964567	C	0.2118	-0.0482	0.0076	2.49E-10	0.2143	0.1127	0.01579	9.47E-13	rs62055546:43964567:A:C
17_43964755_C_T	17	43964755	T	0.2123	-0.0484	0.0076	2.04E-10	0.2145	0.1113	0.01577	1.68E-12	rs62055547:43964755:C:T
17_43964899_A_G	17	43964899	G	0.2123	-0.0483	0.0076	2.13E-10	0.2145	0.1114	0.01577	1.64E-12	rs62055548:43964899:A:G
17_43965063_T_C	17	43965063	C	0.2119	-0.0482	0.0076	2.38E-10	0.2144	0.1127	0.01578	9.08E-13	rs113327263:43965063:T:C
17_43965129_AT_A	17	43965129	A	0.2374	-0.0477	0.0076	3.23E-10	0.2431	0.1039	0.0156	2.73E-11	17:43965129:AT:A
17_43965429_TC_T	17	43965429	T	0.2125	-0.0473	0.0077	6.93E-10	0.2145	0.1115	0.01577	1.56E-12	17:43965429:TC:T
17_43965595_G_C	17	43965595	C	0.2123	-0.0483	0.0076	2.21E-10	0.2145	0.1116	0.01577	1.48E-12	rs62055549:43965595:G:C
17_43965680_G_A	17	43965680	A	0.2119	-0.0482	0.0076	2.39E-10	0.2144	0.1127	0.01578	9.08E-13	rs62055550:43965680:G:A
17_43965687_C_G	17	43965687	G	0.2123	-0.0483	0.0076	2.10E-10	0.2145	0.1113	0.01577	1.69E-12	rs62055551:43965687:C:G
17_43965955_A_G	17	43965955	G	0.2119	-0.0482	0.0076	2.39E-10	0.2144	0.1127	0.01578	9.08E-13	rs62055552:43965955:A:G
17_43966178_C_A	17	43966178	A	0.2119	-0.0482	0.0076	2.39E-10	0.2144	0.1127	0.01578	9.07E-13	rs62055553:43966178:C:A

17_43966260_A_G	17	43966260	G	0.2123	-0.0483	0.0076	2.12E-10	0.2145	0.1115	0.01577	1.55E-12	rs62055554:43966260:A:G
17_43966282_G_T	17	43966282	T	0.2125	-0.0484	0.0076	2.00E-10	0.2147	0.1116	0.01578	1.51E-12	rs62055555:43966282:G:T
17_43966608_A_T	17	43966608	T	0.2119	-0.0482	0.0076	2.37E-10	0.2144	0.1127	0.01578	9.09E-13	rs111941646:43966608:A:T
17_43966749_T_C	17	43966749	C	0.212	-0.0482	0.0076	2.36E-10	0.2144	0.1127	0.01578	9.10E-13	rs62055556:43966749:T:C
17_43966795_C_A	17	43966795	A	0.212	-0.0482	0.0076	2.36E-10	0.2144	0.1127	0.01578	9.10E-13	rs62055557:43966795:C:A
17_43966910_A_AAGG	17	43966910	AAGG	0.2119	-0.0474	0.0077	6.95E-10	0.2141	0.113	0.01578	8.20E-13	17:43966910:A:AAGG
17_43966955_A_G	17	43966955	G	0.212	-0.0482	0.0076	2.34E-10	0.2144	0.1127	0.01578	9.11E-13	rs62055558:43966955:A:G
17_43967138_T_G	17	43967138	G	0.2123	-0.0482	0.0076	2.25E-10	0.2144	0.1111	0.01579	2.00E-12	rs62055559:43967138:T:G
17_43967562_T_C	17	43967562	C	0.212	-0.0481	0.0076	2.72E-10	0.2142	0.1123	0.01579	1.12E-12	rs79193046:43967562:T:C
17_43968219_A_G	17	43968219	G	0.212	-0.0482	0.0076	2.34E-10	0.2143	0.1129	0.01578	8.35E-13	rs17691466:43968219:A:G
17_43968415_G_A	17	43968415	A	0.3317	-0.0309	0.0066	2.61E-06	0.3262	0.07981	0.01392	9.84E-09	rs7210728:43968415:G:A
17_43968463_C_G	17	43968463	G	0.2123	-0.0483	0.0076	2.07E-10	0.2144	0.1118	0.01577	1.38E-12	rs17691508:43968463:C:G
17_43968572_G_A	17	43968572	A	0.2124	-0.0483	0.0076	2.11E-10	0.2144	0.1122	0.01577	1.15E-12	rs62056760:43968572:G:A
17_43968718_T_TACACACA	17	43968718	TACACACAC	0.2121	-0.0472	0.0077	7.65E-10	0.2143	0.1129	0.01578	8.51E-13	40458370:43968718:T:TACACACAC
17_43968874_A_G	17	43968874	G	0.212	-0.0482	0.0076	2.38E-10	0.2143	0.1128	0.01578	8.62E-13	rs55943606:43968874:A:G
17_43968937_T_C	17	43968937	C	0.212	-0.0482	0.0076	2.38E-10	0.2143	0.1128	0.01578	8.66E-13	rs55895732:43968937:T:C
17_43968994_T_C	17	43968994	C	0.212	-0.0482	0.0076	2.39E-10	0.2144	0.1128	0.01578	8.70E-13	rs55960528:43968994:T:C
17_43969019_T_C	17	43969019	C	0.212	-0.0482	0.0076	2.39E-10	0.2143	0.1128	0.01578	8.72E-13	rs55877243:43969019:T:C
17_43969136_C_T	17	43969136	T	0.2118	-0.0482	0.0076	2.41E-10	0.2141	0.1128	0.01578	8.72E-13	rs17770296:43969136:C:T
17_43969168_T_A	17	43969168	A	0.2122	-0.0484	0.0076	2.00E-10	0.2142	0.1116	0.01578	1.49E-12	rs17691556:43969168:T:A
17_43969258_G_GC	17	43969258	GC	0.2124	-0.0472	0.0077	7.62E-10	0.2144	0.1117	0.01577	1.40E-12	17:43969258:G:GC
17_43969686_T_A	17	43969686	A	0.212	-0.0482	0.0076	2.40E-10	0.2144	0.1128	0.01578	8.89E-13	rs62056761:43969686:T:A
17_43969779_G_T	17	43969779	T	0.2123	-0.0485	0.0076	1.87E-10	0.2144	0.1116	0.01577	1.46E-12	rs17770337:43969779:G:T
17_43969833_A_G	17	43969833	G	0.212	-0.0482	0.0076	2.40E-10	0.2144	0.1127	0.01578	8.91E-13	rs62056773:43969833:A:G
17_43969901_G_A	17	43969901	A	0.212	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	8.91E-13	rs62056774:43969901:G:A
17_43969952_T_C	17	43969952	C	0.212	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	8.92E-13	rs62056775:43969952:T:C
17_43969995_C_T	17	43969995	T	0.212	-0.0482	0.0076	2.42E-10	0.2144	0.1127	0.01578	8.92E-13	rs62056776:43969995:C:T
17_43970012_C_CAG	17	43970012	CAG	0.2121	-0.0472	0.0077	7.82E-10	0.2144	0.1127	0.01578	8.92E-13	rs146712066:43970012:C:CAG
17_43970108_C_A	17	43970108	A	0.212	-0.0482	0.0076	2.43E-10	0.2144	0.1127	0.01578	8.93E-13	rs78729125:43970108:C:A
17_43970154_T_C	17	43970154	C	0.2123	-0.0483	0.0076	2.11E-10	0.2144	0.1116	0.01577	1.50E-12	rs17770343:43970154:T:C
17_43970303_G_A	17	43970303	A	0.212	-0.0482	0.0076	2.43E-10	0.2144	0.1127	0.01578	8.95E-13	rs62056777:43970303:G:A
17_43970662_G_T	17	43970662	T	0.2123	-0.0483	0.0076	2.05E-10	0.2144	0.1118	0.01577	1.40E-12	rs17691610:43970662:G:T
17_43971206_CTAATT_C	17	43971206	C	0.2121	-0.0472	0.0077	7.78E-10	0.2143	0.1127	0.01578	9.08E-13	17:43971206:CTAATT:C
17_43971238_T_TTAGATAC	17	43971238	TTAGATACATCA	0.2125	-0.0475	0.0077	5.97E-10	0.2148	0.112	0.01578	1.25E-12	3325961:43971238:T:TTAGATACATCA
17_43971457_G_C	17	43971457	C	0.212	-0.0482	0.0076	2.40E-10	0.2143	0.1127	0.01578	9.13E-13	rs76594404:43971457:G:C
17_43971481_T_C	17	43971481	C	0.212	-0.0482	0.0076	2.40E-10	0.2143	0.1127	0.01578	9.13E-13	rs80233201:43971481:T:C
17_43971604_C_G	17	43971604	G	0.212	-0.0482	0.0076	2.40E-10	0.2143	0.1127	0.01578	9.16E-13	rs62056778:43971604:C:G
17_43971785_A_G	17	43971785	G	0.212	-0.0482	0.0076	2.41E-10	0.2143	0.1127	0.01578	9.19E-13	rs11575895:43971785:A:G
17_43971937_C_A	17	43971937	A	0.212	-0.0482	0.0076	2.41E-10	0.2143	0.1127	0.01578	9.22E-13	rs62056779:43971937:C:A
17_43972025_TC_T	17	43972025	T	0.2121	-0.0471	0.0077	8.09E-10	0.2143	0.1126	0.01578	9.37E-13	rs144722105:43972025:TC:T
17_43972142_G_A	17	43972142	A	0.212	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.26E-13	rs11575896:43972142:G:A
17_43972581_C_T	17	43972581	T	0.212	-0.0482	0.0076	2.41E-10	0.2144	0.1126	0.01578	9.35E-13	rs74457229:43972581:C:T
17_43973080_A_G	17	43973080	G	0.2121	-0.0482	0.0076	2.42E-10	0.2144	0.1124	0.01578	1.02E-12	rs74548327:43973080:A:G
17_43973121_G_C	17	43973121	C	0.212	-0.0482	0.0076	2.41E-10	0.2144	0.1126	0.01578	9.45E-13	rs111972148:43973121:G:C
17_43973233_C_T	17	43973233	T	0.2123	-0.0483	0.0076	2.18E-10	0.2144	0.1118	0.01577	1.34E-12	rs76324150:43973233:C:T
17_43973408_C_T	17	43973408	T	0.2123	-0.0483	0.0076	2.18E-10	0.2144	0.1117	0.01577	1.39E-12	rs113347741:43973408:C:T
17_43973413_A_G	17	43973413	G	0.212	-0.0482	0.0076	2.41E-10	0.2143	0.1126	0.01578	9.47E-13	rs78720789:43973413:A:G
17_43973498_T_G	17	43973498	G	0.3318	-0.0304	0.0066	3.66E-06	0.3265	0.07969	0.01391	1.01E-08	rs4792891:43973498:T:G
17_43973652_C_T	17	43973652	T	0.212	-0.0482	0.0076	2.35E-10	0.2143	0.1126	0.01578	9.41E-13	rs62056780:43973652:C:T
17_43973899_T_C	17	43973899	C	0.212	-0.0482	0.0076	2.35E-10	0.2144	0.1126	0.01578	9.41E-13	rs62056781:43973899:T:C
17_43974065_C_A	17	43974065	A	0.2123	-0.0483	0.0076	2.15E-10	0.2144	0.112	0.01577	1.20E-12	rs74496580:43974065:C:A
17_43974230_C_T	17	43974230	T	0.2123	-0.0483	0.0076	2.17E-10	0.2144	0.1118	0.01577	1.36E-12	rs62056782:43974230:C:T
17_43974343_TCGC_T	17	43974343	T	0.2121	-0.0472	0.0077	7.60E-10	0.2144	0.1126	0.01578	9.53E-13	17:43974343:TCGC:T
17_43974354_G_A	17	43974354	A	0.212	-0.0482	0.0076	2.34E-10	0.2144	0.1126	0.01578	9.54E-13	rs113161176:43974354:G:A
17_43974476_G_T	17	43974476	T	0.2122	-0.0482	0.0076	2.36E-10	0.2145	0.1118	0.01578	1.34E-12	rs80346216:43974476:G:T

17_43974477_A_T	17	43974477	T	0.2122	-0.0482	0.0076	2.36E-10	0.2145	0.1118	0.01578	1.34E-12	rs76632685:43974477:A:T
17_43974549_G_C	17	43974549	C	0.212	-0.0482	0.0076	2.34E-10	0.2144	0.1125	0.01578	9.75E-13	rs62056783:43974549:G:C
17_43974889_C_G	17	43974889	G	0.2123	-0.0482	0.0076	2.37E-10	0.2145	0.1115	0.01577	1.58E-12	rs62056784:43974889:C:G
17_43975263_T_C	17	43975263	C	0.2124	-0.0483	0.0076	2.11E-10	0.2145	0.1112	0.01577	1.77E-12	rs62056785:43975263:T:C
17_43975285_T_C	17	43975285	C	0.212	-0.0482	0.0076	2.37E-10	0.2144	0.1125	0.01578	1.01E-12	rs62056786:43975285:T:C
17_43975360_ATTACTGTAT	17	43975360	A	0.2125	-0.0472	0.0077	7.93E-10	0.2147	0.1129	0.01578	8.36E-13	5:43975360:ATTACTGTATAAGCTGCTTATAT:A
17_43975382_T_A	17	43975382	A	0.1774	-0.05	0.0086	5.84E-09	0.1802	0.1276	0.01801	1.37E-12	rs62056788:43975382:T:A
17_43975415_A_C	17	43975415	C	0.212	-0.0482	0.0076	2.39E-10	0.2144	0.1125	0.01578	1.01E-12	rs62056789:43975415:A:C
17_43975417_G_A	17	43975417	A	0.212	-0.0482	0.0076	2.39E-10	0.2144	0.1125	0.01578	1.01E-12	rs62056790:43975417:G:A
17_43976064_T_C	17	43976064	C	0.2123	-0.0485	0.0076	1.86E-10	0.2145	0.111	0.01577	1.92E-12	rs62056791:43976064:T:C
17_43976627_G_T	17	43976627	T	0.2119	-0.0481	0.0076	2.52E-10	0.2144	0.1124	0.01578	1.06E-12	rs77561671:43976627:G:T
17_43976644_G_A	17	43976644	A	0.2119	-0.0481	0.0076	2.52E-10	0.2144	0.1124	0.01578	1.06E-12	rs62056792:43976644:G:A
17_43976684_T_C	17	43976684	C	0.3317	-0.0306	0.0066	3.27E-06	0.3261	0.07972	0.01392	1.02E-08	rs9303523:43976684:T:C
17_43977018_A_G	17	43977018	G	0.2123	-0.0482	0.0076	2.22E-10	0.2145	0.1115	0.01577	1.55E-12	rs62056793:43977018:A:G
17_43977049_A_G	17	43977049	G	0.2123	-0.0483	0.0076	2.19E-10	0.2145	0.1114	0.01577	1.62E-12	rs62056794:43977049:A:G
17_43977702_C_T	17	43977702	T	0.2123	-0.0483	0.0076	2.06E-10	0.2145	0.1117	0.01577	1.40E-12	rs1864324:43977702:C:T
17_43977748_G_GGCTGGC	17	43977748	GGCTGGCCCATA	0.2119	-0.0472	0.0077	7.62E-10	0.2143	0.112	0.01579	1.32E-12	17:43977748:G:GGCTGGCCCATA
17_43977827_C_T	17	43977827	T	0.2123	-0.0482	0.0076	2.34E-10	0.2145	0.1115	0.01577	1.56E-12	rs1864325:43977827:C:T
17_43977846_T_G	17	43977846	G	0.3318	-0.0308	0.0066	2.80E-06	0.3261	0.08001	0.01392	9.06E-09	rs28646281:43977846:T:G
17_43978041_C_T	17	43978041	T	0.2123	-0.0483	0.0076	2.18E-10	0.2145	0.1115	0.01577	1.56E-12	rs62056795:43978041:C:T
17_43978120_A_G	17	43978120	G	0.2123	-0.0483	0.0076	2.13E-10	0.2145	0.1114	0.01577	1.62E-12	rs62056796:43978120:A:G
17_43978295_G_C	17	43978295	C	0.2119	-0.0481	0.0076	2.53E-10	0.2144	0.1125	0.01578	9.89E-13	rs55691306:43978295:G:C
17_43978306_G_A	17	43978306	A	0.2119	-0.0481	0.0076	2.53E-10	0.2144	0.1125	0.01578	9.89E-13	rs56306380:43978306:G:A
17_43978308_T_C	17	43978308	C	0.2119	-0.0481	0.0076	2.53E-10	0.2144	0.1125	0.01578	9.89E-13	rs55841786:43978308:T:C
17_43978320_G_A	17	43978320	A	0.2123	-0.0482	0.0076	2.23E-10	0.2145	0.1115	0.01577	1.56E-12	rs55823844:43978320:G:A
17_43978534_G_A	17	43978534	A	0.2123	-0.0481	0.0076	2.44E-10	0.2145	0.1118	0.01577	1.35E-12	rs1560310:43978534:G:A
17_43978604_A_G	17	43978604	G	0.2123	-0.0483	0.0076	2.18E-10	0.2145	0.1116	0.01577	1.50E-12	rs1467962:43978604:A:G
17_43978625_T_C	17	43978625	C	0.2119	-0.0481	0.0076	2.53E-10	0.2144	0.1126	0.01578	9.39E-13	rs1560311:43978625:T:C
17_43978934_T_G	17	43978934	G	0.2123	-0.0483	0.0076	2.21E-10	0.2145	0.1113	0.01577	1.69E-12	rs1467963:43978934:T:G
17_43978988_A_G	17	43978988	G	0.3317	-0.0307	0.0066	2.99E-06	0.3261	0.08029	0.01392	8.08E-09	rs1560312:43978988:A:G
17_43979468_T_A	17	43979468	A	0.2119	-0.0481	0.0076	2.49E-10	0.2144	0.1126	0.01578	9.38E-13	rs62056800:43979468:T:A
17_43979504_G_A	17	43979504	A	0.2119	-0.0481	0.0076	2.48E-10	0.2144	0.1126	0.01578	9.38E-13	rs62056801:43979504:G:A
17_43979622_G_A	17	43979622	A	0.2119	-0.0481	0.0076	2.47E-10	0.2144	0.1126	0.01578	9.38E-13	rs113834264:43979622:G:A
17_43979822_A_T	17	43979822	T	0.2123	-0.0485	0.0076	1.85E-10	0.2145	0.111	0.01577	1.94E-12	rs2099151:43979822:A:T
17_43979971_C_T	17	43979971	T	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1127	0.01578	9.23E-13	rs2082068:43979971:C:T
17_43980530_A_C	17	43980530	C	0.2123	-0.0483	0.0076	2.07E-10	0.2145	0.1113	0.01577	1.70E-12	rs1984937:43980530:A:C
17_43980762_A_G	17	43980762	G	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.69E-13	rs62056802:43980762:A:G
17_43980998_G_A	17	43980998	A	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.69E-13	rs112003140:43980998:G:A
17_43981103_C_A	17	43981103	A	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.68E-13	rs111689007:43981103:C:A
17_43981795_G_A	17	43981795	A	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.68E-13	rs113589236:43981795:G:A
17_43981831_A_T	17	43981831	T	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.68E-13	rs113029914:43981831:A:T
17_43981958_C_T	17	43981958	T	0.2121	-0.0484	0.0076	2.03E-10	0.2144	0.1121	0.01578	1.17E-12	rs112275277:43981958:C:T
17_43982062_CTT_C	17	43982062	C	0.2121	-0.0472	0.0077	8.01E-10	0.2144	0.1128	0.01578	8.68E-13	rs372550912:43982062:CTT:C
17_43982069_T_G	17	43982069	G	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.68E-13	rs367820416:43982069:T:G
17_43982159_A_G	17	43982159	G	0.2123	-0.0484	0.0076	2.03E-10	0.2145	0.1116	0.01577	1.46E-12	rs62056803:43982159:A:G
17_43982286_C_T	17	43982286	T	0.2123	-0.0483	0.0076	2.17E-10	0.2145	0.1116	0.01577	1.48E-12	rs62056804:43982286:C:T
17_43982903_A_G	17	43982903	G	0.2123	-0.0483	0.0076	2.08E-10	0.2145	0.1115	0.01577	1.56E-12	rs77084869:43982903:A:G
17_43982961_T_C	17	43982961	C	0.2125	-0.0483	0.0076	1.97E-10	0.2145	0.1107	0.01576	2.18E-12	rs74573628:43982961:T:C
17_43983159_T_C	17	43983159	C	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1128	0.01578	8.67E-13	rs75617973:43983159:T:C
17_43983363_G_A	17	43983363	A	0.2123	-0.0484	0.0076	1.92E-10	0.2145	0.1114	0.01577	1.61E-12	rs62056805:43983363:G:A
17_43983801_A_G	17	43983801	G	0.2123	-0.0483	0.0076	2.10E-10	0.2145	0.1119	0.01577	1.32E-12	rs62056806:43983801:A:G
17_43984253_G_C	17	43984253	C	0.2123	-0.0484	0.0076	2.02E-10	0.2145	0.1118	0.01577	1.39E-12	rs62056807:43984253:G:C
17_43984399_C_T	17	43984399	T	0.2123	-0.0483	0.0076	2.07E-10	0.2145	0.1117	0.01577	1.39E-12	rs1467966:43984399:C:T
17_43984646_T_C	17	43984646	C	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1129	0.01578	8.31E-13	rs62056808:43984646:T:C
17_43984669_A_G	17	43984669	G	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1129	0.01578	8.28E-13	rs62056809:43984669:A:G

17_43984672_T_C	17	43984672	C	0.2119	-0.0481	0.0076	2.46E-10	0.2144	0.1129	0.01578	8.28E-13	rs62056810:43984672:T:C
17_43984864_C_T	17	43984864	T	0.2123	-0.0483	0.0076	2.07E-10	0.2145	0.1119	0.01577	1.27E-12	rs79492906:43984864:C:T
17_43985247_C_T	17	43985247	T	0.2121	-0.0482	0.0076	2.44E-10	0.2146	0.1129	0.01577	8.27E-13	rs62056811:43985247:C:T
17_43985597_C_T	17	43985597	T	0.2123	-0.0481	0.0076	2.61E-10	0.2145	0.1117	0.01577	1.41E-12	rs74509629:43985597:C:T
17_43985662_T_C	17	43985662	C	0.2123	-0.0483	0.0076	2.06E-10	0.2145	0.1118	0.01577	1.33E-12	rs79290980:43985662:T:C
17_43986396_C_T	17	43986396	T	0.2123	-0.0482	0.0076	2.27E-10	0.2145	0.112	0.01577	1.25E-12	rs1467968:43986396:C:T
17_43986420_A_G	17	43986420	G	0.2119	-0.0481	0.0076	2.52E-10	0.2144	0.1129	0.01578	8.46E-13	rs4371195:43986420:A:G
17_43986432_G_A	17	43986432	A	0.2119	-0.0481	0.0076	2.52E-10	0.2144	0.1128	0.01578	8.70E-13	rs12150125:43986432:G:A
17_43986462_A_G	17	43986462	G	0.2124	-0.0484	0.0076	2.01E-10	0.2145	0.111	0.01577	1.94E-12	rs12150527:43986462:A:G
17_43986992_G_C	17	43986992	C	0.2119	-0.0481	0.0076	2.50E-10	0.2144	0.1127	0.01578	9.32E-13	rs7502888:43986992:G:C
17_43987154_G_A	17	43987154	A	0.2119	-0.0481	0.0076	2.50E-10	0.2144	0.1127	0.01578	9.32E-13	rs62056812:43987154:G:A
17_43987184_T_C	17	43987184	C	0.2119	-0.0481	0.0076	2.50E-10	0.2144	0.1127	0.01578	9.32E-13	rs111447859:43987184:T:C
17_43987723_G_A	17	43987723	A	0.2121	-0.0496	0.0076	7.20E-11	0.2144	0.111	0.01578	1.99E-12	rs28439143:43987723:G:A
17_43987801_T_C	17	43987801	C	0.2112	-0.0481	0.0076	2.78E-10	0.2137	0.1138	0.01584	6.83E-13	rs56189701:43987801:T:C
17_43988205_A_G	17	43988205	G	0.2156	-0.0489	0.0076	1.10E-10	0.2189	0.1114	0.01572	1.42E-12	rs2435204:43988205:A:G
17_43988623_G_A	17	43988623	A	0.2125	-0.0481	0.0076	2.51E-10	0.215	0.1116	0.01577	1.46E-12	rs62056835:43988623:G:A
17_43988884_T_C	17	43988884	C	0.2119	-0.0482	0.0076	2.39E-10	0.2144	0.1127	0.01578	9.31E-13	rs62056837:43988884:T:C
17_43989087_A_G	17	43989087	G	0.2119	-0.0482	0.0076	2.38E-10	0.2144	0.1127	0.01578	9.31E-13	rs62056838:43989087:A:G
17_43989129_CA_C	17	43989129	C	0.2121	-0.0472	0.0077	7.78E-10	0.2144	0.1127	0.01578	9.31E-13	rs66760063:43989129:CA:C
17_43989149_A_AAC	17	43989149	AAC	0.2121	-0.0472	0.0077	7.78E-10	0.2144	0.1127	0.01578	9.31E-13	rs199995459:43989149:A:AAC
17_43989151_A_AC	17	43989151	AC	0.2126	-0.0467	0.0077	1.05E-09	0.2145	0.1116	0.01576	1.47E-12	17:43989151:A:AC
17_43989159_G_GC	17	43989159	GC	0.2121	-0.0472	0.0077	7.78E-10	0.2144	0.1127	0.01578	9.31E-13	17:43989159:G:GC
17_43989221_T_C	17	43989221	C	0.2123	-0.0483	0.0076	2.04E-10	0.2145	0.1116	0.01577	1.47E-12	rs62056839:43989221:T:C
17_43989509_TA_T	17	43989509	T	0.2121	-0.0472	0.0077	7.81E-10	0.2144	0.1127	0.01578	9.30E-13	17:43989509:TA:T
17_43989689_T_C	17	43989689	C	0.2119	-0.0482	0.0076	2.40E-10	0.2144	0.1127	0.01578	9.30E-13	rs62056840:43989689:T:C
17_43989898_T_G	17	43989898	G	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.30E-13	rs112116311:43989898:T:G
17_43989909_A_G	17	43989909	G	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.30E-13	rs78209533:43989909:A:G
17_43990041_A_C	17	43990041	C	0.2119	-0.0482	0.0076	2.41E-10	0.2144	0.1127	0.01578	9.30E-13	rs62056841:43990041:A:C
17_43990072_A_G	17	43990072	G	0.2119	-0.0482	0.0076	2.41E-10	0.2145	0.1127	0.01578	9.30E-13	rs79860128:43990072:A:G
17_43990662_G_A	17	43990662	A	0.212	-0.0483	0.0076	2.24E-10	0.2145	0.113	0.01578	7.95E-13	rs9944484:43990662:G:A
17_43990919_A_G	17	43990919	G	0.2123	-0.0483	0.0076	2.10E-10	0.2146	0.1114	0.01577	1.60E-12	rs17563965:43990919:A:G
17_43991252_AC_A	17	43991252	A	0.2121	-0.0472	0.0077	7.97E-10	0.2145	0.1127	0.01578	9.30E-13	17:43991252:AC:A
17_43991272_A_G	17	43991272	G	0.2123	-0.0483	0.0076	2.08E-10	0.2146	0.1115	0.01577	1.55E-12	rs17563986:43991272:A:G
17_43991468_T_TA	17	43991468	TA	0.2125	-0.0474	0.0077	6.56E-10	0.2145	0.1119	0.01577	1.28E-12	17:43991468:T:TA
17_43991515_T_G	17	43991515	G	0.2107	-0.0483	0.0076	2.47E-10	0.2128	0.1121	0.01582	1.37E-12	17:43991515:T:G
17_43991553_A_G	17	43991553	G	0.3278	-0.032	0.0066	1.27E-06	0.3232	0.07917	0.01399	1.52E-08	17:43991553:A:G
17_43991781_G_T	17	43991781	T	0.2124	-0.0482	0.0076	2.36E-10	0.2146	0.1117	0.01577	1.39E-12	rs17564020:43991781:G:T
17_43991888_G_A	17	43991888	A	0.2124	-0.0482	0.0076	2.28E-10	0.2146	0.1114	0.01577	1.60E-12	rs55682376:43991888:G:A
17_43992233_C_T	17	43992233	T	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1127	0.01578	9.32E-13	rs55788678:43992233:C:T
17_43992244_G_A	17	43992244	A	0.2119	-0.0481	0.0076	2.46E-10	0.2145	0.1126	0.01578	9.48E-13	rs56042957:43992244:G:A
17_43992283_A_G	17	43992283	G	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1127	0.01578	9.32E-13	rs55810795:43992283:A:G
17_43992305_G_A	17	43992305	A	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1127	0.01578	9.32E-13	rs55933304:43992305:G:A
17_43992456_G_A	17	43992456	A	0.2123	-0.0483	0.0076	2.07E-10	0.2146	0.1118	0.01577	1.36E-12	rs62056848:43992456:G:A
17_43992463_G_C	17	43992463	C	0.2123	-0.0483	0.0076	2.19E-10	0.2146	0.1114	0.01577	1.62E-12	rs62056849:43992463:G:C
17_43992581_C_T	17	43992581	T	0.2127	-0.0484	0.0076	1.97E-10	0.2148	0.1115	0.01576	1.51E-12	rs62056850:43992581:C:T
17_43992806_A_G	17	43992806	G	0.2119	-0.0481	0.0076	2.48E-10	0.2145	0.1126	0.01578	9.36E-13	rs62056851:43992806:A:G
17_43992939_T_C	17	43992939	C	0.2119	-0.0481	0.0076	2.48E-10	0.2145	0.1126	0.01578	9.37E-13	rs62056856:43992939:T:C
17_43992943_G_A	17	43992943	A	0.3279	-0.0325	0.0066	8.97E-07	0.3234	0.07989	0.01399	1.12E-08	rs9899833:43992943:G:A
17_43994252_T_C	17	43994252	C	0.2137	-0.0471	0.0076	5.70E-10	0.2157	0.1138	0.01577	5.32E-13	rs77926909:43994252:T:C
17_43994358_C_T	17	43994358	T	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1126	0.01578	9.57E-13	rs111541901:43994358:C:T
17_43994386_C_A	17	43994386	A	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1126	0.01578	9.58E-13	rs17649518:43994386:C:A
17_43994435_A_G	17	43994435	G	0.2119	-0.0482	0.0076	2.43E-10	0.2145	0.1126	0.01578	9.58E-13	rs62056859:43994435:A:G
17_43994508_GAGA_G	17	43994508	G	0.2121	-0.0472	0.0077	7.88E-10	0.2145	0.1126	0.01578	9.59E-13	17:43994508:GAGA:G
17_43994623_G_A	17	43994623	A	0.2123	-0.0485	0.0076	1.76E-10	0.2146	0.1117	0.01577	1.45E-12	rs112647192:43994623:G:A
17_43994648_C_T	17	43994648	T	0.2128	-0.0487	0.0076	1.50E-10	0.2152	0.112	0.01576	1.18E-12	rs17649553:43994648:C:T

17_43994952_A_G	17	43994952	G	0.2123	-0.0483	0.0076	2.15E-10	0.2146	0.1115	0.01577	1.59E-12	rs17649571:43994952:A:G
17_43995098_G_A	17	43995098	A	0.2124	-0.0484	0.0076	2.02E-10	0.2146	0.1116	0.01577	1.46E-12	rs17564153:43995098:G:A
17_43995139_TTTTTTTTTTT	17	43995139	T	0.2121	-0.0472	0.0077	7.73E-10	0.2145	0.1125	0.01578	1.00E-12	0326647:43995139:TTTTTTTTTTC:T
17_43995990_A_G	17	43995990	G	0.2119	-0.0482	0.0076	2.36E-10	0.2145	0.1125	0.01578	1.00E-12	rs17649635:43995990:A:G
17_43996430_TA_T	17	43996430	T	0.2376	-0.0428	0.0076	1.60E-08	0.2419	0.09604	0.01568	9.11E-10	rs370497097:43996430:TA:T
17_43996716_GC_G	17	43996716	G	0.2121	-0.0472	0.0077	7.50E-10	0.2145	0.1125	0.01578	1.01E-12	17:43996716:GC:G
17_43996721_C_G	17	43996721	G	0.2119	-0.0483	0.0076	2.20E-10	0.2145	0.1124	0.01578	1.05E-12	17:43996721:C:G
17_43996908_T_G	17	43996908	G	0.212	-0.0482	0.0076	2.30E-10	0.2145	0.1125	0.01578	1.01E-12	rs55760800:43996908:T:G
17_43996960_A_G	17	43996960	G	0.2123	-0.0484	0.0076	1.93E-10	0.2146	0.1115	0.01577	1.53E-12	rs56303672:43996960:A:G
17_43997372_T_C	17	43997372	C	0.2123	-0.0484	0.0076	1.96E-10	0.2146	0.1115	0.01577	1.58E-12	rs17649641:43997372:T:C
17_43997499_A_T	17	43997499	T	0.212	-0.0482	0.0076	2.30E-10	0.2145	0.1125	0.01578	1.01E-12	rs75046472:43997499:A:T
17_43997520_C_T	17	43997520	T	0.2137	-0.0469	0.0076	6.68E-10	0.2161	0.1129	0.01575	7.64E-13	rs17564223:43997520:C:T
17_43997901_G_C	17	43997901	C	0.2123	-0.0478	0.0076	3.14E-10	0.2151	0.1118	0.01577	1.34E-12	rs17649700:43997901:G:C
17_43998151_C_T	17	43998151	T	0.2123	-0.0483	0.0076	2.20E-10	0.2146	0.112	0.01577	1.26E-12	rs62058962:43998151:C:T
17_43998328_C_T	17	43998328	T	0.2123	-0.0485	0.0076	1.87E-10	0.2146	0.1112	0.01577	1.74E-12	rs1467969:43998328:C:T
17_43998574_T_G	17	43998574	G	0.2123	-0.0482	0.0076	2.27E-10	0.2146	0.1116	0.01577	1.49E-12	rs1467970:43998574:T:G
17_43998767_T_C	17	43998767	C	0.2125	-0.0484	0.0076	1.86E-10	0.2146	0.1114	0.01577	1.64E-12	rs767058:43998767:T:C
17_43998822_A_G	17	43998822	G	0.2123	-0.0482	0.0076	2.33E-10	0.2146	0.1113	0.01577	1.67E-12	rs767057:43998822:A:G
17_43998910_C_T	17	43998910	T	0.2123	-0.0484	0.0076	1.93E-10	0.2146	0.1116	0.01577	1.47E-12	rs767056:43998910:C:T
17_43999100_G_C	17	43999100	C	0.2119	-0.0483	0.0076	2.21E-10	0.2145	0.1125	0.01578	1.02E-12	rs767059:43999100:G:C
17_43999406_A_G	17	43999406	G	0.2124	-0.0484	0.0076	1.88E-10	0.2146	0.1112	0.01577	1.75E-12	rs62058964:43999406:A:G
17_43999529_G_C	17	43999529	C	0.212	-0.0483	0.0076	2.18E-10	0.2145	0.1125	0.01578	1.02E-12	rs62058965:43999529:G:C
17_43999785_C_G	17	43999785	G	0.2123	-0.0484	0.0076	1.87E-10	0.2146	0.1113	0.01577	1.69E-12	rs1967981:43999785:C:G
17_43999793_G_A	17	43999793	A	0.212	-0.0483	0.0076	2.14E-10	0.2145	0.1125	0.01578	1.02E-12	rs1476127:43999793:G:A
17_44000202_G_A	17	44000202	A	0.212	-0.0483	0.0076	2.08E-10	0.2145	0.1123	0.01577	1.06E-12	rs55929431:44000202:G:A
17_44000234_A_T	17	44000234	T	0.2123	-0.0484	0.0076	1.93E-10	0.2146	0.1115	0.01577	1.54E-12	rs8079501:44000234:A:T
17_44000505_C_T	17	44000505	T	0.2123	-0.0484	0.0076	1.91E-10	0.2146	0.1115	0.01577	1.56E-12	rs56002706:44000505:C:T
17_44000610_G_A	17	44000610	A	0.212	-0.0483	0.0076	2.13E-10	0.2145	0.1124	0.01578	1.03E-12	rs8078495:44000610:G:A
17_44000914_T_C	17	44000914	C	0.2123	-0.0486	0.0076	1.71E-10	0.2146	0.1113	0.01577	1.67E-12	rs17649866:44000914:T:C
17_44001228_G_A	17	44001228	A	0.2124	-0.0485	0.0076	1.79E-10	0.2146	0.1114	0.01577	1.59E-12	rs62058968:44001228:G:A
17_44001379_C_T	17	44001379	T	0.2123	-0.0484	0.0076	1.99E-10	0.2148	0.1113	0.01577	1.72E-12	rs17564493:44001379:C:T
17_44001549_G_GC	17	44001549	GC	0.2121	-0.0473	0.0077	6.83E-10	0.2145	0.1123	0.01578	1.08E-12	17:44001549:G:GC
17_44001621_A_G	17	44001621	G	0.2123	-0.0485	0.0076	1.86E-10	0.2146	0.1113	0.01577	1.70E-12	rs17649918:44001621:A:G
17_44001661_A_G	17	44001661	G	0.2123	-0.0484	0.0076	1.88E-10	0.2146	0.1113	0.01577	1.69E-12	rs17649954:44001661:A:G
17_44001957_T_G	17	44001957	G	0.212	-0.0483	0.0076	2.11E-10	0.2145	0.1123	0.01578	1.08E-12	rs55685451:44001957:T:G
17_44002062_A_C	17	44002062	C	0.2123	-0.0485	0.0076	1.86E-10	0.2146	0.1114	0.01577	1.62E-12	rs17564591:44002062:A:C
17_44002138_A_G	17	44002138	G	0.2123	-0.0484	0.0076	2.00E-10	0.2146	0.1113	0.01578	1.70E-12	rs17564619:44002138:A:G
17_44002431_C_T	17	44002431	T	0.2123	-0.0485	0.0076	1.83E-10	0.2146	0.1117	0.01577	1.40E-12	rs62059003:44002431:C:T
17_44002555_A_G	17	44002555	G	0.212	-0.0484	0.0076	2.05E-10	0.2145	0.1123	0.01578	1.08E-12	rs17650063:44002555:A:G
17_44002595_C_T	17	44002595	T	0.212	-0.0483	0.0076	2.10E-10	0.2145	0.1123	0.01578	1.08E-12	rs17564703:44002595:C:T
17_44002969_A_C	17	44002969	C	0.2123	-0.0485	0.0076	1.86E-10	0.2146	0.1113	0.01577	1.69E-12	rs76090253:44002969:A:C
17_44003133_A_AAAG	17	44003133	AAAG	0.2121	-0.0474	0.0077	6.78E-10	0.2145	0.1123	0.01578	1.08E-12	rs147319425:44003133:A:AAAG
17_44003397_T_A	17	44003397	A	0.212	-0.0483	0.0076	2.10E-10	0.2145	0.1123	0.01578	1.08E-12	rs55788597:44003397:T:A
17_44003446_A_G	17	44003446	G	0.212	-0.0483	0.0076	2.10E-10	0.2145	0.1123	0.01578	1.08E-12	rs56197117:44003446:A:G
17_44003580_GA_G	17	44003580	G	0.2121	-0.0474	0.0077	6.78E-10	0.2145	0.1123	0.01578	1.08E-12	rs371618052:44003580:GA:G
17_44003599_C_T	17	44003599	T	0.212	-0.0483	0.0076	2.10E-10	0.2145	0.1123	0.01578	1.08E-12	rs56249311:44003599:C:T
17_44003625_T_TAA	17	44003625	TAA	0.2121	-0.0474	0.0077	6.78E-10	0.2145	0.1123	0.01578	1.08E-12	rs137941099:44003625:T:TAA
17_44003893_A_G	17	44003893	G	0.212	-0.0483	0.0076	2.10E-10	0.2146	0.1123	0.01578	1.08E-12	rs62059004:44003893:A:G
17_44004076_T_C	17	44004076	C	0.2123	-0.0484	0.0076	2.00E-10	0.2146	0.1116	0.01577	1.51E-12	rs76500077:44004076:T:C
17_44004472_A_G	17	44004472	G	0.212	-0.0483	0.0076	2.10E-10	0.2146	0.1123	0.01578	1.08E-12	rs62059005:44004472:A:G
17_44005186_G_A	17	44005186	A	0.2133	-0.048	0.0076	2.63E-10	0.2168	0.1099	0.01575	2.96E-12	rs113313477:44005186:G:A
17_44005226_A_C	17	44005226	C	0.2133	-0.048	0.0076	2.63E-10	0.2168	0.1099	0.01575	2.96E-12	rs112439933:44005226:A:C
17_44005254_T_A	17	44005254	A	0.2133	-0.048	0.0076	2.63E-10	0.2168	0.1099	0.01575	2.96E-12	rs113796169:44005254:T:A
17_44005329_G_A	17	44005329	A	0.2133	-0.048	0.0076	2.63E-10	0.2168	0.1099	0.01575	2.96E-12	rs112454267:44005329:G:A
17_44005361_G_A	17	44005361	A	0.2133	-0.048	0.0076	2.63E-10	0.2168	0.1099	0.01575	2.96E-12	rs112166495:44005361:G:A

17_44005413_A_G	17	44005413	G	0.2133	-0.048	0.0076	2.61E-10	0.2168	0.1099	0.01575	2.96E-12	rs17564780:44005413:A:G
17_44005615_A_G	17	44005615	G	0.2123	-0.0484	0.0076	1.92E-10	0.2147	0.1113	0.01577	1.70E-12	rs62059007:44005615:A:G
17_44006085_A_G	17	44006085	G	0.2124	-0.0484	0.0076	1.97E-10	0.215	0.112	0.01577	1.25E-12	rs62059008:44006085:A:G
17_44006130_T_C	17	44006130	C	0.212	-0.0483	0.0076	2.13E-10	0.2146	0.1124	0.01578	1.06E-12	rs62059009:44006130:T:C
17_44006252_T_C	17	44006252	C	0.212	-0.0483	0.0076	2.13E-10	0.2146	0.1124	0.01578	1.05E-12	rs62061705:44006252:T:C
17_44006453_CT_CTT	17	44006453	CTT	0.2122	-0.0472	0.0077	7.66E-10	0.2149	0.1128	0.01578	8.86E-13	17:44006453:CT:CTT
17_44006601_T_C	17	44006601	C	0.212	-0.0483	0.0076	2.15E-10	0.2146	0.1124	0.01578	1.04E-12	rs17564829:44006601:T:C
17_44006896_T_C	17	44006896	C	0.2123	-0.0484	0.0076	1.90E-10	0.2147	0.1116	0.01577	1.46E-12	rs62061706:44006896:T:C
17_44006954_T_C	17	44006954	C	0.2123	-0.0484	0.0076	1.89E-10	0.2147	0.1118	0.01577	1.34E-12	rs62061707:44006954:T:C
17_44006956_A_G	17	44006956	G	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1124	0.01578	1.03E-12	rs62061708:44006956:A:G
17_44007493_C_T	17	44007493	T	0.2123	-0.0484	0.0076	1.96E-10	0.2147	0.1114	0.01577	1.60E-12	rs62061709:44007493:C:T
17_44007727_C_T	17	44007727	T	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1123	0.01578	1.07E-12	rs62061710:44007727:C:T
17_44007764_T_C	17	44007764	C	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1123	0.01578	1.07E-12	rs62061711:44007764:T:C
17_44007773_CAAAA_C	17	44007773	C	0.2124	-0.0478	0.0077	4.67E-10	0.2149	0.1133	0.01577	6.76E-13	17:44007773:CAAAA:C
17_44007785_A_G	17	44007785	G	0.211	-0.0479	0.0076	3.35E-10	0.2133	0.112	0.01583	1.49E-12	17:44007785:A:G
17_44009456_GA_GAA	17	44009456	GAA	0.2151	-0.0457	0.0077	2.80E-09	0.2172	0.1128	0.01579	9.13E-13	rs57389672:44009456:GA:GAA
17_44009876_C_A	17	44009876	A	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1123	0.01578	1.08E-12	rs62061712:44009876:C:A
17_44009921_A_G	17	44009921	G	0.212	-0.0483	0.0076	2.17E-10	0.2146	0.1123	0.01578	1.08E-12	rs7501759:44009921:A:G
17_44010040_A_G	17	44010040	G	0.2124	-0.0485	0.0076	1.78E-10	0.2147	0.1116	0.01577	1.49E-12	rs2316782:44010040:A:G
17_44010118_G_C	17	44010118	C	0.2123	-0.0485	0.0076	1.85E-10	0.2147	0.1115	0.01577	1.55E-12	rs2316783:44010118:G:C
17_44010364_C_G	17	44010364	G	0.212	-0.0483	0.0076	2.18E-10	0.2146	0.1124	0.01578	1.07E-12	rs4255816:44010364:C:G
17_44010405_A_G	17	44010405	G	0.212	-0.0483	0.0076	2.19E-10	0.2146	0.1124	0.01578	1.07E-12	rs62061713:44010405:A:G
17_44010452_C_A	17	44010452	A	0.2121	-0.0482	0.0076	2.37E-10	0.2147	0.1126	0.01577	9.44E-13	rs62061714:44010452:C:A
17_44010463_A_AC	17	44010463	AC	0.2121	-0.0473	0.0077	6.83E-10	0.2146	0.1124	0.01578	1.07E-12	rs200924217:44010463:A:AC
17_44010661_A_G	17	44010661	G	0.212	-0.0483	0.0076	2.20E-10	0.2146	0.1124	0.01578	1.06E-12	rs113952577:44010661:A:G
17_44010984_G_A	17	44010984	A	0.212	-0.0483	0.0076	2.22E-10	0.2146	0.1124	0.01578	1.05E-12	rs78077519:44010984:G:A
17_44011018_A_G	17	44011018	G	0.2123	-0.0484	0.0076	1.93E-10	0.2147	0.1111	0.01577	1.89E-12	rs17564871:44011018:A:G
17_44011073_G_A	17	44011073	A	0.2124	-0.0483	0.0076	2.11E-10	0.2147	0.1115	0.01577	1.58E-12	rs17650258:44011073:G:A
17_44011526_A_G	17	44011526	G	0.2119	-0.0483	0.0076	2.19E-10	0.2146	0.1124	0.01578	1.05E-12	rs62061715:44011526:A:G
17_44011749_A_G	17	44011749	G	0.2119	-0.0483	0.0076	2.18E-10	0.2146	0.1124	0.01578	1.05E-12	rs17564948:44011749:A:G
17_44011825_A_C	17	44011825	C	0.2123	-0.0483	0.0076	2.08E-10	0.2147	0.1114	0.01577	1.61E-12	rs17564983:44011825:A:C
17_44012096_A_G	17	44012096	G	0.2123	-0.0485	0.0076	1.79E-10	0.2147	0.1114	0.01577	1.61E-12	rs62061716:44012096:A:G
17_44012248_T_A	17	44012248	A	0.2123	-0.0484	0.0076	1.96E-10	0.2147	0.1116	0.01577	1.51E-12	rs62061717:44012248:T:A
17_44012257_CG_C	17	44012257	C	0.2129	-0.0473	0.0077	7.21E-10	0.2149	0.1125	0.01578	1.02E-12	rs66755419:44012257:CG:C
17_44012260_T_C	17	44012260	C	0.2119	-0.0483	0.0076	2.17E-10	0.2146	0.1124	0.01578	1.05E-12	17:44012260:T:C
17_44012343_G_A	17	44012343	A	0.2124	-0.0484	0.0076	1.88E-10	0.2147	0.1116	0.01577	1.47E-12	rs17650335:44012343:G:A
17_44012463_T_C	17	44012463	C	0.2128	-0.0486	0.0076	1.67E-10	0.2155	0.1118	0.01576	1.32E-12	rs17565025:44012463:T:C
17_44012915_T_C	17	44012915	C	0.2124	-0.0485	0.0076	1.70E-10	0.2147	0.1113	0.01577	1.65E-12	rs77924424:44012915:T:C
17_44012989_C_T	17	44012989	T	0.2119	-0.0483	0.0076	2.17E-10	0.2146	0.1124	0.01578	1.05E-12	rs62061719:44012989:C:T
17_44013024_T_C	17	44013024	C	0.2124	-0.0485	0.0076	1.83E-10	0.2147	0.1115	0.01577	1.53E-12	rs17650381:44013024:T:C
17_44013103_G_T	17	44013103	T	0.2123	-0.0484	0.0076	1.99E-10	0.2147	0.1117	0.01577	1.39E-12	rs17650417:44013103:G:T
17_44013189_C_T	17	44013189	T	0.2123	-0.0485	0.0076	1.73E-10	0.2147	0.1117	0.01577	1.45E-12	rs62061720:44013189:C:T
17_44013346_T_C	17	44013346	C	0.2123	-0.0485	0.0076	1.83E-10	0.2147	0.1115	0.01577	1.53E-12	rs62061721:44013346:T:C
17_44013475_G_A	17	44013475	A	0.212	-0.0483	0.0076	2.13E-10	0.2146	0.1123	0.01578	1.08E-12	rs79857651:44013475:G:A
17_44013483_A_G	17	44013483	G	0.2123	-0.0485	0.0076	1.87E-10	0.2147	0.1114	0.01577	1.60E-12	rs113756354:44013483:A:G
17_44013938_A_G	17	44013938	G	0.2123	-0.0485	0.0076	1.87E-10	0.2147	0.1112	0.01577	1.77E-12	rs12150111:44013938:A:G
17_44013964_T_TC	17	44013964	TC	0.2116	-0.0472	0.0077	8.08E-10	0.214	0.1128	0.01579	9.25E-13	rs55939347:44013964:T:TC
17_44013966_T_C	17	44013966	C	0.1907	-0.0509	0.0082	5.16E-10	0.1957	0.1202	0.017	1.50E-12	17:44013966:T:C
17_44014137_G_T	17	44014137	T	0.2123	-0.0485	0.0076	1.87E-10	0.2147	0.1116	0.01577	1.51E-12	rs12150460:44014137:G:T
17_44014263_T_C	17	44014263	C	0.2123	-0.0485	0.0076	1.87E-10	0.2147	0.1113	0.01577	1.68E-12	rs12150195:44014263:T:C
17_44014384_G_A	17	44014384	A	0.2123	-0.0485	0.0076	1.87E-10	0.2147	0.1116	0.01577	1.46E-12	rs55874169:44014384:G:A
17_44014981_G_T	17	44014981	T	0.2117	-0.0482	0.0076	2.46E-10	0.2144	0.1124	0.01579	1.06E-12	rs62061723:44014981:G:T
17_44014982_G_T	17	44014982	T	0.2117	-0.0482	0.0076	2.46E-10	0.2144	0.1124	0.01579	1.06E-12	rs62061724:44014982:G:T
17_44015446_A_G	17	44015446	G	0.2123	-0.0484	0.0076	1.89E-10	0.2146	0.1113	0.01577	1.71E-12	rs12150229:44015446:A:G
17_44015464_A_G	17	44015464	G	0.2119	-0.0483	0.0076	2.20E-10	0.2145	0.1123	0.01578	1.08E-12	rs12150230:44015464:A:G

17_44015624_G_A	17	44015624	A	0.2119	-0.0482	0.0076	2.29E-10	0.2144	0.1123	0.01578	1.10E-12	rs12150576:44015624:G:A
17_44015745_A_G	17	44015745	G	0.2123	-0.0484	0.0076	1.95E-10	0.2146	0.1116	0.01577	1.49E-12	rs12150235:44015745:A:G
17_44015816_A_G	17	44015816	G	0.2119	-0.0483	0.0076	2.20E-10	0.2145	0.1123	0.01578	1.08E-12	rs12150242:44015816:A:G
17_44015929_G_A	17	44015929	A	0.2123	-0.0485	0.0076	1.78E-10	0.2146	0.1113	0.01577	1.70E-12	rs12150104:44015929:G:A
17_44016011_A_AT	17	44016011	AT	0.2121	-0.0473	0.0077	6.99E-10	0.2145	0.1123	0.01578	1.08E-12	17:44016011:A:AT
17_44016157_G_C	17	44016157	C	0.2119	-0.0483	0.0076	2.19E-10	0.2145	0.1123	0.01578	1.09E-12	rs62061725:44016157:G:C
17_44016341_G_A	17	44016341	A	0.212	-0.0483	0.0076	2.15E-10	0.2145	0.1123	0.01577	1.10E-12	rs62061726:44016341:G:A
17_44016462_A_G	17	44016462	G	0.2119	-0.0483	0.0076	2.20E-10	0.2145	0.1123	0.01577	1.10E-12	rs113537106:44016462:A:G
17_44016601_A_AG	17	44016601	AG	0.2121	-0.0473	0.0077	7.01E-10	0.2144	0.1123	0.01577	1.10E-12	17:44016601:A:AG
17_44017124_G_T	17	44017124	T	0.2123	-0.0484	0.0076	1.92E-10	0.2145	0.1115	0.01576	1.54E-12	rs62061727:44017124:G:T
17_44017180_T_G	17	44017180	G	0.2123	-0.0484	0.0076	1.99E-10	0.2145	0.1116	0.01576	1.46E-12	rs62061728:44017180:T:G
17_44017283_A_G	17	44017283	G	0.2123	-0.0484	0.0076	1.91E-10	0.2145	0.1114	0.01576	1.60E-12	rs62061729:44017283:A:G
17_44017342_A_G	17	44017342	G	0.2123	-0.0484	0.0076	1.93E-10	0.2145	0.1112	0.01576	1.71E-12	rs62061730:44017342:A:G
17_44017666_C_A	17	44017666	A	0.2123	-0.0481	0.0076	2.57E-10	0.2146	0.1112	0.01576	1.74E-12	rs62061731:44017666:C:A
17_44017941_G_T	17	44017941	T	0.2123	-0.0483	0.0076	2.22E-10	0.2145	0.111	0.01576	1.83E-12	rs62061732:44017941:G:T
17_44018399_A_G	17	44018399	G	0.216	-0.0492	0.0076	8.50E-11	0.217	0.1076	0.01566	6.48E-12	rs62061733:44018399:A:G
17_44018488_T_C	17	44018488	C	0.2103	-0.0526	0.0077	7.90E-12	0.2123	0.111	0.01588	2.71E-12	rs62061734:44018488:T:C
17_44018519_T_C	17	44018519	C	0.2138	-0.0487	0.0076	1.97E-10	0.2174	0.1096	0.01579	3.88E-12	rs7210219:44018519:T:C
17_44019103_T_G	17	44019103	G	0.2639	-0.0447	0.0076	4.95E-09	0.2657	0.1144	0.0159	6.12E-13	17:44019103:T:G
17_44019107_T_G	17	44019107	G	0.2154	-0.0463	0.0076	1.32E-09	0.2174	0.1111	0.01582	2.21E-12	rs111825734:44019107:T:G
17_44019479_C_G	17	44019479	G	0.2123	-0.0483	0.0076	2.10E-10	0.2145	0.1108	0.01574	1.91E-12	rs62062768:44019479:C:G
17_44019643_G_A	17	44019643	A	0.2123	-0.0485	0.0076	1.82E-10	0.2145	0.1103	0.01575	2.53E-12	rs62062769:44019643:G:A
17_44019680_T_C	17	44019680	C	0.2119	-0.0482	0.0076	2.31E-10	0.2144	0.1116	0.01575	1.38E-12	rs62062770:44019680:T:C
17_44020282_G_A	17	44020282	A	0.2119	-0.0482	0.0076	2.31E-10	0.2144	0.1117	0.01575	1.36E-12	rs62062771:44020282:G:A
17_44020314_C_T	17	44020314	T	0.2119	-0.0482	0.0076	2.31E-10	0.2144	0.1117	0.01575	1.36E-12	rs62062772:44020314:C:T
17_44020545_A_G	17	44020545	G	0.2119	-0.0482	0.0076	2.31E-10	0.2144	0.1117	0.01576	1.35E-12	rs62062773:44020545:A:G
17_44021061_C_T	17	44021061	T	0.2123	-0.0484	0.0076	1.91E-10	0.2144	0.1106	0.01575	2.20E-12	rs79115768:44021061:C:T
17_44021218_C_T	17	44021218	T	0.2123	-0.0483	0.0076	2.16E-10	0.2145	0.1108	0.01575	2.04E-12	rs28416808:44021218:C:T
17_44021463_T_C	17	44021463	C	0.2123	-0.0484	0.0076	2.04E-10	0.2144	0.1105	0.01575	2.30E-12	rs62062774:44021463:T:C
17_44021699_G_T	17	44021699	T	0.2123	-0.0484	0.0076	1.95E-10	0.2145	0.1104	0.01575	2.40E-12	rs2316784:44021699:G:T
17_44021717_G_A	17	44021717	A	0.2119	-0.0481	0.0076	2.50E-10	0.2144	0.1118	0.01576	1.30E-12	rs4327091:44021717:G:A
17_44021744_T_C	17	44021744	C	0.2119	-0.0482	0.0076	2.30E-10	0.2144	0.1117	0.01576	1.33E-12	rs4479290:44021744:T:C
17_44022043_A_C	17	44022043	C	0.2123	-0.0485	0.0076	1.89E-10	0.2144	0.111	0.01575	1.84E-12	rs62062776:44022043:A:C
17_44022068_G_A	17	44022068	A	0.2123	-0.0484	0.0076	1.91E-10	0.2144	0.111	0.01575	1.83E-12	rs62062777:44022068:G:A
17_44022319_G_A	17	44022319	A	0.2123	-0.0484	0.0076	2.01E-10	0.2144	0.1108	0.01575	1.99E-12	rs75839508:44022319:G:A
17_44022376_C_T	17	44022376	T	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1118	0.01576	1.30E-12	rs75686108:44022376:C:T
17_44022433_T_C	17	44022433	C	0.2123	-0.0484	0.0076	2.01E-10	0.2144	0.1105	0.01575	2.26E-12	rs79765413:44022433:T:C
17_44022434_G_A	17	44022434	A	0.2123	-0.0484	0.0076	2.05E-10	0.2144	0.1109	0.01575	1.93E-12	rs78834738:44022434:G:A
17_44022528_A_G	17	44022528	G	0.2123	-0.0484	0.0076	1.92E-10	0.2144	0.1104	0.01575	2.43E-12	rs62062778:44022528:A:G
17_44022577_A_C	17	44022577	C	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1118	0.01576	1.30E-12	rs62062779:44022577:A:C
17_44022593_C_T	17	44022593	T	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1118	0.01576	1.30E-12	rs62062780:44022593:C:T
17_44022632_G_A	17	44022632	A	0.2123	-0.0484	0.0076	1.99E-10	0.2144	0.1106	0.01575	2.17E-12	rs62062781:44022632:G:A
17_44023087_G_A	17	44023087	A	0.2119	-0.0482	0.0076	2.40E-10	0.2143	0.1118	0.01576	1.29E-12	rs62062782:44023087:G:A
17_44023520_T_G	17	44023520	G	0.2123	-0.0483	0.0076	2.08E-10	0.2144	0.1105	0.01576	2.30E-12	rs62062783:44023520:T:G
17_44023828_C_CGTG	17	44023828	CGTG	0.212	-0.0473	0.0077	7.10E-10	0.2143	0.1119	0.01576	1.26E-12	rs34232924:44023828:C:CGTG
17_44023842_G_A	17	44023842	A	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1119	0.01576	1.26E-12	rs35163442:44023842:G:A
17_44024552_C_G	17	44024552	G	0.2123	-0.0486	0.0076	1.69E-10	0.2144	0.1107	0.01576	2.10E-12	rs62062784:44024552:C:G
17_44024562_G_T	17	44024562	T	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1119	0.01576	1.23E-12	rs62062785:44024562:G:T
17_44024660_G_C	17	44024660	C	0.2136	-0.0482	0.0076	2.25E-10	0.2188	0.1113	0.01576	1.64E-12	rs62062786:44024660:G:C
17_44024749_CT_C	17	44024749	C	0.2647	-0.0426	0.0076	2.04E-08	0.2634	0.1085	0.0156	3.51E-12	17:44024749:CT:C
17_44024865_T_C	17	44024865	C	0.2119	-0.0482	0.0076	2.29E-10	0.2143	0.112	0.01576	1.22E-12	rs62062787:44024865:T:C
17_44024906_A_G	17	44024906	G	0.2119	-0.0482	0.0076	2.29E-10	0.2143	0.112	0.01576	1.22E-12	rs62062788:44024906:A:G
17_44025033_T_C	17	44025033	C	0.2119	-0.0483	0.0076	2.26E-10	0.2143	0.1119	0.01576	1.26E-12	rs62062789:44025033:T:C
17_44025045_C_T	17	44025045	T	0.2119	-0.0482	0.0076	2.29E-10	0.2143	0.112	0.01576	1.22E-12	rs62062790:44025045:C:T
17_44025273_G_A	17	44025273	A	0.2119	-0.0482	0.0076	2.29E-10	0.2143	0.112	0.01576	1.21E-12	rs62062791:44025273:G:A

17_44025347_T_C	17	44025347	C	0.2119	-0.0482	0.0076	2.28E-10	0.2143	0.112	0.01576	1.21E-12	rs62062792:44025347:T:C
17_44025359_TTTG_T	17	44025359	T	0.2117	-0.048	0.0077	4.33E-10	0.2139	0.1125	0.01579	1.03E-12	rs140618737:44025359:TTTG:T
17_44025407_C_CT	17	44025407	CT	0.212	-0.0473	0.0077	7.05E-10	0.2143	0.112	0.01576	1.21E-12	17:44025407:C:CT
17_44025592_G_C	17	44025592	C	0.2119	-0.0482	0.0076	2.28E-10	0.2143	0.112	0.01577	1.20E-12	rs78026984:44025592:G:C
17_44025650_T_C	17	44025650	C	0.2119	-0.0482	0.0076	2.28E-10	0.2143	0.112	0.01577	1.20E-12	rs113395365:44025650:T:C
17_44025678_G_GCT	17	44025678	GCT	0.212	-0.0473	0.0077	7.06E-10	0.2143	0.112	0.01577	1.20E-12	17:44025678:G:GCT
17_44025888_C_A	17	44025888	C	0.2221	-0.0462	0.0075	9.22E-10	0.2245	0.1094	0.01559	2.22E-12	rs242559:44025888:C:A
17_44026321_T_C	17	44026321	C	0.2123	-0.0484	0.0076	2.00E-10	0.2144	0.1109	0.01576	1.93E-12	rs62062793:44026321:T:C
17_44026394_A_G	17	44026394	G	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1122	0.01577	1.12E-12	rs62062794:44026394:A:G
17_44026478_A_G	17	44026478	G	0.2103	-0.0484	0.0076	2.52E-10	0.212	0.1111	0.01583	2.25E-12	rs78556223:44026478:A:G
17_44026490_A_C	17	44026490	C	0.2103	-0.0484	0.0076	2.52E-10	0.212	0.1111	0.01583	2.25E-12	rs77266933:44026490:A:C
17_44026495_A_G	17	44026495	G	0.2103	-0.0484	0.0076	2.52E-10	0.212	0.1111	0.01583	2.24E-12	rs74531363:44026495:A:G
17_44026548_T_C	17	44026548	T	0.2122	-0.0482	0.0076	2.38E-10	0.2147	0.1113	0.01576	1.63E-12	rs242561:44026548:T:C
17_44027090_C_T	17	44027090	T	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1122	0.01577	1.10E-12	rs62062795:44027090:C:T
17_44027316_G_A	17	44027316	A	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1122	0.01577	1.10E-12	rs62062796:44027316:G:A
17_44027366_T_G	17	44027366	G	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1122	0.01577	1.09E-12	rs62062797:44027366:T:G
17_44027383_A_G	17	44027383	G	0.2119	-0.0482	0.0076	2.30E-10	0.2143	0.1122	0.01577	1.09E-12	rs62062798:44027383:A:G
17_44027521_G_T	17	44027521	T	0.2124	-0.0485	0.0076	1.83E-10	0.2144	0.1138	0.01576	5.01E-13	rs62062799:44027521:G:T
17_44027753_A_G	17	44027753	G	0.2123	-0.0485	0.0076	1.84E-10	0.2143	0.1111	0.01576	1.79E-12	rs62062800:44027753:A:G
17_44027836_GC_G	17	44027836	G	0.212	-0.0473	0.0077	7.27E-10	0.2142	0.1123	0.01577	1.08E-12	17:44027836:GC:G
17_44028011_T_G	17	44028011	G	0.2122	-0.0484	0.0076	1.99E-10	0.2143	0.1112	0.01576	1.75E-12	rs62062801:44028011:T:G
17_44028045_G_T	17	44028045	T	0.2119	-0.0482	0.0076	2.38E-10	0.2142	0.1123	0.01577	1.08E-12	rs62062802:44028045:G:T
17_44028183_T_C	17	44028183	C	0.2145	-0.0471	0.0076	5.60E-10	0.2167	0.1121	0.01575	1.12E-12	rs62062803:44028183:T:C
17_44028469_CA_C	17	44028469	C	0.2124	-0.0475	0.0077	6.19E-10	0.2143	0.1112	0.01576	1.74E-12	17:44028469:CA:C
17_44028707_G_A	17	44028707	A	0.2119	-0.0482	0.0076	2.38E-10	0.2142	0.1123	0.01577	1.06E-12	rs74903707:44028707:G:A
17_44028796_T_C	17	44028796	C	0.2123	-0.0484	0.0076	1.94E-10	0.2143	0.111	0.01577	1.89E-12	rs77017444:44028796:T:C
17_44029178_G_C	17	44029178	C	0.2119	-0.0482	0.0076	2.39E-10	0.2142	0.1123	0.01577	1.05E-12	rs76839282:44029178:G:C
17_44029510_TGATG_T	17	44029510	T	0.212	-0.0473	0.0077	7.39E-10	0.2142	0.1124	0.01577	1.04E-12	17:44029510:TGATG:T
17_44030115_C_T	17	44030115	T	0.2119	-0.0482	0.0076	2.39E-10	0.2142	0.1124	0.01577	1.03E-12	rs17650579:44030115:C:T
17_44030195_A_T	17	44030195	T	0.2122	-0.0485	0.0076	1.85E-10	0.2143	0.1112	0.01577	1.75E-12	rs17650597:44030195:A:T
17_44030231_T_C	17	44030231	C	0.2122	-0.0484	0.0076	2.07E-10	0.2143	0.1111	0.01577	1.82E-12	rs17650633:44030231:T:C
17_44030263_A_AC	17	44030263	AC	0.212	-0.0472	0.0077	7.55E-10	0.2142	0.1124	0.01577	1.02E-12	17:44030263:A:AC
17_44030311_T_G	17	44030311	G	0.2122	-0.0484	0.0076	2.02E-10	0.2143	0.1111	0.01577	1.88E-12	rs17650651:44030311:T:G
17_44030773_A_G	17	44030773	G	0.2122	-0.0484	0.0076	1.94E-10	0.2143	0.1112	0.01577	1.74E-12	rs62062805:44030773:A:G
17_44031420_G_A	17	44031420	A	0.2122	-0.0484	0.0076	1.95E-10	0.2143	0.1112	0.01577	1.80E-12	rs62062806:44031420:G:A
17_44031540_G_T	17	44031540	T	0.2119	-0.0483	0.0076	2.24E-10	0.2142	0.1125	0.01577	1.01E-12	rs55978005:44031540:G:T
17_44031946_A_G	17	44031946	G	0.2118	-0.0482	0.0076	2.38E-10	0.2141	0.1125	0.01578	9.90E-13	rs55946323:44031946:A:G
17_44032073_A_G	17	44032073	G	0.2119	-0.0482	0.0076	2.45E-10	0.2142	0.1125	0.01577	9.82E-13	rs56317731:44032073:A:G
17_44032470_C_G	17	44032470	G	0.2122	-0.0484	0.0076	2.01E-10	0.2142	0.1112	0.01577	1.73E-12	rs55821155:44032470:C:G
17_44032597_G_A	17	44032597	A	0.2119	-0.0481	0.0076	2.61E-10	0.2142	0.1126	0.01577	9.45E-13	rs56080482:44032597:G:A
17_44032768_T_C	17	44032768	C	0.2122	-0.0484	0.0076	2.01E-10	0.2142	0.1111	0.01577	1.83E-12	rs17571718:44032768:T:C
17_44032879_A_G	17	44032879	G	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.63E-13	rs78555354:44032879:A:G
17_44032915_T_C	17	44032915	C	0.2119	-0.0482	0.0076	2.40E-10	0.2141	0.1125	0.01577	9.63E-13	rs17571739:44032915:T:C
17_44032956_G_A	17	44032956	A	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1126	0.01577	9.61E-13	rs62062813:44032956:G:A
17_44033002_T_C	17	44033002	C	0.2122	-0.0483	0.0076	2.25E-10	0.2142	0.111	0.01577	1.92E-12	rs62063262:44033002:T:C
17_44033097_T_TTTTTTTTT	17	44033097	TTTTTTTTTTTC	0.2109	-0.0474	0.0077	7.48E-10	0.2126	0.1125	0.01582	1.13E-12	17:44033097:T:TTTTTTTTTTTC
17_44033132_C_T	17	44033132	T	0.212	-0.0481	0.0076	2.56E-10	0.2142	0.1123	0.01577	1.06E-12	rs113520245:44033132:C:T
17_44033169_T_C	17	44033169	C	0.2119	-0.0482	0.0076	2.45E-10	0.2141	0.1125	0.01577	9.63E-13	rs113277432:44033169:T:C
17_44033188_G_A	17	44033188	A	0.2119	-0.0482	0.0076	2.45E-10	0.2141	0.1125	0.01577	9.63E-13	rs112950348:44033188:G:A
17_44033394_G_C	17	44033394	C	0.2119	-0.0482	0.0076	2.45E-10	0.2141	0.1125	0.01577	9.66E-13	rs62063263:44033394:G:C
17_44033401_C_T	17	44033401	T	0.2119	-0.0482	0.0076	2.40E-10	0.2141	0.1125	0.01577	9.68E-13	rs62063264:44033401:C:T
17_44033468_G_A	17	44033468	A	0.2119	-0.0482	0.0076	2.40E-10	0.2141	0.1125	0.01577	9.69E-13	rs62063265:44033468:G:A
17_44033488_C_T	17	44033488	T	0.2119	-0.0482	0.0076	2.40E-10	0.2141	0.1125	0.01577	9.70E-13	rs62063266:44033488:C:T
17_44033802_T_C	17	44033802	C	0.2119	-0.0482	0.0076	2.40E-10	0.2141	0.1125	0.01577	9.75E-13	rs17571781:44033802:T:C
17_44034340_C_T	17	44034340	T	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.80E-13	rs56201245:44034340:C:T

17_44034486_A_G	17	44034486	G	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.83E-13	rs56302057:44034486:A:G
17_44034575_T_C	17	44034575	C	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.84E-13	rs55746658:44034575:T:C
17_44034673_T_G	17	44034673	G	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.85E-13	rs56367860:44034673:T:G
17_44034833_G_A	17	44034833	A	0.2119	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.88E-13	rs62063269:44034833:G:A
17_44034859_A_G	17	44034859	G	0.2122	-0.0484	0.0076	2.07E-10	0.2142	0.1113	0.01577	1.66E-12	rs17571809:44034859:A:G
17_44035222_GAA_G	17	44035222	G	0.213	-0.048	0.0077	3.87E-10	0.2143	0.1132	0.0158	7.92E-13	rs369337577:44035222:GAA:G
17_44035233_A_T	17	44035233	T	0.2119	-0.0481	0.0076	2.51E-10	0.2142	0.1122	0.01577	1.14E-12	rs80190331:44035233:A:T
17_44035367_A_G	17	44035367	G	0.2122	-0.0483	0.0076	2.12E-10	0.2142	0.1113	0.01577	1.69E-12	rs17650771:44035367:A:G
17_44035516_G_A	17	44035516	A	0.2122	-0.0483	0.0076	2.14E-10	0.2141	0.1115	0.01577	1.58E-12	rs77555455:44035516:G:A
17_44035706_A_G	17	44035706	G	0.2122	-0.0483	0.0076	2.21E-10	0.2142	0.1113	0.01577	1.68E-12	rs17571857:44035706:A:G
17_44036047_G_A	17	44036047	A	0.2121	-0.0483	0.0076	2.27E-10	0.2144	0.1121	0.01576	1.12E-12	rs62063271:44036047:G:A
17_44036129_C_T	17	44036129	T	0.2118	-0.0482	0.0076	2.44E-10	0.2141	0.1125	0.01577	9.66E-13	rs112916880:44036129:C:T
17_44036287_A_G	17	44036287	G	0.2118	-0.0482	0.0076	2.45E-10	0.2141	0.1125	0.01577	9.63E-13	rs62063275:44036287:A:G
17_44036408_T_G	17	44036408	G	0.2125	-0.0482	0.0076	2.40E-10	0.2149	0.1123	0.01576	1.03E-12	rs62063276:44036408:T:G
17_44036462_T_A	17	44036462	A	0.2118	-0.0482	0.0076	2.45E-10	0.2141	0.1125	0.01577	9.60E-13	rs62063277:44036462:T:A
17_44036787_T_C	17	44036787	C	0.2122	-0.0482	0.0076	2.27E-10	0.2142	0.1115	0.01577	1.54E-12	rs17650818:44036787:T:C
17_44036914_C_T	17	44036914	T	0.2118	-0.0481	0.0076	2.56E-10	0.2141	0.1127	0.01577	9.18E-13	rs62063278:44036914:C:T
17_44036936_G_A	17	44036936	A	0.2118	-0.0481	0.0076	2.56E-10	0.2141	0.1127	0.01577	9.12E-13	rs62063279:44036936:G:A
17_44037079_G_A	17	44037079	A	0.2118	-0.0481	0.0076	2.57E-10	0.214	0.1129	0.01578	8.49E-13	rs113793114:44037079:G:A
17_44037106_C_CA	17	44037106	CA	0.2119	-0.0472	0.0077	8.08E-10	0.214	0.1128	0.01578	8.69E-13	17:44037106:C:CA
17_44037299_G_C	17	44037299	C	0.2121	-0.0481	0.0076	2.61E-10	0.2141	0.1119	0.01577	1.29E-12	rs62063280:44037299:G:C
17_44037491_A_G	17	44037491	G	0.2123	-0.0482	0.0076	2.27E-10	0.2142	0.1118	0.01576	1.31E-12	rs17650842:44037491:A:G
17_44038207_CAAA_C	17	44038207	CAAA	0.29	-0.039	0.0072	6.90E-08	0.2858	0.08683	0.01499	6.96E-09	17:44038207:CAAA:C
17_44038536_CA_C	17	44038536	C	0.2233	-0.0461	0.0077	2.26E-09	0.2256	0.1087	0.01593	9.09E-12	rs376368638:44038536:CA:C
17_44038785_A_G	17	44038785	G	0.2128	-0.0484	0.0076	1.98E-10	0.2142	0.1102	0.01574	2.47E-12	rs62063281:44038785:A:G
17_44039008_G_A	17	44039008	A	0.2114	-0.0494	0.0076	9.03E-11	0.2138	0.1114	0.0158	1.78E-12	rs17650860:44039008:G:A
17_44039043_G_A	17	44039043	A	0.212	-0.0483	0.0076	2.29E-10	0.2141	0.1119	0.01577	1.31E-12	rs62063282:44039043:G:A
17_44039141_G_GT	17	44039141	GT	0.2568	-0.0442	0.0075	3.08E-09	0.2555	0.0999	0.01542	9.18E-11	17:44039141:G:GT
17_44039410_A_G	17	44039410	G	0.2128	-0.0486	0.0076	1.62E-10	0.2145	0.113	0.01577	7.65E-13	rs111520035:44039410:A:G
17_44039516_G_T	17	44039516	T	0.2121	-0.0484	0.0076	2.08E-10	0.2141	0.1125	0.01577	9.65E-13	rs17650872:44039516:G:T
17_44039691_A_G	17	44039691	G	0.2121	-0.0486	0.0076	1.62E-10	0.2141	0.1126	0.01577	9.53E-13	rs17650901:44039691:A:G
17_44040120_C_T	17	44040120	T	0.2121	-0.0487	0.0076	1.61E-10	0.214	0.1126	0.01577	9.24E-13	rs55780945:44040120:C:T
17_44040288_C_CA	17	44040288	CA	0.2136	-0.0478	0.0077	5.21E-10	0.2151	0.1134	0.01582	7.46E-13	17:44040288:C:CA
17_44040823_C_T	17	44040823	T	0.2123	-0.048	0.0076	2.67E-10	0.2142	0.1125	0.01575	9.25E-13	rs55711941:44040823:C:T
17_44041101_T_C	17	44041101	C	0.2121	-0.0485	0.0076	1.87E-10	0.2141	0.1129	0.01577	7.90E-13	rs55709241:44041101:T:C
17_44041107_G_A	17	44041107	A	0.2121	-0.0487	0.0076	1.59E-10	0.214	0.1127	0.01577	8.87E-13	rs56280951:44041107:G:A
17_44041562_G_T	17	44041562	T	0.2121	-0.0483	0.0076	2.12E-10	0.2143	0.1116	0.01577	1.49E-12	rs112058117:44041562:G:T
17_44041817_A_G	17	44041817	G	0.2121	-0.0487	0.0076	1.59E-10	0.214	0.1127	0.01577	9.01E-13	rs112206871:44041817:A:G
17_44042221_A_G	17	44042221	G	0.2122	-0.0484	0.0076	1.99E-10	0.2143	0.112	0.01576	1.19E-12	rs56166491:44042221:A:G
17_44042361_T_C	17	44042361	C	0.2121	-0.0486	0.0076	1.69E-10	0.2141	0.1126	0.01577	9.08E-13	rs56226437:44042361:T:C
17_44042366_G_A	17	44042366	A	0.2121	-0.0487	0.0076	1.59E-10	0.214	0.1126	0.01577	9.23E-13	rs55907036:44042366:G:A
17_44042783_G_A	17	44042783	A	0.2121	-0.0486	0.0076	1.63E-10	0.214	0.1126	0.01577	9.23E-13	rs56294117:44042783:G:A
17_44042868_G_A	17	44042868	A	0.2121	-0.0486	0.0076	1.74E-10	0.2141	0.1126	0.01577	9.45E-13	rs112415880:44042868:G:A
17_44042939_G_A	17	44042939	A	0.2111	-0.05	0.0076	5.78E-11	0.2134	0.1128	0.01582	9.91E-13	rs112003311:44042939:G:A
17_44042951_C_T	17	44042951	T	0.2112	-0.0501	0.0076	5.34E-11	0.2134	0.1127	0.01582	1.06E-12	rs111751251:44042951:C:T
17_44043092_CAA_C	17	44043092	C	0.2139	-0.0499	0.0077	8.78E-11	0.2165	0.1124	0.01578	1.06E-12	17:44043092:CAA:C
17_44043378_T_C	17	44043378	C	0.2121	-0.0485	0.0076	1.83E-10	0.2141	0.1127	0.01577	8.76E-13	rs62063291:44043378:T:C
17_44043636_C_T	17	44043636	T	0.2121	-0.0486	0.0076	1.72E-10	0.2141	0.1125	0.01577	9.57E-13	rs62063292:44043636:C:T
17_44043819_G_A	17	44043819	A	0.2121	-0.0486	0.0076	1.72E-10	0.2141	0.1125	0.01577	9.56E-13	rs62063293:44043819:G:A
17_44044157_G_A	17	44044157	A	0.2126	-0.0481	0.0076	2.53E-10	0.2152	0.1127	0.01577	8.62E-13	rs62063294:44044157:G:A
17_44044220_A_T	17	44044220	T	0.2122	-0.0483	0.0076	2.19E-10	0.2141	0.1124	0.01577	9.95E-13	rs17650973:44044220:A:T
17_44044431_C_T	17	44044431	T	0.2121	-0.0485	0.0076	1.83E-10	0.2141	0.1128	0.01577	8.43E-13	rs62063295:44044431:C:T
17_44044508_A_C	17	44044508	C	0.2121	-0.0485	0.0076	1.82E-10	0.2141	0.1128	0.01577	8.43E-13	rs17650991:44044508:A:C
17_44044823_T_A	17	44044823	A	0.2121	-0.0485	0.0076	1.78E-10	0.2141	0.1126	0.01577	9.29E-13	rs75145092:44044823:T:A
17_44044940_T_C	17	44044940	C	0.2121	-0.0487	0.0076	1.51E-10	0.2141	0.1117	0.01577	1.36E-12	rs113857334:44044940:T:C

17_44044985_A_G	17	44044985	G	0.2121	-0.0486	0.0076	1.72E-10	0.2141	0.1126	0.01577	9.15E-13	rs17572147:44044985:A:G
17_44045474_A_G	17	44045474	G	0.2121	-0.0484	0.0076	1.96E-10	0.2141	0.1127	0.01577	8.74E-13	rs77513497:44045474:A:G
17_44045574_AC_A	17	44045574	A	0.2122	-0.0476	0.0077	5.44E-10	0.2141	0.1126	0.01577	9.14E-13	rs112893615:44045574:AC:A
17_44045585_C_A	17	44045585	A	0.2128	-0.0467	0.0076	8.01E-10	0.215	0.1126	0.01575	8.82E-13	17:44045585:C:A
17_44045974_C_T	17	44045974	T	0.2121	-0.0485	0.0076	1.80E-10	0.2141	0.1129	0.01577	8.02E-13	rs17572169:44045974:C:T
17_44046202_C_T	17	44046202	T	0.2121	-0.0485	0.0076	1.81E-10	0.2141	0.113	0.01577	7.78E-13	rs62063296:44046202:C:T
17_44046934_T_A	17	44046934	A	0.2085	-0.0491	0.0077	1.79E-10	0.21	0.1128	0.01597	1.66E-12	rs113925422:44046934:T:A
17_44047037_T_A	17	44047037	A	0.2121	-0.0486	0.0076	1.72E-10	0.2141	0.1126	0.01577	9.14E-13	rs142792793:44047037:T:A
17_44047216_T_G	17	44047216	G	0.212	-0.0485	0.0076	1.82E-10	0.2141	0.1127	0.01577	9.03E-13	rs62641967:44047216:T:G
17_44047449_CCCAT_C	17	44047449	C	0.2152	-0.0479	0.0077	4.83E-10	0.2166	0.1098	0.01579	3.54E-12	rs137876410:44047449:CCCAT:C
17_44047609_C_T	17	44047609	T	0.2121	-0.0485	0.0076	1.84E-10	0.2141	0.1128	0.01577	8.43E-13	rs74373419:44047609:C:T
17_44047802_A_T	17	44047802	T	0.2121	-0.0486	0.0076	1.71E-10	0.2141	0.1126	0.01577	9.13E-13	rs62063297:44047802:A:T
17_44048323_G_T	17	44048323	T	0.2121	-0.0486	0.0076	1.69E-10	0.2141	0.1126	0.01577	9.13E-13	rs62063298:44048323:G:T
17_44048336_T_C	17	44048336	C	0.2121	-0.0486	0.0076	1.69E-10	0.2141	0.1126	0.01577	9.13E-13	rs62063299:44048336:T:C
17_44048350_T_C	17	44048350	C	0.2121	-0.0485	0.0076	1.82E-10	0.2141	0.1128	0.01577	8.42E-13	rs62063300:44048350:T:C
17_44048502_GA_G	17	44048502	G	0.2122	-0.0476	0.0077	5.37E-10	0.2141	0.1126	0.01577	9.13E-13	17:44048502:GA:G
17_44048936_C_A	17	44048936	A	0.2114	-0.0486	0.0076	1.89E-10	0.2134	0.1132	0.01582	8.42E-13	rs77566074:44048936:C:A
17_44048937_T_C	17	44048937	C	0.2114	-0.0486	0.0076	1.89E-10	0.2134	0.1132	0.01582	8.42E-13	17:44048937:T:C
17_44048939_AG_A	17	44048939	A	0.2122	-0.0476	0.0077	5.37E-10	0.2141	0.1126	0.01577	9.11E-13	rs367627274:44048939:AG:A
17_44048941_G_C	17	44048941	C	0.212	-0.0486	0.0076	1.69E-10	0.2141	0.1126	0.01577	9.11E-13	rs62063301:44048941:G:C
17_44048943_G_A	17	44048943	A	0.212	-0.0486	0.0076	1.69E-10	0.2141	0.1126	0.01577	9.11E-13	rs62063302:44048943:G:A
17_44049133_T_C	17	44049133	C	0.2121	-0.0485	0.0076	1.79E-10	0.2141	0.1128	0.01577	8.43E-13	rs62063303:44049133:T:C
17_44049329_C_T	17	44049329	T	0.212	-0.0486	0.0076	1.69E-10	0.214	0.1127	0.01577	8.75E-13	rs75242405:44049329:C:T
17_44049550_G_A	17	44049550	A	0.2118	-0.0485	0.0076	1.88E-10	0.2134	0.113	0.01578	7.95E-13	rs17651093:44049550:G:A
17_44049867_A_G	17	44049867	G	0.2121	-0.0484	0.0076	1.92E-10	0.2141	0.113	0.01577	7.60E-13	rs17572248:44049867:A:G
17_44049900_A_G	17	44049900	G	0.212	-0.0485	0.0076	1.81E-10	0.2139	0.1129	0.01577	7.94E-13	rs62063304:44049900:A:G
17_44050282_G_A	17	44050282	A	0.212	-0.0485	0.0076	1.79E-10	0.2139	0.1129	0.01577	8.07E-13	rs62063305:44050282:G:A
17_44050340_G_A	17	44050340	A	0.2118	-0.0485	0.0076	1.98E-10	0.2135	0.1133	0.01577	6.60E-13	rs17651134:44050340:G:A
17_44050395_C_A	17	44050395	A	0.212	-0.0485	0.0076	1.86E-10	0.2141	0.1134	0.01576	6.21E-13	rs62063306:44050395:C:A
17_44050463_T_C	17	44050463	C	0.2118	-0.0484	0.0076	2.01E-10	0.2135	0.1134	0.01577	6.34E-13	rs62063774:44050463:T:C
17_44050823_G_T	17	44050823	T	0.2121	-0.0484	0.0076	2.00E-10	0.2141	0.1136	0.01576	5.63E-13	rs62063775:44050823:G:T
17_44050850_A_G	17	44050850	G	0.2121	-0.0486	0.0076	1.65E-10	0.214	0.1129	0.01576	7.85E-13	rs62063776:44050850:A:G
17_44051588_C_G	17	44051588	G	0.2121	-0.0486	0.0076	1.67E-10	0.214	0.1129	0.01576	7.94E-13	rs117124984:44051588:C:G
17_44051589_T_G	17	44051589	G	0.2121	-0.0486	0.0076	1.67E-10	0.214	0.1129	0.01576	7.94E-13	rs118087478:44051589:T:G
17_44051612_A_G	17	44051612	G	0.2121	-0.0486	0.0076	1.67E-10	0.214	0.1129	0.01576	7.94E-13	rs77875796:44051612:A:G
17_44051846_A_G	17	44051846	G	0.2121	-0.0486	0.0076	1.68E-10	0.214	0.1129	0.01576	7.98E-13	rs1800547:44051846:A:G
17_44051924_G_A	17	44051924	A	0.2124	-0.0489	0.0076	1.23E-10	0.2142	0.1111	0.01572	1.58E-12	rs17651213:44051924:G:A
17_44052009_T_C	17	44052009	C	0.2121	-0.0483	0.0076	2.09E-10	0.2142	0.1122	0.01576	1.08E-12	rs17572361:44052009:T:C
17_44052284_G_A	17	44052284	A	0.2121	-0.0485	0.0076	1.79E-10	0.2141	0.1115	0.01572	1.32E-12	rs17651243:44052284:G:A
17_44052733_A_G	17	44052733	G	0.2115	-0.0478	0.0076	3.52E-10	0.2141	0.1109	0.01575	1.91E-12	rs78104015:44052733:A:G
17_44053171_A_G	17	44053171	G	0.212	-0.0485	0.0076	1.89E-10	0.2141	0.1108	0.01573	1.88E-12	rs62063777:44053171:A:G
17_44053307_T_TAG	17	44053307	TAG	0.2126	-0.0475	0.0077	6.06E-10	0.2147	0.1124	0.01576	1.01E-12	rs113242154:44053307:T:TAG
17_44053448_A_G	17	44053448	G	0.2121	-0.0484	0.0076	2.07E-10	0.2141	0.1115	0.01572	1.33E-12	rs2217394:44053448:A:G
17_44053989_G_A	17	44053989	A	0.2121	-0.0484	0.0076	2.02E-10	0.2141	0.1111	0.01571	1.53E-12	rs62063778:44053989:G:A
17_44054237_G_A	17	44054237	A	0.2121	-0.0483	0.0076	2.16E-10	0.2141	0.1119	0.01572	1.12E-12	rs17651285:44054237:G:A
17_44054388_T_C	17	44054388	C	0.2121	-0.0484	0.0076	2.04E-10	0.2142	0.1111	0.01571	1.55E-12	rs17572467:44054388:T:C
17_44054596_T_G	17	44054596	G	0.2121	-0.0484	0.0076	1.99E-10	0.2142	0.1109	0.01571	1.71E-12	rs17572495:44054596:T:G
17_44054671_C_T	17	44054671	T	0.2119	-0.0484	0.0076	2.01E-10	0.2139	0.112	0.01575	1.14E-12	rs62063779:44054671:C:T
17_44054696_G_A	17	44054696	G	0.4069	-0.0254	0.0063	0.00005482	0.3994	0.07813	0.01341	5.60E-09	rs754593:44054696:G:A
17_44055638_T_A	17	44055638	A	0.2121	-0.0485	0.0076	1.84E-10	0.2142	0.1103	0.01571	2.24E-12	rs754513:44055638:T:A
17_44055647_A_T	17	44055647	T	0.2121	-0.0485	0.0076	1.76E-10	0.2142	0.1108	0.01571	1.76E-12	rs754512:44055647:A:T
17_44056238_A_G	17	44056238	G	0.212	-0.0485	0.0076	1.82E-10	0.2141	0.1123	0.01575	1.02E-12	rs62063780:44056238:A:G
17_44056433_T_C	17	44056433	C	0.2121	-0.0485	0.0076	1.86E-10	0.2142	0.1105	0.01572	2.05E-12	rs2163129:44056433:T:C
17_44056434_G_A	17	44056434	A	0.2121	-0.0486	0.0076	1.73E-10	0.2141	0.1109	0.01572	1.77E-12	rs2163130:44056434:G:A
17_44056767_G_A	17	44056767	A	0.2121	-0.0486	0.0076	1.67E-10	0.2141	0.1114	0.01575	1.49E-12	rs1981997:44056767:G:A

17_44056833_G_A	17	44056833	A	0.2121	-0.0485	0.0076	1.83E-10	0.2141	0.1128	0.01577	8.59E-13	rs1981998:44056833:G:A
17_44057595_G_A	17	44057595	A	0.2219	-0.0491	0.0075	7.63E-11	0.2226	0.1125	0.01567	7.20E-13	rs3785884:44057595:G:A
17_44057770_G_GGAGGCA	17	44057770	GGAGGCAGGAGA	0.2119	-0.0474	0.0077	7.02E-10	0.2139	0.1124	0.01579	1.11E-12	7:44057770:G:GGAGGCAGGAGAATTGTTACT
17_44058004_A_G	17	44058004	G	0.2121	-0.0486	0.0076	1.71E-10	0.2141	0.1128	0.01577	8.62E-13	rs17572613:44058004:A:G
17_44058017_G_T	17	44058017	T	0.2121	-0.0488	0.0076	1.42E-10	0.2141	0.1127	0.01577	9.16E-13	rs77527347:44058017:G:T
17_44058629_T_A	17	44058629	A	0.212	-0.0485	0.0076	1.86E-10	0.214	0.1124	0.01577	1.00E-12	rs17572627:44058629:T:A
17_44058691_G_T	17	44058691	T	0.2121	-0.0486	0.0076	1.63E-10	0.2141	0.1131	0.01577	7.43E-13	rs62063781:44058691:G:T
17_44058699_TAGG_T	17	44058699	T	0.2122	-0.0476	0.0077	5.44E-10	0.2141	0.1129	0.01577	8.17E-13	rs375542128:44058699:TAGG:T
17_44058716_G_T	17	44058716	T	0.2122	-0.0489	0.0076	1.29E-10	0.2142	0.1125	0.01577	9.69E-13	rs62063782:44058716:G:T
17_44058861_C_A	17	44058861	A	0.212	-0.0487	0.0076	1.54E-10	0.214	0.1134	0.01577	6.41E-13	rs17651483:44058861:C:A
17_44059215_C_T	17	44059215	T	0.2121	-0.0486	0.0076	1.71E-10	0.2141	0.1128	0.01577	8.37E-13	rs62063783:44059215:C:T
17_44059775_A_G	17	44059775	G	0.2121	-0.0485	0.0076	1.78E-10	0.2141	0.1124	0.01577	9.96E-13	rs62063784:44059775:A:G
17_44060248_G_A	17	44060248	A	0.212	-0.0484	0.0076	2.02E-10	0.2141	0.1125	0.01577	9.68E-13	rs56234850:44060248:G:A
17_44060775_C_T	17	44060775	T	0.2121	-0.0485	0.0076	1.76E-10	0.2141	0.1128	0.01577	8.62E-13	rs63750417:44060775:C:T
17_44061023_G_A	17	44061023	A	0.212	-0.0487	0.0076	1.54E-10	0.2141	0.1137	0.01577	5.52E-13	rs62063786:44061023:G:A
17_44061036_T_C	17	44061036	C	0.2121	-0.0484	0.0076	1.95E-10	0.2141	0.1133	0.01577	6.80E-13	rs62063787:44061036:T:C
17_44061278_C_T	17	44061278	T	0.212	-0.0483	0.0076	2.14E-10	0.214	0.1128	0.01577	8.42E-13	rs17651549:44061278:C:T
17_44061608_GT_G	17	44061608	G	0.212	-0.0473	0.0077	7.38E-10	0.2136	0.1131	0.01577	7.48E-13	17:44061608:GT:G
17_44061696_C_T	17	44061696	T	0.2121	-0.0485	0.0076	1.80E-10	0.2141	0.1132	0.01577	7.17E-13	17:44061696:C:T
17_44061898_T_C	17	44061898	C	0.2121	-0.0485	0.0076	1.76E-10	0.2141	0.1128	0.01577	8.60E-13	17:44061898:T:C
17_44062337_G_A	17	44062337	A	0.2121	-0.0482	0.0076	2.38E-10	0.2141	0.1146	0.01577	3.69E-13	17:44062337:G:A
17_44062689_A_C	17	44062689	C	0.2136	-0.0493	0.0076	8.32E-11	0.2156	0.1139	0.01572	4.37E-13	17:44062689:A:C
17_44062915_G_T	17	44062915	T	0.2119	-0.0486	0.0076	1.63E-10	0.214	0.1129	0.01578	8.37E-13	17:44062915:G:T
17_44062993_A_G	17	44062993	G	0.2119	-0.0484	0.0076	2.00E-10	0.2141	0.1121	0.01577	1.21E-12	17:44062993:A:G
17_44063140_A_G	17	44063140	G	0.2119	-0.0486	0.0076	1.68E-10	0.2141	0.1122	0.01578	1.14E-12	17:44063140:A:G
17_44063393_G_A	17	44063393	A	0.2121	-0.0486	0.0076	1.72E-10	0.2141	0.1129	0.01577	7.92E-13	17:44063393:G:A
17_44063563_T_C	17	44063563	C	0.2121	-0.0486	0.0076	1.65E-10	0.2141	0.1125	0.01577	9.77E-13	17:44063563:T:C
17_44063723_A_C	17	44063723	C	0.2124	-0.0482	0.0076	2.34E-10	0.2142	0.1121	0.01576	1.14E-12	17:44063723:A:C
17_44063766_A_G	17	44063766	G	0.2121	-0.0486	0.0076	1.73E-10	0.2141	0.1129	0.01577	8.21E-13	17:44063766:A:G
17_44063787_A_G	17	44063787	G	0.2121	-0.0486	0.0076	1.74E-10	0.2141	0.1129	0.01577	8.21E-13	17:44063787:A:G
17_44064208_G_A	17	44064208	A	0.212	-0.0488	0.0076	1.39E-10	0.2141	0.1123	0.01577	1.06E-12	17:44064208:G:A
17_44064334_T_C	17	44064334	C	0.212	-0.0483	0.0076	2.13E-10	0.2141	0.1127	0.01577	8.98E-13	17:44064334:T:C
17_44064759_A_C	17	44064759	C	0.212	-0.0485	0.0076	1.82E-10	0.2141	0.1129	0.01577	8.20E-13	17:44064759:A:C
17_44065410_G_A	17	44065410	A	0.2121	-0.0486	0.0076	1.70E-10	0.2139	0.1133	0.01578	6.96E-13	rs10445371:44065410:G:A
17_44065669_A_T	17	44065669	T	0.212	-0.0485	0.0076	1.87E-10	0.2139	0.1131	0.01578	7.87E-13	rs919461:44065669:A:T
17_44065740_C_T	17	44065740	T	0.2121	-0.0486	0.0076	1.70E-10	0.2139	0.1133	0.01578	6.96E-13	rs919462:44065740:C:T
17_44065901_C_T	17	44065901	T	0.2122	-0.0484	0.0076	1.94E-10	0.2139	0.1131	0.01578	7.69E-13	rs919464:44065901:C:T
17_44066088_T_A	17	44066088	A	0.2121	-0.0486	0.0076	1.70E-10	0.2139	0.1133	0.01578	6.96E-13	rs62063794:44066088:T:A
17_44066172_A_G	17	44066172	G	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1133	0.01578	6.96E-13	rs112385572:44066172:A:G
17_44066252_AAAACAAAC_	17	44066252	A	0.2123	-0.0477	0.0077	5.23E-10	0.2139	0.1132	0.01578	7.29E-13	39916822:44066252:AAAACAAAC:A
17_44066634_C_G	17	44066634	G	0.2121	-0.0486	0.0076	1.71E-10	0.2139	0.1135	0.01578	6.37E-13	rs17651700:44066634:C:G
17_44066868_C_A	17	44066868	A	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1133	0.01578	6.96E-13	rs372810927:44066868:C:A
17_44066874_G_A	17	44066874	A	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1133	0.01578	6.96E-13	rs111240522:44066874:G:A
17_44066995_C_T	17	44066995	T	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1133	0.01578	6.96E-13	rs113134013:44066995:C:T
17_44067046_G_A	17	44067046	A	0.2121	-0.0486	0.0076	1.65E-10	0.2139	0.1133	0.01578	6.96E-13	rs76357066:44067046:G:A
17_44067400_T_C	17	44067400	C	0.2121	-0.0486	0.0076	1.61E-10	0.2139	0.1132	0.01578	7.25E-13	rs10445337:44067400:T:C
17_44067508_A_G	17	44067508	G	0.2121	-0.0487	0.0076	1.56E-10	0.2139	0.1131	0.01578	7.86E-13	rs79447161:44067508:A:G
17_44067546_T_C	17	44067546	C	0.2121	-0.0485	0.0076	1.77E-10	0.2139	0.1134	0.01578	6.65E-13	rs17651754:44067546:T:C
17_44067682_G_A	17	44067682	A	0.2121	-0.0485	0.0076	1.80E-10	0.2141	0.1132	0.01578	7.39E-13	rs10445338:44067682:G:A
17_44067831_T_C	17	44067831	C	0.2121	-0.0485	0.0076	1.77E-10	0.2139	0.1133	0.01578	6.96E-13	rs111652694:44067831:T:C
17_44068112_C_G	17	44068112	G	0.2125	-0.0486	0.0076	1.61E-10	0.2142	0.1131	0.01577	7.39E-13	rs75743061:44068112:C:G
17_44068238_C_T	17	44068238	T	0.2121	-0.0484	0.0076	2.03E-10	0.214	0.1129	0.01578	8.62E-13	rs62063795:44068238:C:T
17_44068289_G_A	17	44068289	A	0.2125	-0.0482	0.0076	2.31E-10	0.2142	0.1133	0.01578	6.79E-13	rs62063796:44068289:G:A
17_44068294_G_C	17	44068294	C	0.2125	-0.0482	0.0076	2.31E-10	0.2142	0.1133	0.01578	6.79E-13	rs62063797:44068294:G:C
17_44068480_T_C	17	44068480	C	0.2121	-0.0485	0.0076	1.77E-10	0.2139	0.1133	0.01578	6.96E-13	rs77290642:44068480:T:C

17_44068481_G_A	17	44068481	A	0.2121	-0.0485	0.0076	1.77E-10	0.2139	0.1133	0.01578	6.96E-13	rs76618565:44068481:G:A
17_44068543_G_A	17	44068543	A	0.2121	-0.0486	0.0076	1.75E-10	0.2139	0.1135	0.01578	6.49E-13	rs62063798:44068543:G:A
17_44068924_G_A	17	44068924	A	0.212	-0.0485	0.0076	1.88E-10	0.2138	0.1135	0.01579	6.41E-13	rs1052551:44068924:G:A
17_44069180_C_G	17	44069180	G	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1133	0.01578	6.96E-13	rs62063799:44069180:C:G
17_44069198_C_T	17	44069198	T	0.2122	-0.0486	0.0076	1.66E-10	0.2139	0.1135	0.01578	6.43E-13	rs62063800:44069198:C:T
17_44069376_G_T	17	44069376	T	0.2121	-0.0486	0.0076	1.70E-10	0.2139	0.1133	0.01578	7.04E-13	rs62063801:44069376:G:T
17_44069687_A_G	17	44069687	G	0.2121	-0.0486	0.0076	1.69E-10	0.2139	0.1133	0.01578	6.99E-13	rs17651857:44069687:A:G
17_44069768_A_G	17	44069768	G	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1134	0.01578	6.63E-13	rs74759276:44069768:A:G
17_44069840_G_A	17	44069840	A	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1134	0.01578	6.63E-13	rs17651887:44069840:G:A
17_44069970_C_G	17	44069970	G	0.2127	-0.048	0.0076	2.62E-10	0.2145	0.112	0.01578	1.26E-12	rs78599197:44069970:C:G
17_44070111_G_C	17	44070111	C	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	6.95E-13	rs62063842:44070111:G:C
17_44070545_G_A	17	44070545	A	0.2121	-0.0486	0.0076	1.73E-10	0.2139	0.1136	0.01578	6.18E-13	rs55662347:44070545:G:A
17_44070956_T_A	17	44070956	A	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	6.95E-13	rs55913645:44070956:T:A
17_44071089_C_G	17	44071089	G	0.2121	-0.0485	0.0076	1.76E-10	0.2139	0.1134	0.01578	6.63E-13	rs17573175:44071089:C:G
17_44071294_T_C	17	44071294	C	0.2121	-0.0485	0.0076	1.84E-10	0.2139	0.1133	0.01578	7.13E-13	rs62063845:44071294:T:C
17_44071674_A_G	17	44071674	G	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	6.95E-13	rs62063846:44071674:A:G
17_44072017_C_A	17	44072017	A	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	6.99E-13	rs55736025:44072017:C:A
17_44072041_T_A	17	44072041	A	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	6.99E-13	rs55886080:44072041:T:A
17_44072423_A_C	17	44072423	C	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1133	0.01578	7.07E-13	rs75944932:44072423:A:C
17_44072854_T_C	17	44072854	C	0.2125	-0.0489	0.0076	1.25E-10	0.2147	0.1128	0.01578	8.94E-13	rs17573245:44072854:T:C
17_44072881_C_G	17	44072881	G	0.2122	-0.0484	0.0076	2.04E-10	0.2139	0.1133	0.01578	7.14E-13	rs17573266:44072881:C:G
17_44072984_A_G	17	44072984	G	0.2121	-0.0486	0.0076	1.65E-10	0.2139	0.1133	0.01578	7.20E-13	rs112572874:44072984:A:G
17_44073027_G_A	17	44073027	A	0.2121	-0.0486	0.0076	1.65E-10	0.2139	0.1133	0.01578	7.21E-13	rs17652036:44073027:G:A
17_44073062_T_G	17	44073062	G	0.2121	-0.0485	0.0076	1.83E-10	0.2139	0.1133	0.01578	7.10E-13	rs62063849:44073062:T:G
17_44073145_G_C	17	44073145	C	0.2121	-0.0486	0.0076	1.65E-10	0.2139	0.1132	0.01578	7.24E-13	rs17652066:44073145:G:C
17_44073739_G_A	17	44073739	A	0.2125	-0.0491	0.0076	1.10E-10	0.2145	0.1135	0.01578	6.38E-13	rs62063850:44073739:G:A
17_44073889_A_G	17	44073889	G	0.2123	-0.0489	0.0076	1.29E-10	0.214	0.1129	0.01579	8.72E-13	rs1052553:44073889:A:G
17_44073973_T_C	17	44073973	C	0.212	-0.0486	0.0076	1.62E-10	0.2139	0.1138	0.01579	5.62E-13	rs17652121:44073973:T:C
17_44074435_C_G	17	44074435	G	0.2121	-0.0486	0.0076	1.63E-10	0.2139	0.113	0.01578	8.18E-13	rs62063851:44074435:C:G
17_44074581_A_G	17	44074581	G	0.2121	-0.0485	0.0076	1.87E-10	0.2139	0.113	0.01578	8.02E-13	rs62063852:44074581:A:G
17_44074613_A_G	17	44074613	G	0.2121	-0.0486	0.0076	1.71E-10	0.2139	0.1132	0.01578	7.45E-13	rs62063853:44074613:A:G
17_44074619_G_A	17	44074619	A	0.2121	-0.0486	0.0076	1.71E-10	0.2139	0.1132	0.01578	7.45E-13	rs62063854:44074619:G:A
17_44075099_T_C	17	44075099	C	0.2121	-0.0486	0.0076	1.67E-10	0.2139	0.1132	0.01578	7.49E-13	rs2004673:44075099:T:C
17_44075110_A_T	17	44075110	T	0.2121	-0.0486	0.0076	1.72E-10	0.2139	0.1132	0.01578	7.45E-13	rs2004674:44075110:A:T
17_44075535_T_C	17	44075535	C	0.2121	-0.0486	0.0076	1.73E-10	0.2139	0.1132	0.01578	7.44E-13	rs62063855:44075535:T:C
17_44075837_T_C	17	44075837	C	0.2121	-0.0486	0.0076	1.73E-10	0.2139	0.1132	0.01578	7.44E-13	rs1078269:44075837:T:C
17_44075901_A_G	17	44075901	G	0.2121	-0.0486	0.0076	1.74E-10	0.2139	0.1131	0.01578	7.67E-13	rs1078268:44075901:A:G
17_44076466_A_G	17	44076466	G	0.212	-0.0486	0.0076	1.74E-10	0.2139	0.1132	0.01578	7.44E-13	rs62063856:44076466:A:G
17_44076665_A_G	17	44076665	G	0.212	-0.0484	0.0076	2.00E-10	0.2139	0.1132	0.01579	7.61E-13	rs62063857:44076665:A:G
17_44077708_G_T	17	44077708	T	0.2121	-0.0486	0.0076	1.69E-10	0.214	0.1133	0.01578	7.16E-13	rs79959255:44077708:G:T
17_44077850_G_A	17	44077850	A	0.212	-0.0485	0.0076	1.80E-10	0.214	0.1132	0.01578	7.43E-13	rs56301633:44077850:G:A
17_44077851_T_A	17	44077851	A	0.212	-0.0485	0.0076	1.80E-10	0.214	0.1132	0.01578	7.43E-13	rs56108300:44077851:T:A
17_44078616_G_A	17	44078616	A	0.212	-0.0485	0.0076	1.84E-10	0.214	0.1132	0.01578	7.42E-13	rs62063859:44078616:G:A
17_44078680_T_TA	17	44078680	TA	0.2122	-0.0475	0.0077	6.10E-10	0.214	0.1132	0.01578	7.42E-13	rs150334020:44078680:T:TA
17_44078816_TA_T	17	44078816	T	0.2118	-0.0469	0.0077	1.05E-09	0.2137	0.1129	0.01582	9.38E-13	17:44078816:TA:T
17_44078832_G_A	17	44078832	A	0.2122	-0.0488	0.0076	1.37E-10	0.2141	0.1134	0.01579	6.89E-13	rs62064660:44078832:G:A
17_44078892_G_A	17	44078892	A	0.212	-0.0485	0.0076	1.84E-10	0.214	0.1132	0.01579	7.44E-13	rs62064661:44078892:G:A
17_44079567_C_T	17	44079567	T	0.2146	-0.0486	0.0076	1.59E-10	0.2177	0.1133	0.01577	6.62E-13	rs17573447:44079567:C:T
17_44079721_A_G	17	44079721	G	0.212	-0.0486	0.0076	1.75E-10	0.214	0.1131	0.01579	7.75E-13	rs62064662:44079721:A:G
17_44080039_T_G	17	44080039	G	0.2121	-0.0489	0.0076	1.30E-10	0.2141	0.1126	0.01578	9.77E-13	rs62064663:44080039:T:G
17_44080408_G_C	17	44080408	C	0.2119	-0.0486	0.0076	1.72E-10	0.2139	0.1128	0.01579	9.23E-13	rs113894932:44080408:G:C
17_44080465_C_CGTGTGT	17	44080465	CGTGTGT	0.2117	-0.0483	0.0077	3.26E-10	0.2133	0.113	0.0158	8.62E-13	17:44080465:C:CGTGTGT
17_44081064_A_G	17	44081064	G	0.2128	-0.0487	0.0076	1.53E-10	0.2153	0.1104	0.01576	2.47E-12	rs8070723:44081064:A:G
17_44081218_C_CT	17	44081218	CT	0.212	-0.0475	0.0077	6.27E-10	0.214	0.113	0.01579	8.28E-13	17:44081218:C:CT
17_44081224_G_A	17	44081224	A	0.2119	-0.0485	0.0076	1.88E-10	0.214	0.113	0.01579	8.28E-13	rs17573509:44081224:G:A

17_44081462_T_C	17	44081462	C	0.2119	-0.0486	0.0076	1.77E-10	0.214	0.113	0.01579	8.08E-13	rs62064664:44081462:T:C
17_44081527_T_C	17	44081527	C	0.2119	-0.0485	0.0076	1.78E-10	0.214	0.113	0.01579	8.08E-13	rs62064665:44081527:T:C
17_44082181_A_G	17	44082181	G	0.2119	-0.0485	0.0076	1.88E-10	0.2139	0.1131	0.01579	7.89E-13	rs111324579:44082181:A:G
17_44082249_A_T	17	44082249	T	0.2119	-0.0485	0.0076	1.84E-10	0.2139	0.113	0.01579	8.03E-13	rs113201171:44082249:A:T
17_44082432_G_A	17	44082432	A	0.2119	-0.0485	0.0076	1.86E-10	0.2139	0.113	0.01579	8.02E-13	rs112310745:44082432:G:A
17_44082441_T_C	17	44082441	C	0.2119	-0.0485	0.0076	1.86E-10	0.2139	0.113	0.01579	8.02E-13	rs74450848:44082441:T:C
17_44082446_G_A	17	44082446	A	0.2119	-0.0484	0.0076	1.99E-10	0.2139	0.1129	0.01579	8.42E-13	rs74846646:44082446:G:A
17_44082514_T_C	17	44082514	C	0.212	-0.0485	0.0076	1.87E-10	0.214	0.1128	0.01579	9.09E-13	rs62064666:44082514:T:C
17_44082528_A_T	17	44082528	T	0.212	-0.0485	0.0076	1.77E-10	0.214	0.1124	0.01579	1.06E-12	rs62064667:44082528:A:T
17_44082603_A_C	17	44082603	C	0.212	-0.0485	0.0076	1.85E-10	0.214	0.1131	0.01579	7.96E-13	rs17573593:44082603:A:C
17_44082955_A_AT	17	44082955	AT	0.2119	-0.0476	0.0077	5.72E-10	0.214	0.113	0.0158	8.49E-13	17:44082955:A:AT
17_44082981_G_A	17	44082981	A	0.212	-0.0487	0.0076	1.61E-10	0.214	0.1123	0.01578	1.14E-12	rs62064668:44082981:G:A
17_44083081_G_A	17	44083081	A	0.2116	-0.0489	0.0076	1.43E-10	0.2134	0.1134	0.01581	7.34E-13	rs17573607:44083081:G:A
17_44083323_C_T	17	44083323	T	0.2124	-0.0479	0.0076	3.01E-10	0.2144	0.1109	0.01577	2.03E-12	rs17652337:44083323:C:T
17_44083402_G_A	17	44083402	A	0.2143	-0.0481	0.0076	2.66E-10	0.2162	0.1107	0.01582	2.52E-12	rs1991556:44083402:G:A
17_44084002_T_C	17	44084002	C	0.2082	-0.0479	0.0077	4.95E-10	0.2098	0.1162	0.01599	3.65E-13	rs112836774:44084002:T:C
17_44084157_T_C	17	44084157	C	0.212	-0.0487	0.0076	1.59E-10	0.2139	0.1131	0.01579	7.86E-13	rs113316734:44084157:T:C
17_44084533_T_C	17	44084533	C	0.212	-0.0485	0.0076	1.79E-10	0.2139	0.113	0.01579	7.97E-13	rs74829364:44084533:T:C
17_44084676_C_T	17	44084676	T	0.212	-0.0485	0.0076	1.80E-10	0.2139	0.113	0.01579	7.97E-13	rs62064669:44084676:C:T
17_44084844_G_C	17	44084844	C	0.212	-0.0485	0.0076	1.80E-10	0.2139	0.113	0.01579	7.97E-13	rs78962882:44084844:G:C
17_44085743_T_C	17	44085743	C	0.212	-0.0484	0.0076	1.93E-10	0.2139	0.1128	0.01579	8.89E-13	rs78136862:44085743:T:C
17_44085852_T_A	17	44085852	A	0.212	-0.0485	0.0076	1.88E-10	0.2139	0.1131	0.01579	7.91E-13	rs62064670:44085852:T:A
17_44086100_T_C	17	44086100	C	0.212	-0.0484	0.0076	1.95E-10	0.2139	0.1131	0.01579	7.79E-13	rs62064671:44086100:T:C
17_44086521_G_A	17	44086521	A	0.212	-0.0484	0.0076	1.99E-10	0.2139	0.1131	0.01579	7.72E-13	rs62064672:44086521:G:A
17_44086726_T_C	17	44086726	C	0.212	-0.0484	0.0076	2.01E-10	0.2139	0.1131	0.01579	7.69E-13	rs370558872:44086726:T:C
17_44088772_C_A	17	44088772	A	0.212	-0.0483	0.0076	2.18E-10	0.2139	0.1132	0.01578	7.37E-13	rs62064674:44088772:C:A
17_44088926_C_T	17	44088926	T	0.2121	-0.0485	0.0076	1.84E-10	0.214	0.1131	0.01578	7.45E-13	rs62064675:44088926:C:T
17_44088937_G_C	17	44088937	C	0.212	-0.0483	0.0076	2.13E-10	0.2139	0.1132	0.01578	7.36E-13	rs17652449:44088937:G:C
17_44089108_T_C	17	44089108	C	0.2126	-0.0484	0.0076	1.96E-10	0.215	0.1137	0.01579	5.96E-13	rs76723223:44089108:T:C
17_44089563_C_T	17	44089563	T	0.2122	-0.0483	0.0076	2.10E-10	0.2139	0.1155	0.01578	2.49E-13	rs733966:44089563:C:T
17_44089690_T_C	17	44089690	C	0.2121	-0.0483	0.0076	2.23E-10	0.214	0.1126	0.01578	9.62E-13	rs733967:44089690:T:C
17_44089715_C_T	17	44089715	T	0.212	-0.0482	0.0076	2.39E-10	0.2139	0.1131	0.01578	7.82E-13	rs733968:44089715:C:T
17_44089727_G_A	17	44089727	A	0.2133	-0.0482	0.0076	2.27E-10	0.2154	0.1093	0.01577	4.27E-12	rs733969:44089727:G:A
17_44089921_C_T	17	44089921	T	0.2128	-0.0473	0.0076	4.89E-10	0.2148	0.1126	0.01576	8.81E-13	rs4283261:44089921:C:T
17_44090035_C_G	17	44090035	G	0.212	-0.0483	0.0076	2.27E-10	0.2139	0.1131	0.01578	7.79E-13	rs62062265:44090035:C:G
17_44090148_A_C	17	44090148	C	0.212	-0.0483	0.0076	2.27E-10	0.2139	0.1131	0.01578	7.79E-13	rs75666751:44090148:A:C
17_44090236_T_C	17	44090236	C	0.212	-0.0483	0.0076	2.28E-10	0.2139	0.1131	0.01578	7.79E-13	rs4306559:44090236:T:C
17_44090339_T_C	17	44090339	C	0.212	-0.0483	0.0076	2.23E-10	0.2139	0.1131	0.01578	7.76E-13	rs747152:44090339:T:C
17_44090455_T_C	17	44090455	C	0.212	-0.0482	0.0076	2.41E-10	0.2139	0.1129	0.01578	8.49E-13	rs12150254:44090455:T:C
17_44090536_G_A	17	44090536	A	0.212	-0.0482	0.0076	2.28E-10	0.2139	0.1131	0.01578	7.56E-13	17:44090536:G:A
17_44090538_T_G	17	44090538	G	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	17:44090538:T:G
17_44090646_A_G	17	44090646	G	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	rs12150170:44090646:A:G
17_44090685_G_T	17	44090685	T	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	rs12150515:44090685:G:T
17_44090704_A_G	17	44090704	G	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	rs62062266:44090704:A:G
17_44090796_T_C	17	44090796	C	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	rs17573858:44090796:T:C
17_44090854_C_T	17	44090854	T	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1131	0.01578	7.79E-13	rs62062267:44090854:C:T
17_44090858_C_T	17	44090858	T	0.212	-0.0482	0.0076	2.33E-10	0.2139	0.1131	0.01578	7.84E-13	rs62062268:44090858:C:T
17_44091092_G_C	17	44091092	C	0.212	-0.0481	0.0076	2.61E-10	0.2139	0.1124	0.01578	1.05E-12	rs62062269:44091092:G:C
17_44091195_T_C	17	44091195	C	0.212	-0.0482	0.0076	2.39E-10	0.2139	0.1128	0.01578	8.79E-13	rs62062270:44091195:T:C
17_44091724_G_A	17	44091724	A	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1134	0.01579	6.85E-13	rs75534191:44091724:G:A
17_44091886_C_T	17	44091886	T	0.2171	-0.0458	0.0075	1.29E-09	0.2178	0.1106	0.01565	1.64E-12	rs9891103:44091886:C:T
17_44091988_T_C	17	44091988	C	0.2224	-0.0469	0.0075	3.68E-10	0.2272	0.1128	0.01557	4.22E-13	rs62062271:44091988:T:C
17_44092108_T_C	17	44092108	C	0.212	-0.0483	0.0076	2.26E-10	0.2139	0.1135	0.01579	6.60E-13	rs62062272:44092108:T:C
17_44092243_C_T	17	44092243	T	0.212	-0.0483	0.0076	2.24E-10	0.2139	0.1135	0.01579	6.60E-13	rs62062273:44092243:C:T
17_44092497_T_C	17	44092497	C	0.212	-0.0483	0.0076	2.21E-10	0.2139	0.1135	0.01579	6.59E-13	rs12150469:44092497:T:C

17_44092729_TAAA_T	17	44092729	T	0.2124	-0.0474	0.0077	6.85E-10	0.2145	0.1132	0.01578	7.28E-13	rs72169174:44092729:TAAA:T
17_44092744_A_G	17	44092744	G	0.212	-0.0483	0.0076	2.18E-10	0.2139	0.1135	0.01579	6.59E-13	rs112402370:44092744:A:G
17_44092801_G_A	17	44092801	A	0.2121	-0.0483	0.0076	2.25E-10	0.2141	0.1135	0.01578	6.33E-13	rs12149995:44092801:G:A
17_44093319_G_A	17	44093319	A	0.212	-0.0481	0.0076	2.61E-10	0.2139	0.113	0.01577	7.97E-13	rs62062274:44093319:G:A
17_44093496_A_G	17	44093496	G	0.2122	-0.0483	0.0076	2.19E-10	0.2139	0.1142	0.01578	4.55E-13	rs62062275:44093496:A:G
17_44093627_A_G	17	44093627	G	0.212	-0.0483	0.0076	2.12E-10	0.2139	0.1134	0.01578	6.85E-13	rs62062276:44093627:A:G
17_44093753_T_G	17	44093753	G	0.212	-0.0483	0.0076	2.12E-10	0.2139	0.1135	0.01579	6.52E-13	rs62062277:44093753:T:G
17_44093860_A_G	17	44093860	G	0.212	-0.0483	0.0076	2.14E-10	0.2139	0.1132	0.01579	7.31E-13	rs62062278:44093860:A:G
17_44093964_T_C	17	44093964	C	0.212	-0.0483	0.0076	2.16E-10	0.2139	0.1135	0.01579	6.60E-13	rs62062279:44093964:T:C
17_44093993_C_T	17	44093993	T	0.212	-0.0483	0.0076	2.17E-10	0.2139	0.1134	0.01579	6.63E-13	rs62062280:44093993:C:T
17_44094112_A_G	17	44094112	G	0.212	-0.0483	0.0076	2.22E-10	0.2139	0.1134	0.01579	6.72E-13	rs62062281:44094112:A:G
17_44094133_CA_C	17	44094133	C	0.2124	-0.0473	0.0077	7.00E-10	0.2145	0.1132	0.01578	7.45E-13	17:44094133:CA:C
17_44094374_A_G	17	44094374	G	0.212	-0.0482	0.0076	2.32E-10	0.2139	0.1129	0.01578	8.38E-13	rs62062282:44094374:A:G
17_44094471_G_A	17	44094471	A	0.2123	-0.0477	0.0076	3.71E-10	0.2145	0.1138	0.01578	5.56E-13	rs17652502:44094471:G:A
17_44094667_C_G	17	44094667	G	0.212	-0.0483	0.0076	2.12E-10	0.2139	0.1132	0.01579	7.43E-13	rs2316948:44094667:C:G
17_44094871_A_G	17	44094871	G	0.212	-0.0482	0.0076	2.33E-10	0.2139	0.1133	0.01579	7.03E-13	rs9709338:44094871:A:G
17_44095055_C_A	17	44095055	A	0.212	-0.0482	0.0076	2.32E-10	0.2139	0.1133	0.01579	7.10E-13	rs62062283:44095055:C:A
17_44095335_C_A	17	44095335	A	0.212	-0.0482	0.0076	2.35E-10	0.2139	0.1131	0.01578	7.60E-13	rs111976319:44095335:C:A
17_44095467_T_C	17	44095467	C	0.2212	-0.0472	0.0075	3.27E-10	0.2237	0.1111	0.0156	1.08E-12	rs58879558:44095467:T:C
17_44095570_G_A	17	44095570	A	0.212	-0.0482	0.0076	2.33E-10	0.2139	0.1131	0.01578	7.80E-13	rs62062284:44095570:G:A
17_44095661_T_G	17	44095661	G	0.212	-0.0482	0.0076	2.31E-10	0.2139	0.113	0.01578	8.30E-13	rs62062285:44095661:T:G
17_44096486_C_T	17	44096486	T	0.2124	-0.0484	0.0076	2.03E-10	0.2143	0.1133	0.01579	7.24E-13	rs62062286:44096486:C:T
17_44096541_T_G	17	44096541	G	0.2138	-0.0467	0.0076	8.82E-10	0.2143	0.1151	0.01574	2.62E-13	rs62062287:44096541:T:G
17_44096553_G_A	17	44096553	A	0.2047	-0.0477	0.0078	1.07E-09	0.2071	0.1141	0.01617	1.69E-12	rs62062288:44096553:G:A
17_44097235_G_C	17	44097235	C	0.212	-0.0482	0.0076	2.31E-10	0.2139	0.1133	0.01578	7.13E-13	rs62062289:44097235:G:C
17_44098861_G_T	17	44098861	T	0.21	-0.0482	0.0077	2.94E-10	0.2113	0.1115	0.01589	2.35E-12	17:44098861:G:T
17_44098862_A_G	17	44098862	G	0.2106	-0.0484	0.0076	2.42E-10	0.2117	0.1118	0.01587	1.88E-12	17:44098862:A:G
17_44098967_G_A	17	44098967	A	0.2148	-0.0486	0.0076	1.54E-10	0.2157	0.1103	0.01571	2.28E-12	rs17652520:44098967:G:A
17_44099082_C_T	17	44099082	T	0.212	-0.0484	0.0076	1.92E-10	0.2139	0.1133	0.01578	7.01E-13	rs17573907:44099082:C:T
17_44099129_C_A	17	44099129	A	0.2115	-0.048	0.0076	3.10E-10	0.2129	0.1125	0.0158	1.09E-12	rs62062290:44099129:C:A
17_44099669_G_A	17	44099669	A	0.2123	-0.0482	0.0076	2.35E-10	0.2141	0.1134	0.01579	6.92E-13	rs55726761:44099669:G:A
17_44099809_A_C	17	44099809	C	0.212	-0.0484	0.0076	2.08E-10	0.2139	0.1133	0.01578	6.90E-13	rs62062292:44099809:A:C
17_44099827_C_G	17	44099827	G	0.212	-0.0482	0.0076	2.38E-10	0.2139	0.1131	0.01578	7.76E-13	rs77747656:44099827:C:G
17_44099856_G_GC	17	44099856	GC	0.2121	-0.0472	0.0077	7.49E-10	0.2139	0.1132	0.01578	7.28E-13	rs66885608:44099856:G:GC
17_44100553_C_A	17	44100553	A	0.212	-0.0485	0.0076	1.90E-10	0.2139	0.113	0.01578	8.15E-13	rs62062293:44100553:C:A
17_44100666_A_C	17	44100666	C	0.2122	-0.0489	0.0076	1.37E-10	0.2144	0.1131	0.01579	7.80E-13	rs62062294:44100666:A:C
17_44100906_A_G	17	44100906	G	0.212	-0.0483	0.0076	2.25E-10	0.2139	0.1139	0.01578	5.33E-13	rs62062295:44100906:A:G
17_44100916_C_T	17	44100916	T	0.212	-0.0483	0.0076	2.20E-10	0.2138	0.1134	0.01578	6.92E-13	rs62062296:44100916:C:T
17_44101004_A_G	17	44101004	G	0.212	-0.0483	0.0076	2.19E-10	0.2138	0.1133	0.01579	7.03E-13	rs62062297:44101004:A:G
17_44101563_T_C	17	44101563	C	0.2122	-0.0483	0.0076	2.20E-10	0.2144	0.1129	0.01579	8.66E-13	rs9468:44101563:T:C
17_44101775_A_AT	17	44101775	AT	0.2127	-0.0473	0.0077	7.25E-10	0.2144	0.1137	0.01579	6.10E-13	17:44101775:A:AT
17_44101849_T_TC	17	44101849	TC	0.2121	-0.0478	0.0077	4.93E-10	0.2138	0.1138	0.01578	5.40E-13	rs147268270:44101849:T:TC
17_44101871_A_G	17	44101871	G	0.2123	-0.0491	0.0076	1.08E-10	0.2144	0.1126	0.01577	9.68E-13	rs8712:44101871:A:G
17_44102443_C_CCT	17	44102443	CCT	0.2121	-0.0473	0.0077	7.18E-10	0.2138	0.1133	0.01579	7.16E-13	rs141412361:44102443:C:CCT
17_44102604_T_C	17	44102604	C	0.212	-0.0482	0.0076	2.31E-10	0.2138	0.1136	0.01578	6.17E-13	rs1052587:44102604:T:C
17_44102638_A_G	17	44102638	G	0.212	-0.0483	0.0076	2.24E-10	0.2138	0.1134	0.01578	6.91E-13	rs1052590:44102638:A:G
17_44102682_C_CT	17	44102682	CT	0.3993	-0.0256	0.0064	0.00005963	0.3836	0.07693	0.01314	4.73E-09	rs5820605:44102682:C:CT
17_44102689_G_C	17	44102689	C	0.212	-0.0482	0.0076	2.31E-10	0.2138	0.1134	0.01579	6.71E-13	rs1052594:44102689:G:C
17_44102741_TCA_T	17	44102741	T	0.2121	-0.0473	0.0077	7.33E-10	0.2138	0.113	0.01579	8.20E-13	17:44102741:TCA:T
17_44102865_A_C	17	44102865	C	0.212	-0.0483	0.0076	2.27E-10	0.2138	0.1133	0.01578	6.93E-13	rs17574040:44102865:A:C
17_44102933_T_C	17	44102933	C	0.2118	-0.0482	0.0076	2.38E-10	0.2137	0.1121	0.01579	1.26E-12	rs16940799:44102933:T:C
17_44103296_T_C	17	44103296	C	0.212	-0.0483	0.0076	2.14E-10	0.2138	0.1134	0.01579	6.89E-13	rs7687:44103296:T:C
17_44103616_C_T	17	44103616	T	0.212	-0.0483	0.0076	2.23E-10	0.2138	0.1134	0.01578	6.90E-13	rs17652748:44103616:C:T
17_44103825_T_C	17	44103825	C	0.2122	-0.0477	0.0076	3.64E-10	0.2139	0.1132	0.01578	7.26E-13	rs75010486:44103825:T:C
17_44103826_G_A	17	44103826	A	0.212	-0.0485	0.0076	1.80E-10	0.2138	0.1133	0.01578	7.10E-13	rs16940806:44103826:G:A

17_44103927_C_CT	17	44103927	CT	0.2121	-0.0473	0.0077	7.22E-10	0.2138	0.1134	0.01578	6.90E-13	17:44103927:C:CT
17_44104278_TG_T	17	44104278	T	0.2121	-0.0473	0.0077	7.23E-10	0.2138	0.1134	0.01578	6.90E-13	17:44104278:TG:T
17_44104343_A_C	17	44104343	C	0.212	-0.0483	0.0076	2.22E-10	0.2138	0.1134	0.01578	6.90E-13	rs2158257:44104343:A:C
17_44104410_TCTC_T	17	44104410	T	0.2122	-0.0474	0.0077	6.55E-10	0.2138	0.1131	0.01578	7.57E-13	17:44104410:TCTC:T
17_44104509_T_C	17	44104509	C	0.2121	-0.0485	0.0076	1.81E-10	0.2138	0.1131	0.01578	7.82E-13	rs17574228:44104509:T:C
17_44104576_CCTT_C	17	44104576	C	0.215	-0.047	0.0076	7.93E-10	0.2159	0.1149	0.01572	2.66E-13	17:44104576:CCTT:C
17_44106219_C_T	17	44106219	T	0.212	-0.0483	0.0076	2.12E-10	0.2138	0.1129	0.01579	8.48E-13	rs78681971:44106219:C:T
17_44106220_A_G	17	44106220	G	0.2123	-0.048	0.0076	2.61E-10	0.2139	0.115	0.01576	2.95E-13	rs79772576:44106220:A:G
17_44106515_AAAG_A	17	44106515	A	0.2121	-0.0473	0.0077	7.24E-10	0.2138	0.1132	0.01578	7.27E-13	rs149028349:44106515:AAAG:A
17_44106806_G_A	17	44106806	A	0.2121	-0.0484	0.0076	1.97E-10	0.2139	0.1131	0.01578	7.70E-13	rs78229689:44106806:G:A
17_44107321_CT_C	17	44107321	C	0.2175	-0.0464	0.0077	1.40E-09	0.219	0.1127	0.01576	8.44E-13	rs371902677:44107321:CT:C
17_44107487_GT_G	17	44107487	G	0.2146	-0.0475	0.0077	6.23E-10	0.2166	0.1102	0.01579	2.95E-12	17:44107487:GT:G
17_44107513_GT_G	17	44107513	G	0.2128	-0.0466	0.0077	1.32E-09	0.2142	0.1126	0.01579	9.94E-13	17:44107513:GT:G
17_44107606_A_AT	17	44107606	AT	0.213	-0.0475	0.0077	6.75E-10	0.2142	0.1132	0.0158	7.75E-13	17:44107606:A:AT
17_44108100_C_T	17	44108100	T	0.212	-0.0483	0.0076	2.15E-10	0.2138	0.1132	0.01578	7.30E-13	rs7350928:44108100:C:T
17_44108202_A_G	17	44108202	G	0.212	-0.0484	0.0076	1.97E-10	0.2138	0.113	0.01578	8.24E-13	rs17574361:44108202:A:G
17_44108355_G_A	17	44108355	A	0.212	-0.0485	0.0076	1.86E-10	0.2138	0.113	0.01578	7.96E-13	rs17652961:44108355:G:A
17_44108482_A_AGCCCTCT	17	44108482	AGCCCTCT	0.2121	-0.0473	0.0077	7.22E-10	0.2138	0.1133	0.01578	7.24E-13	17:44108482:A:AGCCCTCT
17_44108906_A_G	17	44108906	G	0.212	-0.0482	0.0076	2.46E-10	0.2138	0.113	0.01579	8.28E-13	rs34579536:44108906:A:G
17_44109188_C_G	17	44109188	G	0.212	-0.0482	0.0076	2.31E-10	0.2138	0.1128	0.01579	8.97E-13	rs17574425:44109188:C:G
17_44109248_G_A	17	44109248	A	0.212	-0.0482	0.0076	2.29E-10	0.2138	0.1128	0.01579	9.09E-13	rs55881134:44109248:G:A
17_44109769_C_G	17	44109769	G	0.2118	-0.0483	0.0076	2.26E-10	0.2136	0.1127	0.01579	9.61E-13	rs1076222:44109769:C:G
17_44110271_G_A	17	44110271	A	0.2165	-0.0474	0.0076	3.34E-10	0.2164	0.1132	0.01566	4.89E-13	rs7350980:44110271:G:A
17_44110532_G_A	17	44110532	A	0.212	-0.0482	0.0076	2.29E-10	0.2138	0.1133	0.01578	7.16E-13	rs36076725:44110532:G:A
17_44110541_G_A	17	44110541	A	0.212	-0.0483	0.0076	2.20E-10	0.2138	0.113	0.01579	8.07E-13	rs35833914:44110541:G:A
17_44110670_C_G	17	44110670	G	0.2165	-0.0475	0.0076	3.18E-10	0.2164	0.1133	0.01566	4.68E-13	rs4597358:44110670:C:G
17_44110888_A_T	17	44110888	T	0.212	-0.0482	0.0076	2.30E-10	0.2138	0.1134	0.01578	6.63E-13	rs77009866:44110888:A:T
17_44111109_A_G	17	44111109	G	0.212	-0.0483	0.0076	2.22E-10	0.2138	0.1131	0.01578	7.82E-13	rs62062321:44111109:A:G
17_44111613_A_G	17	44111613	G	0.212	-0.0483	0.0076	2.18E-10	0.2138	0.1131	0.01578	7.62E-13	rs17574604:44111613:A:G
17_44111827_C_A	17	44111827	A	0.212	-0.0484	0.0076	2.08E-10	0.2138	0.1131	0.01579	7.76E-13	rs17653162:44111827:C:A
17_44112385_A_G	17	44112385	G	0.212	-0.0483	0.0076	2.24E-10	0.2138	0.1133	0.01578	7.19E-13	rs62062322:44112385:A:G
17_44112441_G_A	17	44112441	A	0.212	-0.0482	0.0076	2.29E-10	0.2138	0.1131	0.01578	7.62E-13	rs17653193:44112441:G:A
17_44112638_T_C	17	44112638	C	0.212	-0.0483	0.0076	2.23E-10	0.2138	0.1131	0.01578	7.62E-13	rs17653211:44112638:T:C
17_44112743_C_A	17	44112743	A	0.212	-0.0483	0.0076	2.12E-10	0.2138	0.1127	0.01578	9.13E-13	rs17653255:44112743:C:A
17_44113197_G_GA	17	44113197	GA	0.2122	-0.0473	0.0077	7.41E-10	0.2138	0.1131	0.01578	7.62E-13	rs201474071:44113197:G:GA
17_44113224_C_T	17	44113224	T	0.2122	-0.0477	0.0076	3.59E-10	0.214	0.1136	0.01578	6.26E-13	rs62062323:44113224:C:T
17_44113227_T_TG	17	44113227	TG	0.2124	-0.0469	0.0077	1.01E-09	0.214	0.1136	0.01578	6.08E-13	rs141698966:44113227:T:TG
17_44113359_T_C	17	44113359	C	0.212	-0.0483	0.0076	2.27E-10	0.2138	0.1132	0.01579	7.36E-13	rs4608377:44113359:T:C
17_44113392_T_A	17	44113392	A	0.1996	-0.0503	0.008	3.44E-10	0.1967	0.1172	0.01654	1.41E-12	17:44113392:T:A
17_44113491_T_C	17	44113491	C	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs12185225:44113491:T:C
17_44113787_T_TG	17	44113787	TG	0.2121	-0.0472	0.0077	7.59E-10	0.2138	0.1133	0.01579	7.17E-13	17:44113787:T:TG
17_44113963_C_T	17	44113963	T	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs12150438:44113963:C:T
17_44114090_CT_C	17	44114090	C	0.2538	-0.0424	0.0076	2.64E-08	0.2565	0.09073	0.01573	8.11E-09	17:44114090:CT:C
17_44114218_T_C	17	44114218	C	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs12150162:44114218:T:C
17_44114362_A_T	17	44114362	T	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs62062324:44114362:A:T
17_44114364_C_A	17	44114364	A	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs62062325:44114364:C:A
17_44114372_T_C	17	44114372	C	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs62062133:44114372:T:C
17_44114432_A_C	17	44114432	C	0.212	-0.0483	0.0076	2.25E-10	0.2138	0.1138	0.01578	5.42E-13	rs62062134:44114432:A:C
17_44115074_T_C	17	44115074	C	0.212	-0.0483	0.0076	2.28E-10	0.2138	0.1131	0.01578	7.62E-13	rs17574796:44115074:T:C
17_44115107_C_T	17	44115107	T	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.17E-13	rs17574824:44115107:C:T
17_44115351_T_C	17	44115351	C	0.2124	-0.0478	0.0076	3.21E-10	0.214	0.114	0.01578	5.02E-13	rs12185243:44115351:T:C
17_44115440_T_C	17	44115440	C	0.2165	-0.0474	0.0076	3.42E-10	0.2164	0.1133	0.01566	4.60E-13	rs8077487:44115440:T:C
17_44115569_C_A	17	44115569	A	0.212	-0.0483	0.0076	2.15E-10	0.2138	0.1132	0.01579	7.33E-13	rs11079729:44115569:C:A
17_44115730_G_A	17	44115730	A	0.212	-0.0483	0.0076	2.18E-10	0.2138	0.1132	0.01578	7.46E-13	rs12150542:44115730:G:A
17_44115886_C_T	17	44115886	T	0.212	-0.0483	0.0076	2.17E-10	0.2138	0.1132	0.01579	7.55E-13	rs12150090:44115886:C:T

17_44116238_G_A	17	44116238	A	0.212	-0.0482	0.0076	2.30E-10	0.2138	0.1133	0.01579	7.20E-13	rs41437445:44116238:G:A
17_44116312_T_C	17	44116312	C	0.212	-0.0481	0.0076	2.51E-10	0.2138	0.1131	0.01578	7.64E-13	rs62062136:44116312:T:C
17_44116950_T_G	17	44116950	G	0.2165	-0.0474	0.0076	3.50E-10	0.2164	0.1134	0.01566	4.53E-13	rs7221390:44116950:T:G
17_44117119_A_G	17	44117119	G	0.212	-0.0483	0.0076	2.24E-10	0.2138	0.1131	0.01578	7.62E-13	rs34043286:44117119:A:G
17_44117397_A_G	17	44117397	G	0.212	-0.0483	0.0076	2.14E-10	0.2138	0.1131	0.01578	7.62E-13	rs10514897:44117397:A:G
17_44118848_G_A	17	44118848	A	0.212	-0.0482	0.0076	2.36E-10	0.2138	0.1132	0.01579	7.56E-13	rs62062137:44118848:G:A
17_44118999_A_G	17	44118999	G	0.212	-0.0482	0.0076	2.29E-10	0.2138	0.1131	0.01578	7.62E-13	rs41382552:44118999:A:G
17_44119320_C_T	17	44119320	T	0.2119	-0.0481	0.0076	2.63E-10	0.2137	0.1131	0.01579	7.77E-13	rs55893711:44119320:C:T
17_44119463_C_T	17	44119463	T	0.2107	-0.0483	0.0076	2.62E-10	0.2124	0.1124	0.01587	1.41E-12	rs55649944:44119463:C:T
17_44119474_T_C	17	44119474	C	0.2106	-0.0483	0.0076	2.57E-10	0.2123	0.1125	0.01587	1.36E-12	rs56406462:44119474:T:C
17_44119500_C_CTT	17	44119500	CTT	0.2107	-0.0473	0.0077	8.45E-10	0.2123	0.1125	0.01587	1.36E-12	17:44119500:C:CTT
17_44119636_A_C	17	44119636	C	0.212	-0.0484	0.0076	2.05E-10	0.2138	0.1129	0.01578	8.62E-13	rs10514898:44119636:A:C
17_44120442_A_G	17	44120442	G	0.212	-0.0483	0.0076	2.24E-10	0.2138	0.1131	0.01578	7.62E-13	rs41374248:44120442:A:G
17_44120608_A_G	17	44120608	G	0.212	-0.0482	0.0076	2.29E-10	0.2138	0.1126	0.01578	9.57E-13	rs79252344:44120608:A:G
17_44121469_C_T	17	44121469	T	0.212	-0.0483	0.0076	2.14E-10	0.2138	0.113	0.01578	7.97E-13	17:44121469:C:T
17_44121917_C_T	17	44121917	T	0.212	-0.0482	0.0076	2.35E-10	0.2138	0.1134	0.01578	6.90E-13	17:44121917:C:T
17_44122345_A_G	17	44122345	G	0.2078	-0.0485	0.0077	3.27E-10	0.2102	0.1139	0.016	1.09E-12	17:44122345:A:G
17_44122348_C_T	17	44122348	T	0.2078	-0.0485	0.0077	3.34E-10	0.2102	0.1139	0.016	1.09E-12	17:44122348:C:T
17_44122354_A_G	17	44122354	G	0.2078	-0.0484	0.0077	3.68E-10	0.2102	0.1139	0.016	1.09E-12	17:44122354:A:G
17_44122484_C_T	17	44122484	T	0.212	-0.0483	0.0076	2.26E-10	0.2138	0.1131	0.01578	7.63E-13	17:44122484:C:T
17_44122626_C_A	17	44122626	A	0.212	-0.0481	0.0076	2.69E-10	0.2138	0.1131	0.01578	7.63E-13	17:44122626:C:A
17_44122896_G_A	17	44122896	A	0.212	-0.0481	0.0076	2.55E-10	0.2138	0.1131	0.01578	7.63E-13	rs77105679:44122896:G:A
17_44123248_T_C	17	44123248	C	0.2116	-0.0483	0.0076	2.34E-10	0.2134	0.1131	0.01579	7.90E-13	rs62063670:44123248:T:C
17_44123685_G_A	17	44123685	A	0.212	-0.048	0.0076	2.83E-10	0.2138	0.1131	0.01579	7.89E-13	rs74571696:44123685:G:A
17_44123717_C_T	17	44123717	T	0.212	-0.048	0.0076	2.83E-10	0.2138	0.1131	0.01579	7.89E-13	rs79698033:44123717:C:T
17_44124535_T_C	17	44124535	C	0.212	-0.0481	0.0076	2.66E-10	0.2138	0.1136	0.01578	6.22E-13	rs79065019:44124535:T:C
17_44124837_A_G	17	44124837	G	0.212	-0.048	0.0076	2.77E-10	0.2138	0.1131	0.01578	7.63E-13	rs62063671:44124837:A:G
17_44125066_C_T	17	44125066	T	0.212	-0.048	0.0076	2.82E-10	0.2109	0.1132	0.01627	3.46E-12	rs112578465:44125066:C:T
17_44125277_CT_C	17	44125277	C	0.2169	-0.0462	0.0076	1.27E-09	0.217	0.1127	0.01566	6.19E-13	17:44125277:CT:C
17_44125288_A_G	17	44125288	G	0.212	-0.048	0.0076	2.82E-10	0.2082	0.1043	0.01609	9.03E-11	rs62063672:44125288:A:G
17_44125484_T_G	17	44125484	G	0.212	-0.048	0.0076	2.82E-10	0.2082	0.1043	0.01609	8.87E-11	rs62063673:44125484:T:G
17_44125704_C_T	17	44125704	T	0.212	-0.048	0.0076	2.82E-10	0.2082	0.1044	0.01609	8.69E-11	rs12150336:44125704:C:T
17_44126218_G_A	17	44126218	A	0.212	-0.048	0.0076	2.82E-10	0.2082	0.1045	0.01609	8.29E-11	rs12150570:44126218:G:A
17_44126365_C_T	17	44126365	T	0.2165	-0.0474	0.0076	3.48E-10	0.2165	0.113	0.01566	5.32E-13	rs7218319:44126365:C:T
17_44126473_AG_A	17	44126473	A	0.2166	-0.0462	0.0076	1.27E-09	0.2165	0.1133	0.01566	4.65E-13	17:44126473:AG:A
17_44126477_G_A	17	44126477	A	0.2165	-0.0472	0.0076	4.15E-10	0.2164	0.1164	0.01552	6.27E-14	17:44126477:G:A
17_44126478_T_C	17	44126478	C	0.2165	-0.0472	0.0076	4.15E-10	0.2164	0.1163	0.0155	6.23E-14	17:44126478:T:C
17_44126575_C_T	17	44126575	T	0.213	-0.0484	0.0076	1.92E-10	0.215	0.1134	0.01579	6.67E-13	rs62063675:44126575:C:T
17_44126650_C_T	17	44126650	T	0.212	-0.048	0.0076	2.88E-10	0.2137	0.1133	0.0158	7.66E-13	rs112746008:44126650:C:T
17_44126673_A_G	17	44126673	G	0.212	-0.048	0.0076	2.89E-10	0.2137	0.1133	0.0158	7.67E-13	rs112333322:44126673:A:G
17_44126691_G_A	17	44126691	A	0.212	-0.048	0.0076	2.89E-10	0.2137	0.1133	0.0158	7.67E-13	rs111327992:44126691:G:A
17_44126765_C_A	17	44126765	A	0.1854	-0.0478	0.0082	4.70E-09	0.1901	0.1122	0.01682	2.54E-11	rs113434679:44126765:C:A
17_44126977_G_C	17	44126977	C	0.212	-0.048	0.0076	2.91E-10	0.2138	0.1132	0.0158	7.77E-13	rs74977736:44126977:G:C
17_44127285_CTT_C	17	44127285	C	0.2137	-0.0475	0.0077	6.00E-10	0.2147	0.1136	0.01579	6.14E-13	17:44127285:CTT:C
17_44127471_GTGGTTTCA(	17	44127471	G	0.2117	-0.0473	0.0077	7.52E-10	0.2133	0.1135	0.01581	7.03E-13	17:44127471:GTGGTTTCACCA:G
17_44128125_A_C	17	44128125	C	0.212	-0.0479	0.0076	3.00E-10	0.2138	0.113	0.01579	8.17E-13	rs12150447:44128125:A:C
17_44128407_C_A	17	44128407	A	0.212	-0.048	0.0076	2.83E-10	0.2138	0.1128	0.01578	8.94E-13	rs12150064:44128407:C:A
17_44128754_G_GA	17	44128754	GA	0.2121	-0.047	0.0077	9.37E-10	0.2138	0.113	0.01579	8.25E-13	17:44128754:G:GA
17_44128876_T_A	17	44128876	A	0.212	-0.048	0.0076	2.95E-10	0.2138	0.113	0.01579	8.25E-13	rs17653836:44128876:T:A
17_44129253_T_C	17	44129253	C	0.212	-0.048	0.0076	2.74E-10	0.2138	0.1133	0.01578	7.25E-13	rs17575423:44129253:T:C
17_44129398_G_GA	17	44129398	GA	0.2116	-0.0478	0.0077	6.46E-10	0.2124	0.1123	0.01585	1.37E-12	rs66502149:44129398:G:GA
17_44129800_G_A	17	44129800	A	0.212	-0.048	0.0076	2.95E-10	0.2138	0.113	0.01579	8.25E-13	rs62063676:44129800:G:A
17_44129885_C_T	17	44129885	T	0.212	-0.048	0.0076	2.95E-10	0.2138	0.113	0.01579	8.25E-13	rs62063677:44129885:C:T
17_44129949_C_G	17	44129949	G	0.212	-0.048	0.0076	2.95E-10	0.2138	0.113	0.01579	8.25E-13	rs62063678:44129949:C:G
17_44129997_AAAC_A	17	44129997	A	0.2121	-0.047	0.0077	9.37E-10	0.2138	0.113	0.01579	8.25E-13	rs142767245:44129997:AAAC:A

17_44130160_TAAA_T	17	44130160	T	0.2761	-0.0353	0.0072	8.39E-07	0.2788	0.09482	0.01504	2.86E-10	rs367643153:44130160:TAAA:T
17_44130328_TC_T	17	44130328	T	0.2164	-0.0468	0.0076	8.39E-10	0.2188	0.1055	0.01464	5.63E-13	rs35443051:44130328:TC:T
17_44130587_T_G	17	44130587	G	0.212	-0.048	0.0076	2.96E-10	0.2138	0.113	0.01579	8.25E-13	rs79649865:44130587:T:G
17_44130668_T_A	17	44130668	A	0.212	-0.0479	0.0076	3.00E-10	0.2138	0.1129	0.01578	8.65E-13	rs75546272:44130668:T:A
17_44130878_A_G	17	44130878	G	0.212	-0.048	0.0076	2.96E-10	0.2138	0.113	0.01579	8.25E-13	rs111853996:44130878:A:G
17_44130924_A_T	17	44130924	T	0.212	-0.048	0.0076	2.96E-10	0.2138	0.113	0.01579	8.25E-13	rs112674766:44130924:A:T
17_44131022_T_C	17	44131022	C	0.212	-0.048	0.0076	2.96E-10	0.2138	0.113	0.01579	8.25E-13	rs112074397:44131022:T:C
17_44131559_C_A	17	44131559	A	0.2119	-0.0479	0.0076	3.03E-10	0.2138	0.113	0.01579	8.25E-13	rs62063680:44131559:C:A
17_44131592_A_G	17	44131592	G	0.212	-0.0479	0.0076	3.02E-10	0.2138	0.113	0.01579	8.27E-13	rs62063681:44131592:A:G
17_44131622_G_A	17	44131622	A	0.2119	-0.0479	0.0076	3.03E-10	0.2138	0.113	0.01579	8.25E-13	rs62063682:44131622:G:A
17_44131717_G_A	17	44131717	A	0.2119	-0.0479	0.0076	2.99E-10	0.2138	0.113	0.01579	8.25E-13	rs62063683:44131717:G:A
17_44131798_C_T	17	44131798	T	0.212	-0.0481	0.0076	2.58E-10	0.2138	0.1131	0.01578	7.79E-13	rs79180862:44131798:C:T
17_44132269_T_C	17	44132269	C	0.2119	-0.048	0.0076	2.88E-10	0.2138	0.113	0.01579	8.25E-13	rs62063684:44132269:T:C
17_44132379_A_G	17	44132379	G	0.2119	-0.048	0.0076	2.81E-10	0.2138	0.113	0.01579	8.25E-13	rs62063685:44132379:A:G
17_44132458_G_A	17	44132458	A	0.2119	-0.048	0.0076	2.78E-10	0.2138	0.113	0.01579	8.25E-13	rs62063686:44132458:G:A
17_44132592_A_G	17	44132592	G	0.2119	-0.048	0.0076	2.77E-10	0.2138	0.113	0.01579	8.25E-13	rs62063687:44132592:A:G
17_44132887_C_T	17	44132887	T	0.212	-0.0483	0.0076	2.26E-10	0.2138	0.113	0.01578	8.08E-13	rs62060760:44132887:C:T
17_44133031_T_A	17	44133031	A	0.2119	-0.0481	0.0076	2.61E-10	0.2138	0.1128	0.01579	8.84E-13	rs17575437:44133031:T:A
17_44133070_A_T	17	44133070	T	0.2119	-0.0481	0.0076	2.54E-10	0.2138	0.113	0.01578	8.18E-13	rs17653889:44133070:A:T
17_44133142_G_A	17	44133142	A	0.212	-0.0482	0.0076	2.29E-10	0.2139	0.1125	0.01578	1.02E-12	rs17653906:44133142:G:A
17_44133162_A_C	17	44133162	C	0.2119	-0.0481	0.0076	2.65E-10	0.2138	0.113	0.01579	8.24E-13	rs62060761:44133162:A:C
17_44133396_G_A	17	44133396	A	0.2119	-0.0481	0.0076	2.65E-10	0.2138	0.113	0.01579	8.24E-13	rs62060762:44133396:G:A
17_44133403_T_C	17	44133403	C	0.2119	-0.0481	0.0076	2.60E-10	0.2138	0.113	0.01579	8.24E-13	rs62060763:44133403:T:C
17_44133534_C_T	17	44133534	T	0.2119	-0.0481	0.0076	2.67E-10	0.2138	0.113	0.01579	8.24E-13	rs111259120:44133534:C:T
17_44133633_A_G	17	44133633	G	0.2119	-0.0481	0.0076	2.67E-10	0.2138	0.113	0.01579	8.24E-13	rs62060764:44133633:A:G
17_44133648_A_C	17	44133648	C	0.2119	-0.0481	0.0076	2.67E-10	0.2138	0.113	0.01579	8.24E-13	rs62060765:44133648:A:C
17_44133818_TA_T	17	44133818	T	0.2145	-0.0466	0.0077	1.23E-09	0.2177	0.1112	0.01577	1.78E-12	rs71920662:44133818:TA:T
17_44133950_CTGATAGAA	17	44133950	C	0.1776	-0.0535	0.0087	7.70E-10	0.1797	0.1172	0.01797	6.85E-11	44133950:CTGATAGAACATTTACCATCAAACT:C
17_44134095_A_G	17	44134095	G	0.2119	-0.0482	0.0076	2.44E-10	0.2138	0.113	0.01578	8.09E-13	rs17575507:44134095:A:G
17_44134391_G_T	17	44134391	T	0.2119	-0.0482	0.0076	2.46E-10	0.2138	0.1131	0.01578	7.64E-13	rs876944:44134391:G:T
17_44134910_G_A	17	44134910	A	0.2119	-0.0482	0.0076	2.43E-10	0.2138	0.1131	0.01578	7.85E-13	rs62060767:44134910:G:A
17_44134984_G_A	17	44134984	A	0.2119	-0.0481	0.0076	2.65E-10	0.2138	0.113	0.01579	8.25E-13	rs62060768:44134984:G:A
17_44135026_G_C	17	44135026	C	0.2119	-0.0481	0.0076	2.65E-10	0.2138	0.113	0.01579	8.25E-13	rs62060769:44135026:G:C
17_44135359_T_C	17	44135359	C	0.2119	-0.0483	0.0076	2.26E-10	0.2138	0.1131	0.01578	7.61E-13	rs1107820:44135359:T:C
17_44135827_G_A	17	44135827	A	0.2122	-0.0477	0.0076	3.60E-10	0.2144	0.1139	0.01578	5.27E-13	rs17575556:44135827:G:A
17_44135985_A_G	17	44135985	G	0.2119	-0.0481	0.0076	2.69E-10	0.2138	0.113	0.01579	8.25E-13	rs17653998:44135985:A:G
17_44136425_AAAG_A	17	44136425	A	0.2121	-0.0471	0.0077	8.53E-10	0.2138	0.113	0.01579	8.24E-13	rs201194882:44136425:AAAG:A
17_44136577_A_C	17	44136577	C	0.2119	-0.0482	0.0076	2.49E-10	0.2138	0.1131	0.01578	7.64E-13	rs111372048:44136577:A:C
17_44136634_G_A	17	44136634	A	0.2119	-0.0482	0.0076	2.47E-10	0.2138	0.1134	0.01579	6.89E-13	rs62060785:44136634:G:A
17_44136763_C_T	17	44136763	T	0.2119	-0.0481	0.0076	2.71E-10	0.2138	0.113	0.01579	8.24E-13	rs62060786:44136763:C:T
17_44136803_G_T	17	44136803	T	0.2119	-0.0481	0.0076	2.71E-10	0.2138	0.113	0.01579	8.24E-13	rs62060787:44136803:G:T
17_44137009_AAAAAAGAG	17	44137009	A	0.2151	-0.0466	0.0076	1.05E-09	0.2153	0.1127	0.01574	8.20E-13	0791233:44137009:AAAAAAGAG:A
17_44137070_A_G	17	44137070	G	0.2122	-0.0485	0.0076	1.88E-10	0.2145	0.1132	0.01578	7.48E-13	rs41384744:44137070:A:G
17_44137189_A_T	17	44137189	T	0.2119	-0.048	0.0076	2.72E-10	0.2138	0.113	0.01579	8.24E-13	rs55714296:44137189:A:T
17_44137311_G_A	17	44137311	A	0.2119	-0.048	0.0076	2.72E-10	0.2138	0.113	0.01579	8.24E-13	rs55690782:44137311:G:A
17_44137386_T_TAA	17	44137386	TAA	0.2102	-0.0464	0.0077	1.76E-09	0.2114	0.1142	0.01585	5.72E-13	17:44137386:T:TAA
17_44137676_A_T	17	44137676	T	0.2117	-0.0481	0.0076	2.61E-10	0.2121	0.1128	0.01579	9.11E-13	17:44137676:A:T
17_44137678_G_A	17	44137678	A	0.2117	-0.0482	0.0076	2.54E-10	0.2121	0.1129	0.01579	8.79E-13	17:44137678:G:A
17_44137925_T_C	17	44137925	C	0.2119	-0.0481	0.0076	2.58E-10	0.2138	0.1133	0.01578	6.97E-13	rs17654016:44137925:T:C
17_44138201_T_C	17	44138201	C	0.2165	-0.0472	0.0076	3.97E-10	0.2165	0.113	0.01566	5.42E-13	rs7220752:44138201:T:C
17_44138377_G_GA	17	44138377	GA	0.2121	-0.0471	0.0077	8.43E-10	0.2138	0.1131	0.01579	7.79E-13	17:44138377:G:GA
17_44139083_G_C	17	44139083	C	0.212	-0.048	0.0076	2.89E-10	0.214	0.1132	0.01578	7.35E-13	rs2316951:44139083:G:C
17_44139190_G_C	17	44139190	C	0.2119	-0.0481	0.0076	2.67E-10	0.2138	0.1131	0.01579	7.79E-13	rs2316952:44139190:G:C
17_44139472_A_C	17	44139472	C	0.1015	-0.0605	0.0125	1.23E-06	0.1012	0.1647	0.02415	9.28E-12	17:44139472:A:C
17_44139487_A_AC	17	44139487	A	0.4719	-0.0175	0.0072	0.01571	0.4745	0.08703	0.01524	1.13E-08	17:44139487:A:AC

17_44139662_C_T	17	44139662	T	0.2119	-0.0482	0.0076	2.35E-10	0.2138	0.1133	0.01579	7.21E-13	rs17575683:44139662:C:T
17_44139762_C_G	17	44139762	G	0.2119	-0.0481	0.0076	2.67E-10	0.2138	0.1131	0.01579	7.79E-13	rs112411928:44139762:C:G
17_44140341_G_A	17	44140341	A	0.2119	-0.0481	0.0076	2.65E-10	0.2138	0.1131	0.01579	7.79E-13	rs2316953:44140341:G:A
17_44141347_A_G	17	44141347	G	0.2119	-0.0482	0.0076	2.32E-10	0.2138	0.1131	0.01579	7.97E-13	rs2838:44141347:A:G
17_44141732_G_A	17	44141732	A	0.2119	-0.0482	0.0076	2.36E-10	0.2138	0.1134	0.01578	6.77E-13	rs12150127:44141732:G:A
17_44141955_T_A	17	44141955	A	0.2119	-0.0481	0.0076	2.50E-10	0.2138	0.1132	0.01578	7.55E-13	rs62060792:44141955:T:A
17_44142121_G_A	17	44142121	A	0.2119	-0.0481	0.0076	2.62E-10	0.2138	0.1131	0.01579	7.85E-13	rs76307183:44142121:G:A
17_44142231_T_TA	17	44142231	TA	0.212	-0.0471	0.0077	8.32E-10	0.2138	0.1131	0.01579	7.90E-13	rs150514510:44142231:T:TA
17_44142332_T_G	17	44142332	G	0.2119	-0.0481	0.0076	2.61E-10	0.2138	0.1131	0.01579	7.94E-13	17:44142332:T:G
17_44142334_G_T	17	44142334	T	0.2119	-0.0481	0.0076	2.61E-10	0.2138	0.1131	0.01579	7.94E-13	17:44142334:G:T
17_44142427_A_G	17	44142427	G	0.2119	-0.0481	0.0076	2.60E-10	0.2138	0.113	0.01579	7.98E-13	rs62060793:44142427:A:G
17_44142491_C_CCA	17	44142491	CCA	0.2121	-0.0471	0.0077	8.28E-10	0.2138	0.113	0.01579	8.01E-13	rs146149698:44142491:C:CCA
17_44142566_C_T	17	44142566	T	0.2119	-0.0481	0.0076	2.60E-10	0.2138	0.113	0.01579	8.04E-13	rs62060794:44142566:C:T
17_44142663_C_T	17	44142663	T	0.2121	-0.048	0.0076	2.89E-10	0.2139	0.1132	0.01579	7.45E-13	rs62060795:44142663:C:T
17_44142879_C_T	17	44142879	T	0.2119	-0.0481	0.0076	2.59E-10	0.2138	0.113	0.01579	8.18E-13	rs17575773:44142879:C:T
17_44143029_G_T	17	44143029	T	0.212	-0.0484	0.0076	2.01E-10	0.2138	0.1127	0.01578	9.15E-13	rs62060796:44143029:G:T
17_44143344_G_A	17	44143344	A	0.2119	-0.0481	0.0076	2.53E-10	0.2138	0.113	0.01579	8.25E-13	rs62060797:44143344:G:A
17_44143484_G_A	17	44143484	A	0.2119	-0.0481	0.0076	2.50E-10	0.2138	0.113	0.01579	8.25E-13	rs12150344:44143484:G:A
17_44144152_T_C	17	44144152	C	0.2121	-0.0483	0.0076	2.30E-10	0.214	0.1134	0.01578	6.83E-13	rs62060798:44144152:T:C
17_44144251_G_T	17	44144251	T	0.2121	-0.0482	0.0076	2.41E-10	0.214	0.113	0.01579	8.37E-13	rs62060799:44144251:G:T
17_44144345_A_G	17	44144345	G	0.2119	-0.0483	0.0076	2.23E-10	0.2138	0.1127	0.01578	9.17E-13	rs17575822:44144345:A:G
17_44144387_C_A	17	44144387	A	0.2119	-0.0484	0.0076	2.05E-10	0.2138	0.1131	0.01578	7.64E-13	rs17575850:44144387:C:A
17_44144634_G_A	17	44144634	A	0.2119	-0.0483	0.0076	2.19E-10	0.2138	0.113	0.01579	7.99E-13	rs17659731:44144634:G:A
17_44145373_T_C	17	44145373	C	0.2119	-0.0485	0.0076	1.91E-10	0.2138	0.1132	0.01578	7.57E-13	rs75641221:44145373:T:C
17_44145512_CAAG_C	17	44145512	C	0.2121	-0.0474	0.0077	6.62E-10	0.2138	0.1133	0.01579	7.16E-13	17:44145512:CAAG:C
17_44145592_A_G	17	44145592	G	0.2119	-0.0484	0.0076	1.95E-10	0.2138	0.1133	0.01579	7.24E-13	rs62060800:44145592:A:G
17_44145860_A_G	17	44145860	G	0.2119	-0.0483	0.0076	2.17E-10	0.2138	0.113	0.01579	8.25E-13	rs62060801:44145860:A:G
17_44146165_C_G	17	44146165	G	0.2119	-0.0483	0.0076	2.15E-10	0.2138	0.1131	0.01578	7.64E-13	rs17659743:44146165:C:G
17_44146336_A_C	17	44146336	C	0.2118	-0.0483	0.0076	2.11E-10	0.2138	0.113	0.01579	8.20E-13	rs62060802:44146336:A:C
17_44146357_T_C	17	44146357	C	0.2118	-0.0484	0.0076	2.08E-10	0.2138	0.113	0.01579	8.20E-13	rs75975083:44146357:T:C
17_44146451_T_C	17	44146451	C	0.2118	-0.0484	0.0076	2.07E-10	0.2138	0.113	0.01579	8.18E-13	rs77950913:44146451:T:C
17_44146567_T_C	17	44146567	C	0.2118	-0.0484	0.0076	2.02E-10	0.2138	0.113	0.01579	8.15E-13	rs79782347:44146567:T:C
17_44147411_G_A	17	44147411	A	0.2118	-0.0484	0.0076	1.99E-10	0.2138	0.1133	0.01578	7.05E-13	rs56318865:44147411:G:A
17_44147511_G_C	17	44147511	C	0.2119	-0.0483	0.0076	2.22E-10	0.2138	0.1131	0.01578	7.95E-13	rs56041778:44147511:G:C
17_44147574_G_A	17	44147574	A	0.2119	-0.0484	0.0076	1.93E-10	0.2139	0.1133	0.01578	6.93E-13	rs55947022:44147574:G:A
17_44147599_G_C	17	44147599	C	0.2118	-0.0486	0.0076	1.72E-10	0.2138	0.113	0.01578	7.95E-13	rs55929190:44147599:G:C
17_44147721_C_T	17	44147721	T	0.2121	-0.0486	0.0076	1.63E-10	0.2142	0.113	0.01578	8.24E-13	rs56323408:44147721:C:T
17_44148267_C_T	17	44148267	T	0.2123	-0.0489	0.0076	1.31E-10	0.2143	0.1133	0.01578	7.03E-13	rs55831516:44148267:C:T
17_44148613_G_A	17	44148613	A	0.2123	-0.0486	0.0076	1.55E-10	0.2143	0.1133	0.01578	6.89E-13	rs62060809:44148613:G:A
17_44148674_A_G	17	44148674	G	0.2124	-0.0485	0.0076	1.68E-10	0.2144	0.1127	0.01577	9.11E-13	rs62060810:44148674:A:G
17_44149210_G_GA	17	44149210	GA	0.212	-0.0473	0.0077	7.01E-10	0.2138	0.1132	0.01578	7.21E-13	17:44149210:G:GA
17_44149297_A_C	17	44149297	C	0.2118	-0.0483	0.0076	2.17E-10	0.2138	0.1121	0.01578	1.24E-12	rs1117253:44149297:A:C
17_44149348_A_C	17	44149348	C	0.2124	-0.0489	0.0076	1.66E-10	0.2143	0.1141	0.01587	6.56E-13	17:44149348:A:C
17_44149448_C_G	17	44149448	G	0.2118	-0.0484	0.0076	1.97E-10	0.2138	0.1135	0.01578	6.47E-13	rs12150625:44149448:C:G
17_44149537_C_G	17	44149537	G	0.2119	-0.0484	0.0076	1.96E-10	0.2138	0.1138	0.01578	5.50E-13	rs12150627:44149537:C:G
17_44149581_C_T	17	44149581	T	0.2118	-0.0484	0.0076	1.98E-10	0.2138	0.1133	0.01578	7.03E-13	rs12150628:44149581:C:T
17_44149741_G_A	17	44149741	A	0.2118	-0.0486	0.0076	1.70E-10	0.2138	0.1133	0.01578	6.96E-13	rs12150611:44149741:G:A
17_44150042_T_C	17	44150042	C	0.2118	-0.0488	0.0076	1.45E-10	0.2138	0.1137	0.01578	5.68E-13	rs74850776:44150042:T:C
17_44150152_A_T	17	44150152	T	0.2117	-0.0488	0.0076	1.44E-10	0.2138	0.1135	0.01578	6.42E-13	rs974295:44150152:A:T
17_44150161_T_G	17	44150161	G	0.2164	-0.0477	0.0075	2.62E-10	0.2169	0.1126	0.01552	3.87E-13	rs1029463:44150161:T:G
17_44150163_T_G	17	44150163	G	0.2117	-0.0489	0.0076	1.34E-10	0.2138	0.1136	0.01578	6.23E-13	rs974294:44150163:T:G
17_44150233_G_A	17	44150233	A	0.2117	-0.0484	0.0076	2.01E-10	0.2138	0.1134	0.01578	6.62E-13	rs974293:44150233:G:A
17_44150464_T_C	17	44150464	C	0.2118	-0.0485	0.0076	1.83E-10	0.2138	0.1129	0.01578	8.39E-13	rs974292:44150464:T:C
17_44150480_A_T	17	44150480	T	0.2119	-0.0487	0.0076	1.57E-10	0.2138	0.1128	0.01578	8.98E-13	rs974291:44150480:A:T
17_44150920_T_C	17	44150920	C	0.2119	-0.0482	0.0076	2.44E-10	0.2138	0.1131	0.01578	7.88E-13	rs12150551:44150920:T:C

17_44151156_T_C	17	44151156	C	0.2117	-0.0487	0.0076	1.53E-10	0.2138	0.1137	0.01578	5.95E-13	rs12150558:44151156:T:C
17_44151546_T_G	17	44151546	G	0.2164	-0.0478	0.0075	2.48E-10	0.2168	0.1132	0.01556	3.47E-13	rs9907738:44151546:T:G
17_44151667_A_G	17	44151667	G	0.2117	-0.0485	0.0076	1.86E-10	0.2138	0.1138	0.01578	5.45E-13	rs62060812:44151667:A:G
17_44151697_A_T	17	44151697	T	0.2116	-0.0487	0.0076	1.51E-10	0.2138	0.1139	0.01578	5.35E-13	rs62060834:44151697:A:T
17_44151969_C_CA	17	44151969	CA	0.2117	-0.0478	0.0077	4.72E-10	0.2138	0.1139	0.01578	5.28E-13	17:44151969:C:CA
17_44152390_C_T	17	44152390	T	0.2117	-0.0485	0.0076	1.76E-10	0.2138	0.1134	0.01577	6.56E-13	rs62060835:44152390:C:T
17_44152447_G_A	17	44152447	A	0.2115	-0.0483	0.0076	2.17E-10	0.2138	0.1136	0.01577	5.77E-13	rs62060836:44152447:G:A
17_44152736_G_GCT	17	44152736	GCT	0.2116	-0.0478	0.0077	4.85E-10	0.2138	0.1139	0.01578	5.22E-13	rs112597362:44152736:G:GCT
17_44152760_T_G	17	44152760	G	0.2115	-0.0487	0.0076	1.53E-10	0.2138	0.1139	0.01578	5.23E-13	rs62060837:44152760:T:G
17_44152812_T_TGAACCCA	17	44152812	TGAACCCAAGTGA	0.2116	-0.0478	0.0077	4.88E-10	0.2138	0.1139	0.01578	5.24E-13	12:T:TGAACCCAAGTGAGGCACCTGGGTTCAA
17_44153144_A_G	17	44153144	G	0.2115	-0.0482	0.0076	2.39E-10	0.2138	0.1133	0.01577	6.57E-13	rs62060838:44153144:A:G
17_44153227_A_G	17	44153227	G	0.2116	-0.0483	0.0076	2.13E-10	0.2138	0.1134	0.01576	6.23E-13	rs62060839:44153227:A:G
17_44153258_A_G	17	44153258	G	0.2119	-0.0487	0.0076	1.57E-10	0.2138	0.1136	0.01578	5.99E-13	rs62060840:44153258:A:G
17_44153386_A_T	17	44153386	T	0.2114	-0.0479	0.0076	2.94E-10	0.2138	0.1137	0.01577	5.69E-13	rs62060841:44153386:A:T
17_44153607_T_A	17	44153607	A	0.2113	-0.0483	0.0076	2.13E-10	0.2136	0.1136	0.01578	6.08E-13	rs62060842:44153607:T:A
17_44153626_C_T	17	44153626	T	0.2113	-0.0484	0.0076	2.12E-10	0.2137	0.1137	0.01578	5.71E-13	rs62060843:44153626:C:T
17_44153836_C_T	17	44153836	T	0.212	-0.0488	0.0076	1.44E-10	0.2159	0.1128	0.01578	8.87E-13	rs62060844:44153836:C:T
17_44153909_A_G	17	44153909	G	0.2112	-0.0477	0.0076	3.43E-10	0.2138	0.1134	0.01576	6.26E-13	17:44153909:A:G
17_44153977_C_<INS:ME:S	17	44153977	<INS:ME:SVA>	0.1842	-0.0475	0.0084	1.92E-08	0.183	0.1262	0.01724	2.49E-13	4153977:C:<INS:ME:SVA>:44155359
17_44154033_T_C	17	44154033	C	0.2114	-0.048	0.0076	2.86E-10	0.2138	0.113	0.01576	7.51E-13	rs76154201:44154033:T:C
17_44154048_C_T	17	44154048	T	0.2114	-0.0479	0.0076	3.10E-10	0.2138	0.1129	0.01576	7.91E-13	rs75530705:44154048:C:T
17_44154105_A_G	17	44154105	G	0.2115	-0.048	0.0076	2.79E-10	0.2138	0.113	0.01577	7.49E-13	rs112197756:44154105:A:G
17_44154393_A_G	17	44154393	G	0.2115	-0.0478	0.0076	3.19E-10	0.2138	0.1131	0.01577	7.41E-13	rs62060845:44154393:A:G
17_44154461_A_C	17	44154461	C	0.2113	-0.0482	0.0076	2.49E-10	0.2138	0.1139	0.01578	5.23E-13	rs62060846:44154461:A:C
17_44154607_T_C	17	44154607	C	0.2113	-0.0482	0.0076	2.40E-10	0.2138	0.1139	0.01578	5.21E-13	rs74481389:44154607:T:C
17_44154946_C_T	17	44154946	T	0.2114	-0.0483	0.0076	2.22E-10	0.2138	0.114	0.01578	5.16E-13	rs62060847:44154946:C:T
17_44155157_C_T	17	44155157	T	0.2114	-0.0484	0.0076	2.12E-10	0.2138	0.114	0.01578	5.14E-13	rs56100031:44155157:C:T
17_44155299_CT_C	17	44155299	C	0.2115	-0.0474	0.0077	6.61E-10	0.2138	0.114	0.01578	5.18E-13	17:44155299:CT:C
17_44155707_C_T	17	44155707	T	0.2114	-0.0485	0.0076	1.89E-10	0.2138	0.114	0.01578	5.10E-13	rs55972730:44155707:C:T
17_44155732_C_T	17	44155732	T	0.2163	-0.0475	0.0075	3.22E-10	0.2165	0.1133	0.01565	4.59E-13	rs2066899:44155732:C:T
17_44155925_TACAA_T	17	44155925	T	0.2116	-0.0476	0.0077	5.85E-10	0.2138	0.114	0.01578	5.06E-13	17:44155925:TACAA:T
17_44156132_T_TTTA	17	44156132	TTTA	0.2116	-0.0476	0.0077	5.76E-10	0.2138	0.114	0.01578	5.01E-13	rs111750615:44156132:T:TTTA
17_44156167_G_A	17	44156167	A	0.2114	-0.0485	0.0076	1.82E-10	0.2138	0.114	0.01578	5.00E-13	rs2316954:44156167:G:A
17_44156180_A_G	17	44156180	G	0.2109	-0.0493	0.0076	1.05E-10	0.2117	0.1143	0.01581	4.93E-13	17:44156180:A:G
17_44156181_T_A	17	44156181	A	0.2109	-0.0493	0.0076	1.05E-10	0.2117	0.1143	0.01581	4.93E-13	17:44156181:T:A
17_44156401_T_TA	17	44156401	TA	0.2116	-0.0476	0.0077	5.65E-10	0.2138	0.1141	0.01578	4.94E-13	17:44156401:T:TA
17_44157597_A_G	17	44157597	G	0.2115	-0.0486	0.0076	1.64E-10	0.2137	0.1142	0.01578	4.69E-13	rs17659881:44157597:A:G
17_44157622_T_G	17	44157622	G	0.2115	-0.0486	0.0076	1.64E-10	0.2137	0.1142	0.01578	4.68E-13	rs78938131:44157622:T:G
17_44157676_CT_C	17	44157676	C	0.2116	-0.0476	0.0077	5.74E-10	0.2137	0.1141	0.01578	4.85E-13	17:44157676:CT:C
17_44157982_A_T	17	44157982	T	0.2118	-0.0485	0.0076	1.79E-10	0.2138	0.1131	0.01578	7.50E-13	rs62060850:44157982:A:T
17_44157992_T_C	17	44157992	C	0.2118	-0.0483	0.0076	2.11E-10	0.2138	0.1132	0.01578	7.16E-13	rs62060851:44157992:T:C
17_44159102_C_T	17	44159102	T	0.2119	-0.0483	0.0076	2.24E-10	0.2138	0.113	0.01578	8.24E-13	rs1476554:44159102:C:T
17_44159555_C_A	17	44159555	A	0.2119	-0.0482	0.0076	2.46E-10	0.2138	0.1131	0.01579	7.77E-13	rs77138434:44159555:C:A
17_44159631_T_G	17	44159631	G	0.2119	-0.0481	0.0076	2.55E-10	0.2138	0.1132	0.01578	7.51E-13	rs111913701:44159631:T:G
17_44159672_A_G	17	44159672	G	0.2116	-0.0483	0.0076	2.15E-10	0.2138	0.1139	0.01578	5.31E-13	rs111519055:44159672:A:G
17_44159695_C_T	17	44159695	T	0.2116	-0.0483	0.0076	2.15E-10	0.2138	0.1139	0.01578	5.31E-13	rs77925835:44159695:C:T
17_44159725_C_T	17	44159725	T	0.2119	-0.0481	0.0076	2.57E-10	0.2138	0.113	0.01578	8.07E-13	rs17659953:44159725:C:T
17_44159849_T_C	17	44159849	C	0.2119	-0.0482	0.0076	2.48E-10	0.2138	0.1131	0.01579	7.64E-13	rs17576165:44159849:T:C
17_44159988_G_A	17	44159988	A	0.2119	-0.0482	0.0076	2.49E-10	0.2138	0.1133	0.01578	7.00E-13	rs17576200:44159988:G:A
17_44160050_G_A	17	44160050	A	0.2118	-0.0481	0.0076	2.58E-10	0.2138	0.113	0.01579	8.04E-13	rs62060852:44160050:G:A
17_44160592_G_A	17	44160592	A	0.2119	-0.0483	0.0076	2.25E-10	0.2138	0.1132	0.01578	7.35E-13	rs62060853:44160592:G:A
17_44160674_G_C	17	44160674	C	0.2119	-0.0481	0.0076	2.57E-10	0.2138	0.1134	0.01578	6.80E-13	rs17660017:44160674:G:C
17_44161091_GCTCCCCTG	17	44161091	G	0.2121	-0.0474	0.0077	6.73E-10	0.2138	0.1132	0.01579	7.40E-13	161091:GCTCCCCTGGTAAGTCCTAAA:G
17_44161146_T_G	17	44161146	G	0.2118	-0.048	0.0076	2.87E-10	0.2137	0.1131	0.01579	7.64E-13	rs55987700:44161146:T:G
17_44161302_A_G	17	44161302	G	0.2116	-0.0484	0.0076	2.07E-10	0.2138	0.1139	0.01578	5.28E-13	rs113788190:44161302:A:G

17_44161360_A_T	17	44161360	T	0.2114	-0.0485	0.0076	1.86E-10	0.2136	0.1139	0.01579	5.39E-13	rs112364920:44161360:A:T
17_44161470_A_C	17	44161470	C	0.2116	-0.0483	0.0076	2.13E-10	0.2138	0.1139	0.01578	5.37E-13	rs80028338:44161470:A:C
17_44161478_CTCACACCTG	17	44161478	C	0.2117	-0.0474	0.0077	6.72E-10	0.2138	0.1139	0.01578	5.37E-13	CTGTAATCCCAGCACTTTGGGAAGCTGAGGCGGGTGGA:C
17_44161522_A_C	17	44161522	C	0.2116	-0.0483	0.0076	2.14E-10	0.2138	0.1139	0.01578	5.38E-13	rs113955100:44161522:A:C
17_44161747_C_CCAACAA	17	44161747	CCAACAA	0.2117	-0.0474	0.0077	6.73E-10	0.2138	0.1139	0.01578	5.42E-13	201722973:44161747:C:CCAACAA
17_44161860_C_T	17	44161860	T	0.2116	-0.0483	0.0076	2.14E-10	0.2138	0.1139	0.01578	5.44E-13	rs62060855:44161860:C:T
17_44161875_A_C	17	44161875	C	0.2116	-0.0483	0.0076	2.18E-10	0.2138	0.1141	0.01578	4.83E-13	rs62060856:44161875:A:C
17_44161985_T_G	17	44161985	G	0.2116	-0.0483	0.0076	2.14E-10	0.2138	0.1139	0.01578	5.47E-13	rs2316955:44161985:T:G
17_44162056_T_A	17	44162056	A	0.2049	-0.0516	0.0078	4.02E-11	0.2041	0.1166	0.01602	3.32E-13	rs2316956:44162056:T:A
17_44162284_T_C	17	44162284	C	0.2119	-0.0481	0.0076	2.56E-10	0.2138	0.113	0.01578	8.11E-13	rs17660065:44162284:T:C
17_44162597_C_A	17	44162597	A	0.2164	-0.0473	0.0076	3.84E-10	0.2165	0.1131	0.01566	5.08E-13	rs8080583:44162597:C:A
17_44163411_T_C	17	44163411	C	0.2116	-0.0483	0.0076	2.19E-10	0.2138	0.1138	0.01578	5.52E-13	rs55864131:44163411:T:C
17_44163547_ACG_A	17	44163547	A	0.2114	-0.0477	0.0077	5.39E-10	0.2135	0.1142	0.0158	4.91E-13	rs67335396:44163547:ACG:A
17_44163551_AGT_A	17	44163551	A	0.2117	-0.0474	0.0077	6.91E-10	0.2138	0.1138	0.01578	5.52E-13	17:44163551:AGT:A
17_44164090_G_C	17	44164090	C	0.2116	-0.0483	0.0076	2.26E-10	0.2138	0.1138	0.01578	5.52E-13	rs62060858:44164090:G:C
17_44164133_G_A	17	44164133	A	0.2116	-0.0483	0.0076	2.25E-10	0.2138	0.1138	0.01578	5.64E-13	rs62060859:44164133:G:A
17_44164323_G_A	17	44164323	A	0.2116	-0.0483	0.0076	2.26E-10	0.2138	0.1138	0.01578	5.52E-13	rs55692232:44164323:G:A
17_44165049_A_G	17	44165049	G	0.2115	-0.0481	0.0076	2.61E-10	0.2137	0.1138	0.01579	5.74E-13	rs3912063:44165049:A:G
17_44165069_A_G	17	44165069	G	0.2116	-0.0483	0.0076	2.30E-10	0.2138	0.1138	0.01578	5.52E-13	rs3912062:44165069:A:G
17_44165098_C_T	17	44165098	T	0.2116	-0.0483	0.0076	2.30E-10	0.2138	0.1138	0.01578	5.52E-13	rs3912061:44165098:C:T
17_44165169_C_T	17	44165169	T	0.2164	-0.0473	0.0076	3.93E-10	0.2165	0.1131	0.01566	5.22E-13	rs3865315:44165169:C:T
17_44165435_C_T	17	44165435	T	0.2113	-0.0486	0.0076	1.80E-10	0.2133	0.1141	0.0158	5.15E-13	rs3912060:44165435:C:T
17_44165594_C_A	17	44165594	A	0.2116	-0.048	0.0076	2.95E-10	0.2133	0.1128	0.01579	8.98E-13	rs55955207:44165594:C:A
17_44165596_C_T	17	44165596	T	0.2112	-0.0483	0.0076	2.31E-10	0.2133	0.1137	0.01579	6.02E-13	rs55735563:44165596:C:T
17_44165803_T_C	17	44165803	C	0.2114	-0.0482	0.0076	2.56E-10	0.2135	0.1134	0.0158	7.12E-13	rs17660132:44165803:T:C
17_44165852_A_G	17	44165852	G	0.2114	-0.0482	0.0076	2.55E-10	0.2135	0.1134	0.0158	7.07E-13	rs74348235:44165852:A:G
17_44166080_T_A	17	44166080	A	0.2079	-0.0478	0.0077	5.60E-10	0.2098	0.1153	0.01602	6.21E-13	rs201489508:44166080:T:A
17_44166197_A_G	17	44166197	G	0.2116	-0.0482	0.0076	2.36E-10	0.2138	0.1138	0.01579	5.55E-13	rs62061764:44166197:A:G
17_44166311_C_T	17	44166311	T	0.2116	-0.0482	0.0076	2.40E-10	0.2138	0.1138	0.01579	5.56E-13	rs17660167:44166311:C:T
17_44166362_G_GA	17	44166362	GA	0.2109	-0.0469	0.0077	1.09E-09	0.2129	0.1151	0.01582	3.43E-13	17:44166362:G:GA
17_44166500_G_A	17	44166500	A	0.2111	-0.0492	0.0076	1.19E-10	0.2131	0.1132	0.01584	8.90E-13	rs17660228:44166500:G:A
17_44166646_C_T	17	44166646	T	0.2116	-0.0482	0.0076	2.41E-10	0.2138	0.1138	0.01579	5.58E-13	rs17660251:44166646:C:T
17_44166764_C_CTTT	17	44166764	CTTT	0.159	-0.0601	0.0094	1.95E-10	0.1619	0.1237	0.01979	4.09E-10	rs67516111:44166764:C:CTTT
17_44167101_T_C	17	44167101	C	0.2116	-0.0482	0.0076	2.42E-10	0.2138	0.1138	0.01579	5.60E-13	rs17660294:44167101:T:C
17_44167464_G_A	17	44167464	A	0.2116	-0.0482	0.0076	2.39E-10	0.2138	0.1138	0.01579	5.68E-13	rs62061766:44167464:G:A
17_44167661_G_T	17	44167661	T	0.2116	-0.0482	0.0076	2.44E-10	0.2138	0.1138	0.01579	5.63E-13	rs79923630:44167661:G:T
17_44167729_A_G	17	44167729	G	0.2116	-0.0482	0.0076	2.51E-10	0.2138	0.1138	0.01579	5.64E-13	rs62061767:44167729:A:G
17_44168295_CTTA_C	17	44168295	C	0.2117	-0.0472	0.0077	7.88E-10	0.2138	0.1138	0.01579	5.67E-13	17:44168295:CTTA:C
17_44168508_C_T	17	44168508	T	0.2116	-0.0481	0.0076	2.53E-10	0.2138	0.1137	0.01579	6.04E-13	rs111364350:44168508:C:T
17_44168677_A_G	17	44168677	G	0.2164	-0.0473	0.0076	3.89E-10	0.2165	0.1134	0.01566	4.36E-13	rs2097760:44168677:A:G
17_44169377_G_C	17	44169377	C	0.2116	-0.0481	0.0076	2.57E-10	0.2138	0.1138	0.01579	5.73E-13	rs62061770:44169377:G:C
17_44169406_G_A	17	44169406	A	0.2116	-0.0481	0.0076	2.57E-10	0.2138	0.1138	0.01579	5.73E-13	rs62061771:44169406:G:A
17_44169437_T_C	17	44169437	C	0.2116	-0.0481	0.0076	2.57E-10	0.2138	0.1138	0.01579	5.73E-13	rs62061772:44169437:T:C
17_44169581_T_C	17	44169581	C	0.2112	-0.0483	0.0076	2.30E-10	0.2135	0.1139	0.0158	5.61E-13	rs111970616:44169581:T:C
17_44169605_T_C	17	44169605	C	0.2112	-0.0483	0.0076	2.30E-10	0.2135	0.1139	0.0158	5.61E-13	rs17660337:44169605:T:C
17_44169759_G_A	17	44169759	A	0.2113	-0.048	0.0076	3.08E-10	0.2131	0.1143	0.0158	4.70E-13	rs62061788:44169759:G:A
17_44169769_C_T	17	44169769	T	0.2113	-0.048	0.0076	3.08E-10	0.2131	0.1143	0.0158	4.70E-13	rs62061789:44169769:C:T
17_44170018_G_C	17	44170018	C	0.2116	-0.0481	0.0076	2.58E-10	0.2138	0.1138	0.01579	5.77E-13	rs17576631:44170018:G:C
17_44170129_C_CAA	17	44170129	CAA	0.2117	-0.0472	0.0077	8.08E-10	0.2138	0.1138	0.01579	5.78E-13	rs68132028:44170129:C:CAA
17_44170238_G_A	17	44170238	A	0.2116	-0.0481	0.0076	2.59E-10	0.2138	0.1138	0.01579	5.78E-13	rs112596352:44170238:G:A
17_44170414_G_A	17	44170414	A	0.2116	-0.0481	0.0076	2.59E-10	0.2138	0.1138	0.01579	5.79E-13	rs62061790:44170414:G:A
17_44170612_C_T	17	44170612	T	0.2119	-0.048	0.0076	2.98E-10	0.2138	0.1131	0.01579	8.04E-13	rs17660398:44170612:C:T
17_44171024_T_C	17	44171024	C	0.2116	-0.0481	0.0076	2.60E-10	0.2138	0.1137	0.01579	5.81E-13	rs62061791:44171024:T:C
17_44171554_G_A	17	44171554	A	0.2116	-0.0481	0.0076	2.61E-10	0.2138	0.1137	0.01579	5.81E-13	rs62061792:44171554:G:A
17_44171565_C_A	17	44171565	A	0.2116	-0.0481	0.0076	2.61E-10	0.2138	0.1137	0.01579	5.81E-13	rs62061793:44171565:C:A

17_44172205_CA_C	17	44172205	C	0.2117	-0.0472	0.0077	8.15E-10	0.2138	0.1137	0.01579	5.81E-13	17:44172205:CA:C
17_44172327_T_A	17	44172327	A	0.2119	-0.0481	0.0076	2.71E-10	0.2138	0.1129	0.01579	8.54E-13	rs17576695:44172327:T:A
17_44172391_C_T	17	44172391	T	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.81E-13	rs80020809:44172391:C:T
17_44172408_C_G	17	44172408	G	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.81E-13	rs77044307:44172408:C:G
17_44172493_A_AT	17	44172493	AT	0.2113	-0.0473	0.0077	7.61E-10	0.2136	0.1135	0.0158	6.89E-13	rs146453014:44172493:A:AT
17_44172698_T_C	17	44172698	C	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.81E-13	rs79348289:44172698:T:C
17_44172773_C_T	17	44172773	T	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.81E-13	rs75412750:44172773:C:T
17_44173179_C_A	17	44173179	A	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.81E-13	rs62061795:44173179:C:A
17_44173356_C_G	17	44173356	G	0.2119	-0.0478	0.0076	3.26E-10	0.2138	0.1129	0.01579	8.85E-13	rs17576709:44173356:C:G
17_44173408_G_A	17	44173408	A	0.2115	-0.0481	0.0076	2.62E-10	0.2138	0.1138	0.01579	5.80E-13	rs62061796:44173408:G:A
17_44173812_G_A	17	44173812	A	0.2098	-0.0483	0.0077	2.75E-10	0.2115	0.1157	0.01589	3.33E-13	rs62061798:44173812:G:A
17_44173878_G_GT	17	44173878	GT	0.2099	-0.0473	0.0077	8.95E-10	0.2115	0.1157	0.01589	3.33E-13	rs139282381:44173878:G:GT
17_44174068_T_C	17	44174068	C	0.2109	-0.0478	0.0077	4.17E-10	0.2134	0.113	0.01588	1.12E-12	rs62061799:44174068:T:C
17_44174109_G_C	17	44174109	C	0.21	-0.0479	0.0077	3.81E-10	0.2124	0.1135	0.01586	8.37E-13	rs62061800:44174109:G:C
17_44174235_A_G	17	44174235	G	0.2115	-0.0481	0.0076	2.63E-10	0.2138	0.1138	0.01579	5.74E-13	rs62061801:44174235:A:G
17_44174351_T_A	17	44174351	A	0.2115	-0.0481	0.0076	2.63E-10	0.2138	0.1138	0.01579	5.73E-13	rs62061802:44174351:T:A
17_44174513_C_A	17	44174513	A	0.2115	-0.0481	0.0076	2.65E-10	0.2137	0.1137	0.01579	5.94E-13	rs62061803:44174513:C:A
17_44176092_G_A	17	44176092	A	0.2115	-0.0481	0.0076	2.65E-10	0.2138	0.1138	0.01579	5.61E-13	rs55900347:44176092:G:A
17_44176170_C_G	17	44176170	G	0.2115	-0.0481	0.0076	2.65E-10	0.2138	0.1138	0.01579	5.60E-13	rs56240678:44176170:C:G
17_44176215_G_A	17	44176215	A	0.2112	-0.0479	0.0076	3.35E-10	0.2134	0.1135	0.01581	7.04E-13	rs55825513:44176215:G:A
17_44177097_C_T	17	44177097	T	0.2115	-0.0481	0.0076	2.66E-10	0.2138	0.1139	0.01579	5.54E-13	rs62061807:44177097:C:T
17_44177304_TA_T	17	44177304	T	0.2117	-0.0471	0.0077	8.27E-10	0.2138	0.1139	0.01579	5.52E-13	17:44177304:TA:T
17_44177337_C_T	17	44177337	T	0.2115	-0.0481	0.0076	2.66E-10	0.2138	0.1139	0.01579	5.52E-13	rs62061808:44177337:C:T
17_44177669_C_T	17	44177669	T	0.2115	-0.0481	0.0076	2.66E-10	0.2138	0.1139	0.01579	5.50E-13	rs77604208:44177669:C:T
17_44177755_C_G	17	44177755	G	0.2115	-0.0481	0.0076	2.66E-10	0.2138	0.1139	0.01579	5.49E-13	rs80120913:44177755:C:G
17_44177993_C_A	17	44177993	A	0.2118	-0.0479	0.0076	3.23E-10	0.2136	0.1135	0.01579	6.58E-13	rs17660464:44177993:C:A
17_44178272_C_T	17	44178272	T	0.2119	-0.048	0.0076	2.94E-10	0.2138	0.1131	0.01579	7.86E-13	rs17576779:44178272:C:T
17_44178337_T_C	17	44178337	C	0.2119	-0.048	0.0076	2.92E-10	0.2138	0.113	0.01579	8.29E-13	rs17660488:44178337:T:C
17_44178839_T_C	17	44178839	C	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.49E-13	rs62061809:44178839:T:C
17_44178884_G_A	17	44178884	A	0.2116	-0.0482	0.0076	2.39E-10	0.2138	0.1133	0.01579	6.99E-13	rs62061810:44178884:G:A
17_44179168_AACC_A	17	44179168	A	0.2117	-0.0472	0.0077	7.65E-10	0.2138	0.1139	0.01579	5.49E-13	17:44179168:AACC:A
17_44179723_T_C	17	44179723	C	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.49E-13	rs111957446:44179723:T:C
17_44179749_G_A	17	44179749	A	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.49E-13	rs112102887:44179749:G:A
17_44179969_G_A	17	44179969	A	0.2119	-0.048	0.0076	2.76E-10	0.2138	0.113	0.01579	8.41E-13	rs112893440:44179969:G:A
17_44179992_A_G	17	44179992	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.49E-13	rs17576842:44179992:A:G
17_44180173_T_G	17	44180173	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.46E-13	rs62061811:44180173:T:G
17_44180442_A_G	17	44180442	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.43E-13	rs17576870:44180442:A:G
17_44180954_A_G	17	44180954	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.37E-13	rs17660595:44180954:A:G
17_44180997_C_T	17	44180997	T	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.37E-13	rs62061812:44180997:C:T
17_44181118_G_A	17	44181118	A	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.35E-13	rs62061813:44181118:G:A
17_44181454_C_T	17	44181454	T	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.32E-13	rs111952388:44181454:C:T
17_44181508_T_G	17	44181508	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.1139	0.01579	5.31E-13	rs62061814:44181508:T:G
17_44181681_A_G	17	44181681	G	0.2115	-0.0482	0.0076	2.46E-10	0.2138	0.114	0.01579	5.29E-13	rs62061815:44181681:A:G
17_44181933_T_C	17	44181933	C	0.2117	-0.048	0.0076	2.90E-10	0.2128	0.1125	0.01579	1.07E-12	rs17576954:44181933:T:C
17_44182181_T_C	17	44182181	C	0.2119	-0.0481	0.0076	2.66E-10	0.2138	0.1131	0.01579	7.90E-13	rs77924366:44182181:T:C
17_44182336_C_A	17	44182336	A	0.2115	-0.0482	0.0076	2.40E-10	0.2138	0.114	0.01579	5.24E-13	rs62061816:44182336:C:A
17_44182706_A_G	17	44182706	G	0.2119	-0.048	0.0076	2.86E-10	0.2138	0.1134	0.01579	6.72E-13	rs62061817:44182706:A:G
17_44182845_T_TG	17	44182845	TG	0.2117	-0.0473	0.0077	7.38E-10	0.2138	0.114	0.01579	5.29E-13	17:44182845:T:TG
17_44182917_C_G	17	44182917	G	0.209	-0.0487	0.0077	2.37E-10	0.212	0.1155	0.01593	4.06E-13	rs62061818:44182917:C:G
17_44182955_C_T	17	44182955	T	0.209	-0.0487	0.0077	2.37E-10	0.212	0.1155	0.01593	4.07E-13	rs75330746:44182955:C:T
17_44182956_A_G	17	44182956	G	0.209	-0.0487	0.0077	2.37E-10	0.212	0.1155	0.01593	4.07E-13	rs75183956:44182956:A:G
17_44182983_A_G	17	44182983	G	0.172	-0.0611	0.0089	5.43E-12	0.1732	0.1193	0.01822	5.87E-11	rs78381082:44182983:A:G
17_44183002_C_A	17	44183002	A	0.2116	-0.0482	0.0076	2.39E-10	0.2138	0.1139	0.01579	5.34E-13	17:44183002:C:A
17_44183232_C_G	17	44183232	G	0.2116	-0.0482	0.0076	2.40E-10	0.2138	0.1139	0.01579	5.42E-13	17:44183232:C:G
17_44183317_C_A	17	44183317	A	0.2157	-0.046	0.0076	1.39E-09	0.2179	0.1116	0.01574	1.33E-12	rs371996525:44183317:C:A

17_44183403_A_G	17	44183403	G	0.2119	-0.0479	0.0076	3.23E-10	0.2138	0.1132	0.01579	7.68E-13	rs111676341:44183403:A:G
17_44183616_C_A	17	44183616	A	0.2117	-0.0475	0.0076	4.27E-10	0.2138	0.113	0.01579	8.13E-13	rs17576989:44183616:C:A
17_44183790_G_A	17	44183790	A	0.2116	-0.0482	0.0076	2.41E-10	0.2138	0.1137	0.01579	5.96E-13	rs79923708:44183790:G:A
17_44184194_G_GAACTGA	17	44184194	GAACTGAGGAGAT	0.2117	-0.0473	0.0077	7.10E-10	0.2138	0.1141	0.01579	4.97E-13	35:44184194:G:GAACTGAGGAGATATGGA
17_44184375_A_G	17	44184375	G	0.2119	-0.0481	0.0076	2.71E-10	0.2138	0.1128	0.01579	9.21E-13	rs79346219:44184375:A:G
17_44184404_G_A	17	44184404	A	0.2118	-0.0486	0.0076	1.73E-10	0.2141	0.1142	0.01579	4.64E-13	rs73984689:44184404:G:A
17_44184428_T_C	17	44184428	C	0.2118	-0.048	0.0076	2.89E-10	0.2138	0.113	0.01579	8.35E-13	rs111295615:44184428:T:C
17_44184808_C_G	17	44184808	G	0.2114	-0.048	0.0076	3.31E-10	0.2121	0.115	0.01581	3.62E-13	rs111905143:44184808:C:G
17_44184819_CAAAGGT_C	17	44184819	C	0.2109	-0.0466	0.0077	1.49E-09	0.2119	0.1151	0.01583	3.54E-13	17:44184819:CAAAGGT:C
17_44184828_G_T	17	44184828	T	0.3929	-0.0262	0.0063	0.00003738	0.3766	0.07791	0.01346	7.06E-09	rs4510068:44184828:G:T
17_44185245_C_A	17	44185245	A	0.2119	-0.0479	0.0076	3.21E-10	0.2138	0.1131	0.01579	7.74E-13	rs76761511:44185245:C:A
17_44185427_A_AT	17	44185427	AT	0.2112	-0.047	0.0077	9.78E-10	0.2131	0.1146	0.01582	4.39E-13	rs67503183:44185427:A:AT
17_44185431_T_C	17	44185431	C	0.2145	-0.0475	0.0076	3.90E-10	0.2144	0.1141	0.01574	4.19E-13	rs62061820:44185431:T:C
17_44186055_G_A	17	44186055	A	0.2115	-0.0481	0.0076	2.54E-10	0.2138	0.1139	0.01579	5.49E-13	rs62061821:44186055:G:A
17_44186063_C_T	17	44186063	T	0.2164	-0.0469	0.0076	5.33E-10	0.2165	0.1136	0.01566	4.01E-13	rs16940904:44186063:C:T
17_44186252_G_A	17	44186252	A	0.2119	-0.0479	0.0076	3.08E-10	0.2138	0.1134	0.01579	6.75E-13	rs17577024:44186252:G:A
17_44186301_T_C	17	44186301	C	0.2115	-0.0482	0.0076	2.49E-10	0.2138	0.1139	0.01579	5.49E-13	rs17577052:44186301:T:C
17_44186593_T_C	17	44186593	C	0.2115	-0.0482	0.0076	2.48E-10	0.2138	0.1139	0.01579	5.49E-13	rs77635460:44186593:T:C
17_44186894_A_C	17	44186894	C	0.2117	-0.0483	0.0076	2.28E-10	0.2139	0.1141	0.01579	4.98E-13	rs62061822:44186894:A:C
17_44187257_A_G	17	44187257	G	0.2163	-0.0468	0.0076	5.77E-10	0.2165	0.1132	0.01567	5.06E-13	rs9303525:44187257:A:G
17_44187492_A_G	17	44187492	G	0.2119	-0.048	0.0076	2.85E-10	0.2138	0.1133	0.01579	7.00E-13	rs17577094:44187492:A:G
17_44188477_T_G	17	44188477	G	0.2115	-0.0482	0.0076	2.45E-10	0.2138	0.1139	0.01579	5.49E-13	rs17577159:44188477:T:G
17_44188645_C_T	17	44188645	T	0.2115	-0.0482	0.0076	2.45E-10	0.2138	0.1139	0.01579	5.49E-13	rs62061823:44188645:C:T
17_44188672_G_GTT	17	44188672	GTT	0.2117	-0.0472	0.0077	7.63E-10	0.2138	0.1139	0.01579	5.49E-13	17:44188672:G:GTT
17_44188755_T_C	17	44188755	C	0.2114	-0.0484	0.0076	2.15E-10	0.2136	0.1136	0.0158	6.32E-13	rs62061824:44188755:T:C
17_44188764_T_C	17	44188764	C	0.2115	-0.0482	0.0076	2.45E-10	0.2138	0.1139	0.01579	5.49E-13	rs55794067:44188764:T:C
17_44189067_A_G	17	44189067	G	0.3976	-0.0262	0.0063	0.0000338	0.3808	0.07764	0.01341	6.96E-09	rs7225002:44189067:A:G
17_44189373_C_T	17	44189373	T	0.2119	-0.048	0.0076	2.93E-10	0.2138	0.1132	0.01579	7.41E-13	rs17660847:44189373:C:T
17_44189408_T_C	17	44189408	C	0.2115	-0.0482	0.0076	2.44E-10	0.2138	0.1139	0.01579	5.50E-13	rs17660865:44189408:T:C
17_44189799_T_C	17	44189799	C	0.2087	-0.0493	0.0077	1.39E-10	0.2113	0.1143	0.01597	8.42E-13	rs112480703:44189799:T:C
17_44189855_G_A	17	44189855	A	0.2033	-0.0489	0.0078	3.71E-10	0.2063	0.1131	0.01626	3.50E-12	rs79772780:44189855:G:A
17_44189858_G_A	17	44189858	A	0.2033	-0.0489	0.0078	3.71E-10	0.2063	0.1131	0.01626	3.50E-12	rs76640332:44189858:G:A
17_44189910_A_G	17	44189910	G	0.2089	-0.0491	0.0077	1.60E-10	0.2113	0.1144	0.01596	7.56E-13	rs78929339:44189910:A:G
17_44190156_T_C	17	44190156	C	0.2094	-0.049	0.0077	1.59E-10	0.2121	0.1133	0.01593	1.16E-12	rs62061845:44190156:T:C
17_44191085_G_A	17	44191085	A	0.2119	-0.0481	0.0076	2.56E-10	0.214	0.1139	0.01579	5.56E-13	rs17660907:44191085:G:A
17_44191159_C_T	17	44191159	T	0.2119	-0.0479	0.0076	3.16E-10	0.2138	0.1134	0.01579	6.84E-13	rs17660936:44191159:C:T
17_44191682_G_A	17	44191682	A	0.2116	-0.0482	0.0076	2.50E-10	0.2138	0.1137	0.01579	5.84E-13	rs62061847:44191682:G:A
17_44191835_A_G	17	44191835	G	0.2119	-0.048	0.0076	2.91E-10	0.2138	0.1133	0.01579	7.17E-13	rs17577313:44191835:A:G
17_44192395_G_T	17	44192395	T	0.2116	-0.0482	0.0076	2.50E-10	0.2138	0.1138	0.01579	5.82E-13	rs4548919:44192395:G:T
17_44192568_C_T	17	44192568	T	0.1891	-0.0465	0.0081	8.08E-09	0.1925	0.1088	0.01668	6.79E-11	rs4630591:44192568:C:T
17_44192590_T_A	17	44192590	A	0.2125	-0.0481	0.0076	2.78E-10	0.2132	0.1124	0.01581	1.17E-12	rs35524223:44192590:T:A
17_44192592_A_AT	17	44192592	AT	0.2121	-0.0472	0.0077	8.13E-10	0.2145	0.1134	0.01579	6.82E-13	17:44192592:A:AT
17_44192618_A_G	17	44192618	G	0.211	-0.048	0.0076	3.21E-10	0.2121	0.1134	0.01581	7.30E-13	rs4606752:44192618:A:G
17_44192923_A_G	17	44192923	G	0.2121	-0.0482	0.0076	2.48E-10	0.214	0.112	0.01579	1.33E-12	rs17577369:44192923:A:G
17_44192946_C_T	17	44192946	T	0.2109	-0.0484	0.0076	2.33E-10	0.2131	0.1142	0.01582	5.23E-13	rs62061848:44192946:C:T
17_44192957_T_C	17	44192957	C	0.2108	-0.0482	0.0076	2.69E-10	0.2131	0.1142	0.01582	5.21E-13	rs17661015:44192957:T:C
17_44193097_C_A	17	44193097	A	0.2115	-0.0475	0.0076	4.46E-10	0.2137	0.1137	0.01581	6.26E-13	rs17661027:44193097:C:A
17_44193882_C_T	17	44193882	T	0.2116	-0.0481	0.0076	2.58E-10	0.2138	0.1137	0.01579	5.83E-13	rs62061849:44193882:C:T
17_44193908_C_CCAACAA	17	44193908	CCAACAA	0.2117	-0.0471	0.0077	8.29E-10	0.2138	0.1137	0.01579	5.84E-13	17:44193908:C:CCAACAA
17_44194152_T_A	17	44194152	A	0.212	-0.0479	0.0076	3.09E-10	0.2138	0.1136	0.01579	6.29E-13	rs17661045:44194152:T:A
17_44194381_T_A	17	44194381	A	0.2116	-0.0481	0.0076	2.60E-10	0.2138	0.1137	0.01579	5.84E-13	rs17577447:44194381:T:A
17_44194519_T_C	17	44194519	C	0.212	-0.0478	0.0076	3.30E-10	0.2138	0.1131	0.01579	7.73E-13	rs62061850:44194519:T:C
17_44194621_C_G	17	44194621	G	0.212	-0.0479	0.0076	3.16E-10	0.2138	0.113	0.01579	8.41E-13	rs111880194:44194621:C:G
17_44194735_G_T	17	44194735	T	0.212	-0.0479	0.0076	3.08E-10	0.2138	0.1133	0.01579	7.29E-13	rs10514901:44194735:G:T
17_44194835_T_C	17	44194835	C	0.2116	-0.0481	0.0076	2.60E-10	0.2138	0.1137	0.01579	5.84E-13	rs17577496:44194835:T:C

17_44194891_C_T	17	44194891	T	0.2116	-0.0481	0.0076	2.61E-10	0.2138	0.1137	0.01579	5.84E-13	rs62061851:44194891:C:T
17_44195424_A_C	17	44195424	C	0.2116	-0.0481	0.0076	2.65E-10	0.2138	0.1137	0.01579	5.84E-13	rs62061852:44195424:A:C
17_44195495_G_A	17	44195495	A	0.212	-0.0478	0.0076	3.47E-10	0.2138	0.1135	0.01579	6.62E-13	rs727425:44195495:G:A
17_44195611_CA_C	17	44195611	C	0.2118	-0.0472	0.0077	8.12E-10	0.2138	0.1137	0.01579	5.87E-13	17:44195611:CA:C
17_44196015_C_G	17	44196015	G	0.2115	-0.0476	0.0076	4.47E-10	0.2135	0.1136	0.0158	6.51E-13	rs17661141:44196015:C:G
17_44196125_T_C	17	44196125	C	0.2116	-0.0481	0.0076	2.66E-10	0.2138	0.1137	0.01579	5.85E-13	rs62061853:44196125:T:C
17_44196153_A_G	17	44196153	G	0.212	-0.0478	0.0076	3.48E-10	0.2138	0.1134	0.01579	6.90E-13	rs1468241:44196153:A:G
17_44196447_T_A	17	44196447	A	0.2119	-0.0479	0.0076	3.18E-10	0.2134	0.1135	0.0158	6.70E-13	rs1468240:44196447:T:A
17_44196653_G_A	17	44196653	A	0.2116	-0.0481	0.0076	2.69E-10	0.2138	0.1137	0.01579	5.85E-13	rs75229280:44196653:G:A
17_44196799_G_A	17	44196799	A	0.2116	-0.0481	0.0076	2.71E-10	0.2138	0.1137	0.01579	5.85E-13	rs112813897:44196799:G:A
17_44196822_G_A	17	44196822	A	0.2116	-0.0481	0.0076	2.71E-10	0.2138	0.1137	0.01579	5.85E-13	rs113909426:44196822:G:A
17_44197032_T_C	17	44197032	C	0.212	-0.0477	0.0076	3.55E-10	0.2138	0.113	0.01579	8.32E-13	rs111678697:44197032:T:C
17_44197417_T_TGAA	17	44197417	TGAA	0.2118	-0.0471	0.0077	8.64E-10	0.2138	0.1137	0.01579	5.84E-13	rs138190012:44197417:T:TGAA
17_44197603_T_C	17	44197603	C	0.2127	-0.0474	0.0076	4.72E-10	0.2143	0.1129	0.01579	8.69E-13	rs4383188:44197603:T:C
17_44197775_G_GCA	17	44197775	GCA	0.2118	-0.0471	0.0077	8.49E-10	0.2138	0.1137	0.01579	5.85E-13	17:44197775:G:GCA
17_44197806_T_C	17	44197806	C	0.212	-0.0477	0.0076	3.71E-10	0.2139	0.1137	0.01579	6.07E-13	rs1966345:44197806:T:C
17_44198080_C_T	17	44198080	T	0.212	-0.0478	0.0076	3.42E-10	0.2138	0.1135	0.01579	6.53E-13	rs62061854:44198080:C:T
17_44198806_T_C	17	44198806	C	0.2121	-0.0482	0.0076	2.42E-10	0.2139	0.113	0.01579	8.18E-13	rs3087534:44198806:T:C
17_44198962_T_TA	17	44198962	TA	0.2117	-0.0468	0.0077	1.12E-09	0.2137	0.1153	0.01581	2.99E-13	17:44198962:T:TA
17_44199029_T_C	17	44199029	C	0.2123	-0.0475	0.0076	4.18E-10	0.2141	0.1131	0.01579	7.89E-13	rs76924476:44199029:T:C
17_44199670_G_A	17	44199670	A	0.2117	-0.0478	0.0076	3.39E-10	0.2134	0.1125	0.0158	1.04E-12	rs62061855:44199670:G:A
17_44200015_T_C	17	44200015	C	0.2104	-0.0481	0.0076	3.16E-10	0.2118	0.1157	0.01586	3.00E-13	rs62061856:44200015:T:C
17_44200033_T_C	17	44200033	C	0.2101	-0.0476	0.0077	4.86E-10	0.21	0.1158	0.01586	2.87E-13	rs62061858:44200033:T:C
17_44200078_A_T	17	44200078	T	0.2116	-0.048	0.0076	2.77E-10	0.2138	0.1137	0.01579	5.85E-13	rs112560196:44200078:A:T
17_44200510_C_A	17	44200510	A	0.2116	-0.048	0.0076	2.77E-10	0.2138	0.1137	0.01579	5.85E-13	rs75652502:44200510:C:A
17_44201109_C_G	17	44201109	G	0.2116	-0.048	0.0076	2.95E-10	0.2141	0.114	0.0158	5.30E-13	rs62061859:44201109:C:G
17_44201344_G_C	17	44201344	C	0.212	-0.0478	0.0076	3.41E-10	0.2138	0.1134	0.01579	6.78E-13	rs55802590:44201344:G:C
17_44201358_TG_T	17	44201358	T	0.2115	-0.0467	0.0077	1.21E-09	0.2136	0.114	0.0158	5.35E-13	17:44201358:TG:T
17_44201667_G_A	17	44201667	A	0.2116	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.89E-13	rs56257094:44201667:G:A
17_44201680_A_C	17	44201680	C	0.2116	-0.0481	0.0076	2.62E-10	0.2138	0.1137	0.01579	5.89E-13	rs55672516:44201680:A:C
17_44201791_G_C	17	44201791	C	0.2116	-0.0481	0.0076	2.67E-10	0.2138	0.1137	0.01579	5.90E-13	rs112073200:44201791:G:C
17_44201865_C_T	17	44201865	T	0.21	-0.0481	0.0077	3.37E-10	0.2122	0.1138	0.01588	7.88E-13	rs62063163:44201865:C:T
17_44201887_C_T	17	44201887	T	0.21	-0.0481	0.0077	3.25E-10	0.2122	0.1138	0.01588	7.88E-13	rs62063164:44201887:C:T
17_44202147_A_G	17	44202147	G	0.2117	-0.0482	0.0076	2.48E-10	0.2138	0.1137	0.01579	5.94E-13	rs62063165:44202147:A:G
17_44202231_A_G	17	44202231	G	0.2117	-0.0482	0.0076	2.43E-10	0.2138	0.1137	0.01579	5.95E-13	rs62063166:44202231:A:G
17_44202564_G_A	17	44202564	A	0.2117	-0.0482	0.0076	2.43E-10	0.2138	0.1137	0.01579	5.99E-13	rs55669501:44202564:G:A
17_44202608_C_T	17	44202608	T	0.2117	-0.0482	0.0076	2.43E-10	0.2138	0.1137	0.01579	6.00E-13	rs55686102:44202608:C:T
17_44202952_C_G	17	44202952	G	0.2117	-0.0482	0.0076	2.43E-10	0.2138	0.1137	0.01579	6.04E-13	rs55885063:44202952:C:G
17_44203131_C_G	17	44203131	G	0.2132	-0.048	0.0076	2.70E-10	0.2162	0.1115	0.01578	1.61E-12	rs56273589:44203131:C:G
17_44203311_C_T	17	44203311	T	0.2132	-0.0481	0.0076	2.57E-10	0.2162	0.1116	0.01578	1.55E-12	rs62063171:44203311:C:T
17_44203366_T_C	17	44203366	C	0.2128	-0.0482	0.0076	2.28E-10	0.2162	0.1119	0.01578	1.35E-12	rs62063172:44203366:T:C
17_44203413_C_T	17	44203413	T	0.2128	-0.0482	0.0076	2.31E-10	0.2162	0.1119	0.01578	1.35E-12	rs76380490:44203413:C:T
17_44203520_C_T	17	44203520	T	0.2128	-0.0482	0.0076	2.38E-10	0.2162	0.1117	0.01578	1.48E-12	rs113120855:44203520:C:T
17_44203806_C_CA	17	44203806	CA	0.21	-0.0475	0.0077	7.40E-10	0.2111	0.1133	0.01589	1.02E-12	rs149079649:44203806:C:CA
17_44203855_C_CTCAA	17	44203855	CTCAA	0.2116	-0.0474	0.0077	7.03E-10	0.2136	0.1137	0.01579	6.20E-13	rs140412994:44203855:C:CTCAA
17_44204299_AC_A	17	44204299	A	0.2122	-0.0471	0.0077	8.84E-10	0.2138	0.1137	0.01579	5.95E-13	rs66883448:44204299:AC:A
17_44204304_T_G	17	44204304	G	0.212	-0.0479	0.0076	3.09E-10	0.2138	0.1133	0.01579	7.29E-13	rs77095128:44204304:T:G
17_44204739_T_C	17	44204739	C	0.212	-0.0479	0.0076	3.12E-10	0.2138	0.1135	0.01579	6.48E-13	rs4581739:44204739:T:C
17_44204749_A_G	17	44204749	G	0.212	-0.0478	0.0076	3.35E-10	0.2138	0.1134	0.01579	6.79E-13	rs113638513:44204749:A:G
17_44205122_C_G	17	44205122	G	0.2117	-0.0482	0.0076	2.52E-10	0.2138	0.1136	0.01579	6.20E-13	rs62063174:44205122:C:G
17_44205350_A_ATT	17	44205350	ATT	0.2113	-0.0471	0.0077	9.08E-10	0.2134	0.1137	0.01582	6.57E-13	17:44205350:A:ATT
17_44205500_A_G	17	44205500	G	0.2123	-0.0482	0.0076	2.48E-10	0.2159	0.1134	0.01579	6.69E-13	rs17577650:44205500:A:G
17_44205690_C_T	17	44205690	T	0.2145	-0.0461	0.0076	1.17E-09	0.2164	0.108	0.01571	6.33E-12	rs4471723:44205690:C:T
17_44205839_A_G	17	44205839	G	0.2117	-0.0481	0.0076	2.58E-10	0.2138	0.1136	0.01579	6.21E-13	rs1122381:44205839:A:G
17_44206079_C_T	17	44206079	T	0.212	-0.0479	0.0076	3.20E-10	0.2138	0.1133	0.01579	7.16E-13	rs1122380:44206079:C:T

17_44206455_G_GA	17	44206455	GA	0.2116	-0.0469	0.0077	1.08E-09	0.2137	0.1135	0.01581	7.04E-13	rs66472415:44206455:G:GA
17_44206482_C_T	17	44206482	T	0.212	-0.0479	0.0076	3.05E-10	0.2138	0.1134	0.01579	6.80E-13	rs62063200:44206482:C:T
17_44206646_C_G	17	44206646	G	0.212	-0.048	0.0076	2.94E-10	0.2138	0.1132	0.01579	7.65E-13	rs10514903:44206646:C:G
17_44207066_A_G	17	44207066	G	0.212	-0.0479	0.0076	3.08E-10	0.2138	0.1133	0.01579	7.06E-13	rs17661348:44207066:A:G
17_44207360_C_T	17	44207360	T	0.2115	-0.0481	0.0076	2.64E-10	0.2133	0.1134	0.0158	7.10E-13	rs62063201:44207360:C:T
17_44207415_G_GGTGGCA	17	44207415	GGTGGCAT	0.2118	-0.0472	0.0077	8.02E-10	0.2138	0.1136	0.01579	6.21E-13	17:44207415:G:GGTGGCAT
17_44207523_T_A	17	44207523	A	0.2117	-0.0481	0.0076	2.59E-10	0.2138	0.1136	0.01579	6.21E-13	rs113758975:44207523:T:A
17_44207778_A_G	17	44207778	G	0.212	-0.048	0.0076	2.96E-10	0.2138	0.1134	0.01579	6.75E-13	rs17661385:44207778:A:G
17_44207887_C_T	17	44207887	T	0.212	-0.0469	0.0076	7.72E-10	0.2135	0.1113	0.01578	1.75E-12	rs10514904:44207887:C:T
17_44207900_A_ACT	17	44207900	ACT	0.2114	-0.0472	0.0077	8.19E-10	0.2133	0.1138	0.0158	6.11E-13	rs142524806:44207900:A:ACT
17_44207932_A_G	17	44207932	G	0.2113	-0.0482	0.0076	2.58E-10	0.2134	0.1137	0.0158	6.24E-13	rs79301522:44207932:A:G
17_44208144_C_G	17	44208144	G	0.2113	-0.0477	0.0076	4.01E-10	0.212	0.1132	0.01581	7.94E-13	rs17661428:44208144:C:G
17_44208218_A_G	17	44208218	G	0.2111	-0.048	0.0076	3.19E-10	0.212	0.1135	0.01581	6.97E-13	rs17577877:44208218:A:G
17_44208312_G_T	17	44208312	T	0.2164	-0.0473	0.0076	4.14E-10	0.216	0.1134	0.01569	4.80E-13	rs6503457:44208312:G:T
17_44208674_G_T	17	44208674	T	0.2166	-0.0469	0.0076	5.32E-10	0.2165	0.1136	0.01567	4.16E-13	rs8070942:44208674:G:T
17_44208945_C_T	17	44208945	T	0.212	-0.0481	0.0076	2.65E-10	0.2137	0.1135	0.0158	6.79E-13	rs62063202:44208945:C:T
17_44209313_T_C	17	44209313	C	0.2117	-0.0482	0.0076	2.53E-10	0.2138	0.1136	0.01579	6.25E-13	rs62063203:44209313:T:C
17_44209364_G_A	17	44209364	A	0.2118	-0.0483	0.0076	2.27E-10	0.2138	0.1135	0.01579	6.42E-13	rs111724389:44209364:G:A
17_44209474_A_T	17	44209474	T	0.2117	-0.0482	0.0076	2.53E-10	0.2138	0.1136	0.01579	6.23E-13	rs112401617:44209474:A:T
17_44209628_T_C	17	44209628	C	0.2121	-0.0481	0.0076	2.75E-10	0.2138	0.1136	0.01579	6.26E-13	rs17577954:44209628:T:C
17_44209875_T_C	17	44209875	C	0.2117	-0.0482	0.0076	2.53E-10	0.2138	0.1136	0.01579	6.22E-13	rs55780786:44209875:T:C
17_44209919_C_G	17	44209919	G	0.2117	-0.0482	0.0076	2.53E-10	0.2138	0.1136	0.01579	6.21E-13	rs3089:44209919:C:G
17_44209957_A_G	17	44209957	G	0.2117	-0.0482	0.0076	2.53E-10	0.2138	0.1136	0.01579	6.22E-13	rs55909047:44209957:A:G
17_44209985_T_C	17	44209985	C	0.2121	-0.0481	0.0076	2.62E-10	0.2138	0.1133	0.01579	7.30E-13	rs56119705:44209985:T:C
17_44210247_T_TGCAGTG	17	44210247	TGCAGTGAGCCAT	0.2118	-0.0472	0.0077	7.80E-10	0.2138	0.1136	0.01579	6.13E-13	68:44210247:T:TGCAGTGAGCCATCATCATA
17_44210442_C_T	17	44210442	T	0.212	-0.0479	0.0076	3.09E-10	0.2137	0.1133	0.01579	7.34E-13	rs17577975:44210442:C:T
17_44210933_A_G	17	44210933	G	0.2166	-0.047	0.0076	4.93E-10	0.2165	0.1136	0.01567	4.17E-13	rs7207582:44210933:A:G
17_44210988_C_G	17	44210988	G	0.212	-0.0479	0.0076	3.10E-10	0.2138	0.1133	0.01579	7.09E-13	rs12150087:44210988:C:G
17_44211502_G_A	17	44211502	A	0.2116	-0.0481	0.0076	2.74E-10	0.2138	0.1138	0.01579	5.78E-13	rs111424940:44211502:G:A
17_44211902_A_G	17	44211902	G	0.2115	-0.048	0.0076	2.91E-10	0.2138	0.1139	0.0158	5.51E-13	rs62063207:44211902:A:G
17_44212032_C_A	17	44212032	A	0.2115	-0.048	0.0076	2.98E-10	0.2137	0.1139	0.0158	5.43E-13	rs62063208:44212032:C:A
17_44212211_C_CA	17	44212211	CA	0.2113	-0.0484	0.0078	6.52E-10	0.2099	0.1159	0.01605	5.15E-13	rs67006527:44212211:C:CA
17_44212310_G_A	17	44212310	A	0.2167	-0.0469	0.0076	5.26E-10	0.2165	0.1135	0.01567	4.41E-13	rs10221243:44212310:G:A
17_44212525_GA_G	17	44212525	G	0.2116	-0.047	0.0077	9.54E-10	0.214	0.1142	0.01579	4.76E-13	rs67775973:44212525:GA:G
17_44212527_A_G	17	44212527	G	0.2115	-0.0479	0.0076	3.18E-10	0.214	0.1142	0.01579	4.76E-13	rs372980169:44212527:A:G
17_44212782_T_C	17	44212782	C	0.2173	-0.0466	0.0075	6.92E-10	0.2168	0.1121	0.01564	7.67E-13	rs9915547:44212782:T:C
17_44212908_AT_A	17	44212908	AT	0.4504	-0.0183	0.0064	0.004466	0.4284	0.08261	0.01348	8.92E-10	rs34258265:44212908:AT:A
17_44213164_C_A	17	44213164	A	0.1915	-0.0538	0.0082	5.62E-11	0.1889	0.1247	0.01676	9.97E-14	rs12150319:44213164:C:A
17_44213187_G_T	17	44213187	T	0.1915	-0.054	0.0082	4.97E-11	0.1889	0.1248	0.01676	9.36E-14	17:44213187:G:T
17_44213204_C_T	17	44213204	T	0.2112	-0.0478	0.0076	3.49E-10	0.2135	0.1155	0.0158	2.66E-13	17:44213204:C:T
17_44213547_AAAT_A	17	44213547	A	0.2013	-0.0517	0.008	9.11E-11	0.1984	0.1175	0.01612	3.03E-13	rs67220719:44213547:AAAT:A
17_44213712_G_A	17	44213712	A	0.211	-0.0481	0.0076	2.74E-10	0.2135	0.1145	0.0158	4.18E-13	17:44213712:G:A
17_44213921_A_C	17	44213921	C	0.2124	-0.0474	0.0076	4.85E-10	0.2141	0.1131	0.01579	7.98E-13	17:44213921:A:C
17_44213934_G_A	17	44213934	A	0.2114	-0.0471	0.0076	6.30E-10	0.2142	0.1132	0.01579	7.66E-13	17:44213934:G:A
17_44214094_A_G	17	44214094	G	0.2111	-0.0476	0.0076	4.11E-10	0.2136	0.1144	0.0158	4.49E-13	17:44214094:A:G
17_44214386_A_G	17	44214386	G	0.1929	-0.0516	0.0081	1.50E-10	0.1893	0.1132	0.0164	5.09E-12	17:44214386:A:G
17_44214518_C_T	17	44214518	T	0.1927	-0.0516	0.0081	1.53E-10	0.1891	0.1133	0.01641	5.14E-12	17:44214518:C:T
17_44214814_G_A	17	44214814	A	0.2111	-0.0477	0.0076	3.88E-10	0.2136	0.1144	0.0158	4.51E-13	17:44214814:G:A
17_44214815_C_G	17	44214815	G	0.2111	-0.0477	0.0076	3.88E-10	0.2136	0.1144	0.0158	4.51E-13	17:44214815:C:G
17_44214888_T_C	17	44214888	C	0.2016	-0.0523	0.0079	3.58E-11	0.2	0.1168	0.01608	3.70E-13	17:44214888:T:C
17_44215045_T_C	17	44215045	C	0.2112	-0.0474	0.0076	4.76E-10	0.2139	0.114	0.0158	5.33E-13	17:44215045:T:C
17_44215065_T_TA	17	44215065	TA	0.2151	-0.0464	0.0077	1.78E-09	0.2151	0.1131	0.01592	1.23E-12	rs199737620:44215065:T:TA
17_44215416_A_AG	17	44215416	AG	0.2112	-0.0467	0.0077	1.25E-09	0.2136	0.1143	0.0158	4.66E-13	17:44215416:A:AG
17_44215823_A_G	17	44215823	G	0.2112	-0.0476	0.0076	4.26E-10	0.2144	0.1141	0.0158	5.07E-13	17:44215823:A:G
17_44215896_C_T	17	44215896	T	0.2011	-0.0527	0.0079	2.71E-11	0.1995	0.1163	0.01608	4.86E-13	17:44215896:C:T

17_44216158_T_C	17	44216158	C	0.2111	-0.0476	0.0076	4.14E-10	0.2136	0.1143	0.0158	4.72E-13	17:44216158:T:C
17_44216226_A_G	17	44216226	G	0.2112	-0.0476	0.0076	3.92E-10	0.2137	0.1143	0.0158	4.69E-13	17:44216226:A:G
17_44216817_A_T	17	44216817	T	0.1926	-0.0515	0.0081	1.76E-10	0.1891	0.1125	0.01641	7.23E-12	17:44216817:A:T
17_44216966_G_GC	17	44216966	GC	0.2112	-0.0467	0.0077	1.23E-09	0.2136	0.1142	0.0158	4.88E-13	17:44216966:G:GC
17_44217020_T_C	17	44217020	C	0.1888	-0.0469	0.0081	8.32E-09	0.1842	0.1101	0.01677	5.25E-11	17:44217020:T:C
17_44217112_G_T	17	44217112	T	0.2111	-0.0476	0.0076	4.05E-10	0.2136	0.114	0.0158	5.20E-13	17:44217112:G:T
17_44217226_A_G	17	44217226	G	0.2111	-0.0476	0.0076	4.04E-10	0.2136	0.1142	0.0158	4.91E-13	17:44217226:A:G
17_44217267_A_T	17	44217267	T	0.2015	-0.0525	0.0079	3.00E-11	0.1995	0.1157	0.01608	6.18E-13	17:44217267:A:T
17_44217293_G_A	17	44217293	A	0.2111	-0.0481	0.0076	2.71E-10	0.2144	0.1122	0.0158	1.23E-12	17:44217293:G:A
17_44217791_A_C	17	44217791	C	0.1931	-0.0517	0.008	1.36E-10	0.1896	0.1125	0.0164	6.79E-12	17:44217791:A:C
17_44217905_A_AC	17	44217905	AC	0.125	-0.0595	0.0109	4.66E-08	0.1246	0.1311	0.02254	5.97E-09	rs142629715:44217905:A:AC
17_44218017_C_G	17	44218017	G	0.1926	-0.0516	0.0081	1.57E-10	0.1891	0.1138	0.01642	4.21E-12	17:44218017:C:G
17_44218044_A_T	17	44218044	T	0.2015	-0.0527	0.0079	2.63E-11	0.1995	0.1157	0.01608	6.21E-13	17:44218044:A:T
17_44218138_C_T	17	44218138	T	0.1971	-0.0528	0.008	5.02E-11	0.1955	0.1164	0.01634	1.04E-12	17:44218138:C:T
17_44218242_C_T	17	44218242	T	0.2111	-0.0477	0.0076	3.88E-10	0.2136	0.1139	0.0158	5.54E-13	17:44218242:C:T
17_44219831_T_A	17	44219831	A	0.2123	-0.0471	0.0076	6.22E-10	0.2145	0.1135	0.01577	6.15E-13	rs1819040:44219831:T:A
17_44219888_C_T	17	44219888	T	0.1922	-0.0519	0.0081	1.37E-10	0.1885	0.1133	0.01648	6.38E-12	17:44219888:C:T
17_44219905_G_A	17	44219905	A	0.2004	-0.0536	0.0079	1.57E-11	0.1977	0.1165	0.01616	5.56E-13	rs1358439:44219905:G:A
17_44219978_TCAAAA_T	17	44219978	T	0.1928	-0.0509	0.0081	3.76E-10	0.1891	0.112	0.01642	9.20E-12	s139628243:44219978:TCAAAA:T
17_44220454_T_G	17	44220454	G	0.2126	-0.0472	0.0076	5.42E-10	0.2158	0.1131	0.01579	7.78E-13	17:44220454:T:G
17_44220785_G_A	17	44220785	A	0.2114	-0.0477	0.0076	3.72E-10	0.2138	0.1121	0.0158	1.27E-12	17:44220785:G:A
17_44220790_A_G	17	44220790	G	0.2114	-0.048	0.0076	3.04E-10	0.2137	0.1132	0.0158	7.85E-13	17:44220790:A:G
17_44220863_AAAAT_A	17	44220863	A	0.2113	-0.0469	0.0077	1.03E-09	0.2137	0.1133	0.0158	7.30E-13	s141588384:44220863:AAAAT:A
17_44220942_G_A	17	44220942	A	0.2112	-0.0478	0.0076	3.37E-10	0.2137	0.1133	0.0158	7.31E-13	17:44220942:G:A
17_44221042_C_T	17	44221042	T	0.2112	-0.0478	0.0076	3.57E-10	0.2136	0.1134	0.0158	6.99E-13	rs62063212:44221042:C:T
17_44221169_CAAAAAAAA	17	44221169	C	0.2811	-0.0348	0.0074	2.18E-06	0.2779	0.1089	0.01531	1.14E-12	17:44221169:CAAAAAAAAAA:C
17_44221350_G_A	17	44221350	A	0.2112	-0.0477	0.0076	3.67E-10	0.2138	0.1132	0.0158	7.62E-13	rs2532307:44221350:G:A
17_44221476_A_T	17	44221476	T	0.2016	-0.0528	0.0079	2.39E-11	0.1995	0.1151	0.01608	8.11E-13	17:44221476:A:T
17_44221602_G_C	17	44221602	C	0.2116	-0.0479	0.0076	3.14E-10	0.2139	0.1137	0.0158	6.33E-13	17:44221602:G:C
17_44221836_C_T	17	44221836	T	0.2015	-0.0528	0.0079	2.51E-11	0.1993	0.1152	0.01609	8.16E-13	17:44221836:C:T
17_44222019_G_T	17	44222019	T	0.2011	-0.0525	0.0079	3.08E-11	0.1994	0.1157	0.01608	6.27E-13	17:44222019:G:T
17_44222067_T_G	17	44222067	G	0.2112	-0.0478	0.0076	3.57E-10	0.2136	0.1133	0.0158	7.43E-13	17:44222067:T:G
17_44222080_A_C	17	44222080	C	0.1923	-0.0518	0.0081	1.42E-10	0.1888	0.1132	0.01643	5.74E-12	17:44222080:A:C
17_44222335_G_A	17	44222335	A	0.2112	-0.0475	0.0076	4.29E-10	0.2142	0.112	0.01579	1.32E-12	17:44222335:G:A
17_44222460_T_G	17	44222460	G	0.2126	-0.047	0.0076	6.51E-10	0.2142	0.1132	0.01579	7.59E-13	17:44222460:T:G
17_44223034_A_C	17	44223034	C	0.1842	-0.0531	0.0083	1.81E-10	0.1812	0.1141	0.01701	1.96E-11	17:44223034:A:C
17_44223060_G_A	17	44223060	A	0.2112	-0.0477	0.0076	3.63E-10	0.2136	0.1132	0.0158	7.77E-13	17:44223060:G:A
17_44223243_G_A	17	44223243	A	0.2112	-0.0478	0.0076	3.59E-10	0.2136	0.1132	0.0158	7.86E-13	17:44223243:G:A
17_44223387_T_C	17	44223387	C	0.2108	-0.0478	0.0076	3.55E-10	0.2135	0.1126	0.0158	1.03E-12	17:44223387:T:C
17_44223491_C_G	17	44223491	G	0.1929	-0.0517	0.0081	1.39E-10	0.1893	0.1121	0.0164	8.15E-12	17:44223491:C:G
17_44223593_T_C	17	44223593	C	0.193	-0.0518	0.0081	1.23E-10	0.1893	0.1121	0.0164	8.31E-12	17:44223593:T:C
17_44224569_CAG_C	17	44224569	C	0.2013	-0.0515	0.008	1.00E-10	0.1993	0.1155	0.01609	7.14E-13	17:44224569:CAG:C
17_44224686_A_T	17	44224686	T	0.2113	-0.0479	0.0076	3.15E-10	0.2137	0.113	0.0158	8.43E-13	17:44224686:A:T
17_44224782_A_T	17	44224782	T	0.2014	-0.053	0.0079	2.12E-11	0.1994	0.1148	0.0161	9.66E-13	rs1918794:44224782:A:T
17_44224939_A_T	17	44224939	T	0.211	-0.0482	0.0076	2.57E-10	0.2131	0.1143	0.01581	4.82E-13	17:44224939:A:T
17_44224940_A_T	17	44224940	T	0.211	-0.0482	0.0076	2.57E-10	0.2131	0.1143	0.01581	4.82E-13	rs80103986:44224940:A:T
17_44225234_T_C	17	44225234	C	0.2112	-0.0478	0.0076	3.50E-10	0.2136	0.1131	0.01579	7.85E-13	17:44225234:T:C
17_44225440_T_C	17	44225440	C	0.1929	-0.0517	0.0081	1.39E-10	0.1893	0.1122	0.0164	8.03E-12	17:44225440:T:C
17_44225485_T_C	17	44225485	C	0.2112	-0.0478	0.0076	3.51E-10	0.2136	0.1131	0.01579	7.85E-13	17:44225485:T:C
17_44225607_C_T	17	44225607	T	0.1919	-0.0516	0.0081	1.74E-10	0.1884	0.1128	0.01646	7.23E-12	17:44225607:C:T
17_44225802_C_T	17	44225802	T	0.2118	-0.0473	0.0076	4.96E-10	0.2138	0.1131	0.01578	7.67E-13	17:44225802:C:T
17_44225886_G_A	17	44225886	A	0.2018	-0.0521	0.0079	3.85E-11	0.2001	0.116	0.01607	5.33E-13	17:44225886:G:A
17_44226030_G_A	17	44226030	A	0.2112	-0.0478	0.0076	3.51E-10	0.2136	0.1132	0.01579	7.77E-13	17:44226030:G:A
17_44226126_A_C	17	44226126	C	0.2112	-0.0478	0.0076	3.50E-10	0.2136	0.1131	0.01579	7.86E-13	17:44226126:A:C
17_44226325_A_T	17	44226325	T	0.1962	-0.0527	0.0081	6.35E-11	0.1953	0.1199	0.0164	2.66E-13	17:44226325:A:T

17_44226331_A_G	17	44226331	G	0.1962	-0.0527	0.0081	5.96E-11	0.1953	0.1199	0.0164	2.59E-13	17:44226331:A:G
17_44226561_T_G	17	44226561	G	0.2112	-0.0478	0.0076	3.51E-10	0.2136	0.1131	0.01579	7.86E-13	17:44226561:T:G
17_44226817_G_A	17	44226817	A	0.1929	-0.0517	0.0081	1.42E-10	0.1893	0.112	0.0164	8.50E-12	17:44226817:G:A
17_44226980_A_G	17	44226980	G	0.2013	-0.0529	0.0079	2.10E-11	0.1996	0.1158	0.01608	6.04E-13	17:44226980:A:G
17_44227186_G_A	17	44227186	A	0.2113	-0.0478	0.0076	3.51E-10	0.2137	0.1133	0.0158	7.24E-13	17:44227186:G:A
17_44227196_T_C	17	44227196	C	0.2112	-0.0478	0.0076	3.57E-10	0.2136	0.1131	0.01579	7.87E-13	17:44227196:T:C
17_44227393_T_A	17	44227393	A	0.3046	-0.0443	0.0075	4.23E-09	0.2989	0.1013	0.01576	1.30E-10	17:44227393:T:A
17_44227510_A_T	17	44227510	T	0.2121	-0.047	0.0076	6.57E-10	0.2142	0.1148	0.01578	3.48E-13	17:44227510:A:T
17_44227531_T_C	17	44227531	C	0.2122	-0.0468	0.0076	7.60E-10	0.2143	0.1146	0.01578	3.85E-13	17:44227531:T:C
17_44227623_T_C	17	44227623	C	0.2165	-0.047	0.0076	5.09E-10	0.2165	0.1126	0.01566	6.57E-13	17:44227623:T:C
17_44227882_C_G	17	44227882	G	0.2014	-0.0521	0.0079	4.31E-11	0.1996	0.1154	0.01608	7.20E-13	17:44227882:C:G
17_44228169_C_T	17	44228169	T	0.2182	-0.0466	0.0075	6.44E-10	0.2177	0.1101	0.01564	1.96E-12	17:44228169:C:T
17_44228529_G_A	17	44228529	A	0.2122	-0.0472	0.0076	5.60E-10	0.215	0.1126	0.01579	9.98E-13	17:44228529:G:A
17_44228609_C_G	17	44228609	G	0.2117	-0.0471	0.0076	6.42E-10	0.2139	0.1126	0.01579	1.02E-12	17:44228609:C:G
17_44228619_C_T	17	44228619	T	0.2022	-0.0521	0.0079	4.40E-11	0.1998	0.1145	0.01607	1.08E-12	17:44228619:C:T
17_44228621_T_A	17	44228621	A	0.1931	-0.051	0.0081	2.46E-10	0.1893	0.1114	0.01641	1.14E-11	17:44228621:T:A
17_44228770_A_G	17	44228770	G	0.2124	-0.0468	0.0076	7.73E-10	0.2141	0.1132	0.01579	7.38E-13	17:44228770:A:G
17_44228824_A_G	17	44228824	G	0.2128	-0.0472	0.0076	5.77E-10	0.2149	0.112	0.01579	1.29E-12	17:44228824:A:G
17_44229073_G_A	17	44229073	A	0.1935	-0.0501	0.0081	5.41E-10	0.1893	0.1109	0.01641	1.42E-11	17:44229073:G:A
17_44229364_T_C	17	44229364	C	0.2006	-0.052	0.0079	5.45E-11	0.1983	0.1161	0.01614	6.28E-13	17:44229364:T:C
17_44229415_T_C	17	44229415	C	0.2003	-0.0521	0.0079	5.30E-11	0.1979	0.1157	0.01614	7.81E-13	17:44229415:T:C
17_44229708_GACAA_G	17	44229708	G	0.2005	-0.0514	0.008	1.39E-10	0.1979	0.1166	0.01617	5.53E-13	17:44229708:GACAA:G
17_44229986_T_C	17	44229986	C	0.2118	-0.0472	0.0076	5.56E-10	0.214	0.1121	0.01579	1.28E-12	17:44229986:T:C
17_44230097_C_T	17	44230097	T	0.2016	-0.0523	0.0079	4.05E-11	0.1993	0.115	0.01611	9.42E-13	17:44230097:C:T
17_44230166_G_A	17	44230166	A	0.1931	-0.0507	0.0081	3.19E-10	0.1891	0.1115	0.01641	1.06E-11	17:44230166:G:A
17_44230269_G_C	17	44230269	C	0.1908	-0.0503	0.0081	6.25E-10	0.1867	0.1115	0.01654	1.61E-11	17:44230269:G:C
17_44230647_C_T	17	44230647	T	0.211	-0.0474	0.0076	4.79E-10	0.2137	0.1125	0.01579	1.04E-12	17:44230647:C:T
17_44231117_T_C	17	44231117	C	0.2125	-0.0466	0.0076	8.88E-10	0.2141	0.1122	0.01579	1.18E-12	17:44231117:T:C
17_44231295_G_A	17	44231295	A	0.2121	-0.047	0.0076	6.87E-10	0.2156	0.1114	0.01579	1.70E-12	17:44231295:G:A
17_44231326_G_A	17	44231326	A	0.2116	-0.047	0.0076	6.55E-10	0.2154	0.1131	0.01579	7.88E-13	17:44231326:G:A
17_44231617_A_T	17	44231617	T	0.2116	-0.0471	0.0076	5.95E-10	0.2138	0.1123	0.01579	1.16E-12	17:44231617:A:T
17_44231827_T_C	17	44231827	C	0.2019	-0.0524	0.0079	3.41E-11	0.1996	0.1139	0.01609	1.41E-12	17:44231827:T:C
17_44231932_G_A	17	44231932	A	0.1916	-0.0513	0.0081	2.51E-10	0.1881	0.1141	0.01648	4.49E-12	17:44231932:G:A
17_44232169_A_G	17	44232169	G	0.1932	-0.0508	0.0081	2.77E-10	0.1894	0.1113	0.0164	1.15E-11	17:44232169:A:G
17_44232408_G_A	17	44232408	A	0.2025	-0.0518	0.0079	5.45E-11	0.2	0.1141	0.01607	1.24E-12	17:44232408:G:A
17_44232721_G_A	17	44232721	A	0.1933	-0.0509	0.0081	2.65E-10	0.1894	0.1113	0.0164	1.15E-11	17:44232721:G:A
17_44232959_G_A	17	44232959	A	0.2118	-0.0471	0.0076	6.16E-10	0.2141	0.112	0.01579	1.29E-12	17:44232959:G:A
17_44232990_T_C	17	44232990	C	0.1927	-0.051	0.0081	2.76E-10	0.1886	0.1127	0.01646	7.52E-12	17:44232990:T:C
17_44233433_G_C	17	44233433	C	0.2133	-0.0467	0.0076	8.26E-10	0.2152	0.1137	0.01578	6.00E-13	17:44233433:G:C
17_44233589_T_C	17	44233589	C	0.2117	-0.0474	0.0076	4.97E-10	0.2139	0.1122	0.01579	1.20E-12	17:44233589:T:C
17_44233699_C_T	17	44233699	T	0.1933	-0.051	0.0081	2.45E-10	0.1894	0.1114	0.0164	1.12E-11	17:44233699:C:T
17_44233776_T_C	17	44233776	C	0.2128	-0.0471	0.0076	6.19E-10	0.215	0.114	0.01579	5.15E-13	17:44233776:T:C
17_44233811_C_T	17	44233811	T	0.213	-0.0469	0.0076	7.42E-10	0.2151	0.1134	0.01579	6.96E-13	17:44233811:C:T
17_44234060_A_G	17	44234060	G	0.212	-0.0473	0.0076	5.24E-10	0.214	0.112	0.01579	1.34E-12	17:44234060:A:G
17_44234064_G_A	17	44234064	A	0.2024	-0.0523	0.0079	3.62E-11	0.1999	0.1139	0.01607	1.40E-12	17:44234064:G:A
17_44234265_C_CAAA	17	44234265	CAAA	0.2115	-0.0467	0.0077	1.18E-09	0.2136	0.1122	0.0158	1.24E-12	17:44234265:C:CAAA
17_44234526_C_T	17	44234526	T	0.2123	-0.0469	0.0076	7.27E-10	0.2159	0.1138	0.0158	5.74E-13	17:44234526:C:T
17_44235893_C_T	17	44235893	T	0.2119	-0.0473	0.0076	5.10E-10	0.2156	0.112	0.01579	1.29E-12	17:44235893:C:T
17_44236108_T_C	17	44236108	C	0.201	-0.0531	0.0079	2.20E-11	0.1988	0.1126	0.01613	2.92E-12	17:44236108:T:C
17_44236209_G_A	17	44236209	A	0.1923	-0.0512	0.0081	2.37E-10	0.1887	0.111	0.01644	1.47E-11	17:44236209:G:A
17_44236321_C_G	17	44236321	G	0.1609	-0.0474	0.0088	8.43E-08	0.1603	0.107	0.01806	3.20E-09	17:44236321:C:G
17_44236725_C_A	17	44236725	A	0.2112	-0.0473	0.0076	5.57E-10	0.2136	0.1131	0.0158	8.22E-13	17:44236725:C:A
17_44237068_A_T	17	44237068	T	0.2115	-0.0475	0.0076	4.27E-10	0.214	0.1113	0.01579	1.82E-12	17:44237068:A:T
17_44237372_G_C	17	44237372	C	0.2114	-0.0477	0.0076	3.90E-10	0.2138	0.1117	0.01579	1.55E-12	17:44237372:G:C
17_44237790_G_A	17	44237790	A	0.2117	-0.0477	0.0076	3.67E-10	0.2139	0.1104	0.01579	2.69E-12	17:44237790:G:A

17_44238130_AT_A	17	44238130	A	0.2115	-0.0467	0.0077	1.17E-09	0.2138	0.1117	0.01579	1.53E-12	17:44238130:AT:A
17_44238424_G_A	17	44238424	A	0.2117	-0.0476	0.0076	3.96E-10	0.2139	0.1141	0.01579	5.06E-13	17:44238424:G:A
17_44238490_G_A	17	44238490	A	0.2001	-0.0535	0.0079	1.59E-11	0.1988	0.1134	0.01619	2.49E-12	17:44238490:G:A
17_44238571_C_G	17	44238571	G	0.2162	-0.047	0.0076	5.04E-10	0.2161	0.1104	0.01567	1.80E-12	17:44238571:C:G
17_44238616_TAAAAAAAA	17	44238616	T	0.4157	-0.0226	0.0064	0.0004456	0.4008	0.08294	0.01346	7.25E-10	17:44238616:TAAAAAAAA:T
17_44238938_T_C	17	44238938	C	0.2134	-0.0461	0.0076	1.43E-09	0.2164	0.1121	0.01579	1.25E-12	17:44238938:T:C
17_44238966_T_C	17	44238966	C	0.2134	-0.0461	0.0076	1.44E-09	0.2164	0.1123	0.01578	1.12E-12	17:44238966:T:C
17_44239225_G_A	17	44239225	A	0.1907	-0.0523	0.0081	1.09E-10	0.1874	0.1086	0.01652	4.92E-11	17:44239225:G:A
17_44239556_T_C	17	44239556	C	0.1931	-0.0513	0.0081	1.85E-10	0.1894	0.1112	0.0164	1.21E-11	17:44239556:T:C
17_44239639_C_A	17	44239639	A	0.1918	-0.0511	0.0081	2.66E-10	0.1884	0.1104	0.01649	2.15E-11	17:44239639:C:A
17_44239958_C_T	17	44239958	T	0.2114	-0.0472	0.0076	5.76E-10	0.214	0.1112	0.01579	1.91E-12	17:44239958:C:T
17_44240107_T_C	17	44240107	C	0.2126	-0.0464	0.0076	1.12E-09	0.2141	0.1138	0.01579	5.51E-13	17:44240107:T:C
17_44240497_T_C	17	44240497	C	0.193	-0.0512	0.0081	2.03E-10	0.1894	0.1114	0.0164	1.12E-11	17:44240497:T:C
17_44240797_T_C	17	44240797	C	0.1922	-0.0511	0.0081	2.67E-10	0.1885	0.1117	0.01645	1.13E-11	17:44240797:T:C
17_44240850_T_C	17	44240850	C	0.193	-0.0512	0.0081	2.10E-10	0.1894	0.1114	0.0164	1.09E-11	17:44240850:T:C
17_44240986_C_A	17	44240986	A	0.2114	-0.0472	0.0076	5.70E-10	0.2138	0.1123	0.0158	1.21E-12	17:44240986:C:A
17_44241304_C_G	17	44241304	G	0.2113	-0.0474	0.0076	4.71E-10	0.2138	0.1123	0.0158	1.17E-12	17:44241304:C:G
17_44241487_CTT_C	17	44241487	C	0.2013	-0.0516	0.008	9.40E-11	0.1991	0.1144	0.0161	1.18E-12	17:44241487:CTT:C
17_44241664_T_C	17	44241664	C	0.2119	-0.0472	0.0076	5.54E-10	0.2148	0.1117	0.01579	1.52E-12	17:44241664:T:C
17_44241797_T_C	17	44241797	C	0.1928	-0.0511	0.0081	2.30E-10	0.1892	0.1116	0.0164	1.01E-11	17:44241797:T:C
17_44242536_C_T	17	44242536	T	0.1915	-0.052	0.0082	1.77E-10	0.1923	0.1112	0.01654	1.76E-11	17:44242536:C:T
17_44242574_G_A	17	44242574	A	0.1914	-0.0521	0.0082	1.68E-10	0.1921	0.1114	0.01655	1.68E-11	17:44242574:G:A
17_44242606_C_CTTAT	17	44242606	CTTAT	0.2018	-0.046	0.0078	4.49E-09	0.2032	0.1084	0.01618	2.15E-11	17:44242606:C:CTTAT
17_44242637_C_T	17	44242637	T	0.2011	-0.0524	0.0079	3.60E-11	0.1994	0.115	0.01609	8.91E-13	17:44242637:C:T
17_44242759_C_T	17	44242759	T	0.1922	-0.0507	0.0081	3.49E-10	0.1885	0.1125	0.01646	8.27E-12	17:44242759:C:T
17_44242788_C_T	17	44242788	T	0.2113	-0.0473	0.0076	5.25E-10	0.2138	0.1126	0.0158	1.01E-12	17:44242788:C:T
17_44242969_T_C	17	44242969	C	0.2115	-0.0473	0.0076	5.44E-10	0.2141	0.112	0.0158	1.34E-12	17:44242969:T:C
17_44243179_A_G	17	44243179	G	0.2112	-0.0473	0.0076	5.37E-10	0.2137	0.1127	0.0158	9.64E-13	17:44243179:A:G
17_44243351_T_TCG	17	44243351	TCG	0.2115	-0.0462	0.0077	1.77E-09	0.2139	0.1129	0.0158	9.03E-13	rs76475392:44243351:T:TCG
17_44243354_A_AG	17	44243354	AG	0.2114	-0.0462	0.0077	1.77E-09	0.2139	0.1129	0.0158	9.03E-13	17:44243354:A:AG
17_44243543_TA_T	17	44243543	T	0.2113	-0.0463	0.0077	1.67E-09	0.2137	0.1128	0.0158	9.32E-13	17:44243543:TA:T
17_44243863_A_T	17	44243863	T	0.2104	-0.047	0.0076	7.70E-10	0.213	0.113	0.01583	9.52E-13	17:44243863:A:T
17_44243868_C_T	17	44243868	T	0.2104	-0.047	0.0076	7.71E-10	0.213	0.113	0.01583	9.51E-13	17:44243868:C:T
17_44243870_T_C	17	44243870	C	0.2104	-0.047	0.0076	7.71E-10	0.213	0.113	0.01583	9.51E-13	17:44243870:T:C
17_44243979_C_T	17	44243979	T	0.2113	-0.0469	0.0076	7.48E-10	0.2138	0.114	0.01579	5.19E-13	17:44243979:C:T
17_44244397_G_A	17	44244397	A	0.2118	-0.0476	0.0076	4.20E-10	0.2145	0.1121	0.0158	1.29E-12	17:44244397:G:A
17_44244581_T_C	17	44244581	C	0.2112	-0.0472	0.0076	5.60E-10	0.2137	0.1128	0.0158	9.26E-13	17:44244581:T:C
17_44244639_A_G	17	44244639	G	0.1925	-0.0511	0.0081	2.28E-10	0.1891	0.1118	0.01642	9.84E-12	17:44244639:A:G
17_44244896_C_G	17	44244896	G	0.2012	-0.0523	0.0079	3.53E-11	0.1996	0.1148	0.01608	9.40E-13	17:44244896:C:G
17_44244926_T_G	17	44244926	G	0.2112	-0.0472	0.0076	5.57E-10	0.2137	0.1128	0.0158	9.45E-13	17:44244926:T:G
17_44245171_G_T	17	44245171	T	0.2011	-0.0522	0.0079	4.03E-11	0.1995	0.1147	0.01608	1.01E-12	17:44245171:G:T
17_44245359_G_A	17	44245359	A	0.2011	-0.0522	0.0079	4.00E-11	0.1995	0.1146	0.01608	1.04E-12	17:44245359:G:A
17_44245766_G_A	17	44245766	A	0.2111	-0.0472	0.0076	5.51E-10	0.2137	0.1127	0.0158	1.00E-12	17:44245766:G:A
17_44245876_A_G	17	44245876	G	0.2111	-0.0473	0.0076	5.50E-10	0.2137	0.1126	0.0158	1.01E-12	17:44245876:A:G
17_44246143_C_A	17	44246143	A	0.19	-0.0463	0.0081	1.11E-08	0.1855	0.1101	0.01668	4.08E-11	17:44246143:C:A
17_44246211_A_G	17	44246211	G	0.211	-0.0472	0.0076	5.81E-10	0.2137	0.1131	0.0158	8.07E-13	17:44246211:A:G
17_44246330_T_C	17	44246330	C	0.1927	-0.0511	0.0081	2.39E-10	0.1888	0.1118	0.01641	9.60E-12	17:44246330:T:C
17_44246405_C_A	17	44246405	A	0.212	-0.0477	0.0076	3.81E-10	0.2161	0.1107	0.0158	2.39E-12	17:44246405:C:A
17_44246527_T_C	17	44246527	C	0.2015	-0.0521	0.0079	4.52E-11	0.1995	0.1143	0.01608	1.16E-12	rs2532277:44246527:T:C
17_44246624_C_A	17	44246624	A	0.2126	-0.0471	0.0076	6.10E-10	0.2147	0.1146	0.01579	3.97E-13	rs2532276:44246624:C:A
17_44246689_GAACT_G	17	44246689	G	0.1915	-0.0505	0.0082	6.68E-10	0.1872	0.1142	0.01654	5.02E-12	s150546962:44246689:GAACT:G
17_44246997_G_A	17	44246997	A	0.2111	-0.0471	0.0076	6.09E-10	0.2137	0.1128	0.0158	9.32E-13	17:44246997:G:A
17_44247164_A_G	17	44247164	G	0.2167	-0.0452	0.0076	2.29E-09	0.2162	0.112	0.01567	8.98E-13	17:44247164:A:G
17_44247314_C_T	17	44247314	T	0.2115	-0.047	0.0076	6.57E-10	0.2144	0.1126	0.0158	1.01E-12	17:44247314:C:T
17_44247673_G_A	17	44247673	A	0.2113	-0.0473	0.0076	5.27E-10	0.2144	0.1124	0.0158	1.13E-12	17:44247673:G:A

17_44248042_G_A	17	44248042	A	0.2111	-0.0471	0.0076	6.43E-10	0.2137	0.113	0.0158	8.33E-13	17:44248042:G:A
17_44248769_T_C	17	44248769	C	0.2111	-0.047	0.0076	6.47E-10	0.2138	0.1132	0.0158	7.86E-13	17:44248769:T:C
17_44248814_G_A	17	44248814	A	0.2111	-0.0471	0.0076	6.40E-10	0.2137	0.113	0.0158	8.39E-13	17:44248814:G:A
17_44248837_T_C	17	44248837	C	0.1926	-0.0509	0.0081	2.70E-10	0.189	0.1126	0.01642	6.94E-12	17:44248837:T:C
17_44249096_A_C	17	44249096	C	0.1927	-0.051	0.0081	2.52E-10	0.189	0.1129	0.01641	6.04E-12	17:44249096:A:C
17_44249199_T_G	17	44249199	G	0.1927	-0.051	0.0081	2.51E-10	0.189	0.1129	0.01641	6.04E-12	17:44249199:T:G
17_44249621_A_G	17	44249621	G	0.2112	-0.0472	0.0076	5.81E-10	0.2138	0.1137	0.0158	6.09E-13	17:44249621:A:G
17_44249800_G_A	17	44249800	A	0.2112	-0.0472	0.0076	5.67E-10	0.2138	0.1136	0.0158	6.38E-13	17:44249800:G:A
17_44249911_T_TA	17	44249911	TA	0.2119	-0.045	0.0077	4.96E-09	0.2142	0.1132	0.01581	7.99E-13	17:44249911:T:TA
17_44250108_T_C	17	44250108	C	0.2142	-0.0464	0.0076	1.09E-09	0.2151	0.1138	0.01578	5.44E-13	17:44250108:T:C
17_44250236_T_G	17	44250236	G	0.1927	-0.051	0.0081	2.57E-10	0.189	0.1129	0.01641	6.01E-12	17:44250236:T:G
17_44250473_G_C	17	44250473	C	0.2002	-0.0522	0.0079	4.92E-11	0.1977	0.116	0.01613	6.30E-13	17:44250473:G:C
17_44250616_G_A	17	44250616	A	0.2112	-0.0472	0.0076	5.81E-10	0.2138	0.1137	0.0158	6.05E-13	17:44250616:G:A
17_44250669_TA_T	17	44250669	T	0.2113	-0.0462	0.0077	1.76E-09	0.2138	0.1137	0.0158	6.04E-13	17:44250669:TA:T
17_44250883_C_A	17	44250883	A	0.199	-0.0519	0.008	7.52E-11	0.1967	0.1152	0.0162	1.15E-12	17:44250883:C:A
17_44251230_T_C	17	44251230	C	0.2112	-0.0472	0.0076	5.80E-10	0.2138	0.1137	0.0158	6.02E-13	17:44251230:T:C
17_44251243_C_T	17	44251243	T	0.1919	-0.0508	0.0081	3.27E-10	0.1879	0.1127	0.01647	7.84E-12	17:44251243:C:T
17_44251491_GAAAACTT_	17	44251491	G	0.1907	-0.05	0.0082	9.93E-10	0.186	0.1142	0.01657	5.42E-12	17:44251491:GAAAACTT:G
17_44251548_G_A	17	44251548	A	0.2112	-0.0472	0.0076	5.80E-10	0.2138	0.1137	0.0158	6.01E-13	17:44251548:G:A
17_44251554_ATG_A	17	44251554	A	0.2151	-0.047	0.0077	9.20E-10	0.2172	0.1131	0.0158	8.19E-13	17:44251554:ATG:A
17_44251582_T_C	17	44251582	C	0.2112	-0.0472	0.0076	5.80E-10	0.2138	0.1137	0.0158	6.01E-13	17:44251582:T:C
17_44251698_G_A	17	44251698	A	0.2112	-0.0472	0.0076	5.80E-10	0.2138	0.1137	0.0158	6.01E-13	17:44251698:G:A
17_44251769_A_G	17	44251769	G	0.2112	-0.0472	0.0076	5.80E-10	0.2138	0.1137	0.0158	6.00E-13	17:44251769:A:G
17_44251907_C_T	17	44251907	T	0.2112	-0.0474	0.0076	4.69E-10	0.2138	0.1126	0.01579	1.02E-12	17:44251907:C:T
17_44251972_G_A	17	44251972	A	0.2116	-0.0474	0.0076	4.72E-10	0.2139	0.1129	0.01579	8.80E-13	17:44251972:G:A
17_44252098_C_T	17	44252098	T	0.2112	-0.0472	0.0076	5.78E-10	0.2138	0.1138	0.0158	5.86E-13	17:44252098:C:T
17_44252197_G_T	17	44252197	T	0.2112	-0.0472	0.0076	5.68E-10	0.2138	0.1137	0.0158	6.06E-13	17:44252197:G:T
17_44252416_G_C	17	44252416	C	0.2112	-0.0473	0.0076	5.47E-10	0.2138	0.1136	0.0158	6.34E-13	17:44252416:G:C
17_44252461_C_G	17	44252461	G	0.182	-0.0603	0.0084	7.89E-13	0.182	0.1231	0.01713	6.51E-13	17:44252461:C:G
17_44252468_G_A[c]	**17**	**44252468**	**A**	**0.182**	**-0.0605**	**0.0084**	**6.86E-13**	**0.1821**	**0.1232**	**0.01712**	**6.29E-13**	**17:44252468:G:A**
17_44252510_T_C	17	44252510	C	0.2112	-0.0473	0.0076	5.38E-10	0.2138	0.1136	0.0158	6.47E-13	17:44252510:T:C
17_44253203_A_C	17	44253203	C	0.2112	-0.0474	0.0076	4.71E-10	0.2138	0.1132	0.0158	7.52E-13	17:44253203:A:C
17_44253275_T_C	17	44253275	C	0.195	-0.0571	0.008	1.33E-12	0.1946	0.1139	0.01633	3.08E-12	17:44253275:T:C
17_44253364_G_A	17	44253364	A	0.212	-0.0477	0.0076	3.70E-10	0.2144	0.1128	0.01579	9.21E-13	17:44253364:G:A
17_44253951_G_A	17	44253951	A	0.1949	-0.0557	0.008	4.56E-12	0.1945	0.1148	0.01635	2.22E-12	17:44253951:G:A
17_44254291_C_T	17	44254291	T	0.1956	-0.0559	0.008	3.37E-12	0.195	0.1148	0.01631	1.99E-12	17:44254291:C:T
17_44254379_C_T	17	44254379	T	0.2113	-0.0472	0.0076	5.92E-10	0.2137	0.1139	0.0158	5.54E-13	17:44254379:C:T
17_44254413_A_G	17	44254413	G	0.2151	-0.0464	0.0076	9.67E-10	0.2164	0.1115	0.01578	1.57E-12	17:44254413:A:G
17_44254467_A_G	17	44254467	G	0.1925	-0.0508	0.0081	3.08E-10	0.1889	0.1126	0.01642	7.23E-12	17:44254467:A:G
17_44254494_T_C	17	44254494	C	0.2121	-0.0471	0.0076	6.40E-10	0.2147	0.1142	0.01579	4.72E-13	17:44254494:T:C
17_44254686_T_TAATGCAC	17	44254686	TAATGCACAGGAA	0.2113	-0.046	0.0077	2.12E-09	0.2138	0.1134	0.0158	7.08E-13	:44254686:T:TAATGCACAGGAAAA
17_44254993_GT_G	17	44254993	G	0.2114	-0.0459	0.0077	2.29E-09	0.2138	0.1134	0.0158	7.03E-13	17:44254993:GT:G
17_44255002_C_A	17	44255002	A	0.1911	-0.0505	0.0081	4.93E-10	0.1878	0.1123	0.01652	1.05E-11	17:44255002:C:A
17_44255017_T_C	17	44255017	C	0.2114	-0.0468	0.0076	7.84E-10	0.2145	0.1136	0.0158	6.29E-13	17:44255017:T:C
17_44255146_C_CT	17	44255146	CT	0.2252	-0.0425	0.0076	2.68E-08	0.2269	0.1122	0.01573	9.61E-13	17:44255146:C:CT
17_44255532_T_C	17	44255532	C	0.2116	-0.0468	0.0076	7.99E-10	0.2138	0.115	0.01579	3.26E-13	17:44255532:T:C
17_44255550_A_G	17	44255550	G	0.19	-0.051	0.0082	3.91E-10	0.1858	0.1165	0.01657	2.12E-12	17:44255550:A:G
17_44255777_G_A	17	44255777	A	0.2113	-0.0469	0.0076	7.18E-10	0.2138	0.1134	0.0158	7.10E-13	17:44255777:G:A
17_44255784_A_G	17	44255784	G	0.1927	-0.0505	0.0081	3.66E-10	0.189	0.1128	0.01641	6.26E-12	17:44255784:A:G
17_44256053_G_A	17	44256053	A	0.1948	-0.0565	0.0081	2.29E-12	0.194	0.1151	0.01637	2.07E-12	17:44256053:G:A
17_44256296_G_A	17	44256296	A	0.1953	-0.0563	0.008	2.55E-12	0.1948	0.1146	0.01632	2.20E-12	17:44256296:G:A
17_44256655_G_A	17	44256655	A	0.195	-0.0564	0.008	2.37E-12	0.1945	0.1151	0.01635	1.90E-12	17:44256655:G:A
17_44256710_G_C	17	44256710	C	0.1922	-0.0506	0.0081	3.61E-10	0.189	0.1126	0.01642	7.02E-12	17:44256710:G:C
17_44256811_A_AACAAG	17	44256811	AACAAG	0.2113	-0.0459	0.0077	2.21E-09	0.2138	0.1134	0.0158	7.04E-13	113089855:44256811:A:AACAAG
17_44257473_T_C	17	44257473	C	0.2117	-0.0466	0.0076	9.06E-10	0.2143	0.1133	0.0158	7.38E-13	17:44257473:T:C

17_44257783_A_G	17	44257783	G	0.2164	-0.0461	0.0076	1.06E-09	0.2166	0.1137	0.01567	3.95E-13	17:44257783:A:G
17_44257788_T_C	17	44257788	C	0.2112	-0.0469	0.0076	7.51E-10	0.2138	0.1134	0.0158	7.00E-13	17:44257788:T:C
17_44257923_G_A	17	44257923	A	0.2006	-0.0528	0.0079	2.73E-11	0.1987	0.1155	0.01611	7.55E-13	17:44257923:G:A
17_44258231_A_G	17	44258231	G	0.2112	-0.0469	0.0076	7.60E-10	0.2138	0.1134	0.0158	6.98E-13	17:44258231:A:G
17_44258354_G_C	17	44258354	C	0.2123	-0.0466	0.0076	9.17E-10	0.2142	0.1127	0.01579	9.52E-13	17:44258354:G:C
17_44258422_G_T	17	44258422	T	0.2113	-0.0473	0.0076	5.07E-10	0.214	0.1144	0.0158	4.48E-13	17:44258422:G:T
17_44258446_A_G	17	44258446	G	0.1905	-0.0516	0.0081	2.26E-10	0.1849	0.1127	0.01656	1.02E-11	17:44258446:A:G
17_44258914_A_G	17	44258914	G	0.2112	-0.0469	0.0076	7.62E-10	0.2143	0.1138	0.01583	6.35E-13	17:44258914:A:G
17_44258938_G_A	17	44258938	A	0.1908	-0.052	0.0081	1.59E-10	0.1854	0.112	0.01655	1.33E-11	17:44258938:G:A
17_44258954_G_C	17	44258954	C	0.2112	-0.0469	0.0076	7.09E-10	0.2138	0.1138	0.0158	5.92E-13	17:44258954:G:C
17_44259040_G_C	17	44259040	C	0.2119	-0.0473	0.0076	5.22E-10	0.2147	0.114	0.0158	5.42E-13	17:44259040:G:C
17_44259261_T_G	17	44259261	G	0.2019	-0.0465	0.0078	2.23E-09	0.2034	0.1088	0.01617	1.70E-11	17:44259261:T:G
17_44259313_T_TA	17	44259313	TA	0.1914	-0.0503	0.0082	7.64E-10	0.1859	0.1116	0.01652	1.41E-11	rs141371634:44259313:T:TA
17_44259519_A_G	17	44259519	G	0.1986	-0.0525	0.008	4.84E-11	0.1965	0.1168	0.01621	5.83E-13	17:44259519:A:G
17_44259539_A_C	17	44259539	C	0.1986	-0.0525	0.008	4.84E-11	0.1965	0.1168	0.01621	5.83E-13	17:44259539:A:C
17_44259792_G_A	17	44259792	A	0.2114	-0.0475	0.0076	4.33E-10	0.214	0.1133	0.01579	7.38E-13	17:44259792:G:A
17_44259919_A_G	17	44259919	G	0.1991	-0.0527	0.008	3.53E-11	0.1974	0.1153	0.01619	1.07E-12	17:44259919:A:G
17_44260416_T_C	17	44260416	C	0.2126	-0.0471	0.0076	6.12E-10	0.2142	0.113	0.01579	8.19E-13	17:44260416:T:C
17_44260644_AT_A	17	44260644	A	0.2159	-0.0458	0.0077	2.55E-09	0.2192	0.1117	0.01585	1.85E-12	17:44260644:AT:A
17_44260845_G_A	17	44260845	A	0.1877	-0.046	0.0082	1.85E-08	0.1818	0.1108	0.01688	5.20E-11	17:44260845:G:A
17_44260931_GGAGAGA_G	17	44260931	G	0.2109	-0.0463	0.0077	1.78E-09	0.2133	0.1128	0.01583	1.03E-12	17:44260931:GGAGAGA:G
17_44260933_A_G	17	44260933	G	0.211	-0.0477	0.0076	4.11E-10	0.2134	0.1126	0.01581	1.06E-12	17:44260933:A:G
17_44260939_GA_G	17	44260939	G	0.2109	-0.0463	0.0077	1.79E-09	0.2133	0.1128	0.01583	1.03E-12	17:44260939:GA:G
17_44260967_G_A	17	44260967	A	0.2117	-0.0471	0.0076	6.17E-10	0.2141	0.1119	0.0158	1.44E-12	17:44260967:G:A
17_44261137_C_T	17	44261137	T	0.2115	-0.0471	0.0076	6.21E-10	0.2138	0.1124	0.01579	1.10E-12	17:44261137:C:T
17_44261613_T_TCC	17	44261613	TCC	0.2131	-0.0461	0.0077	1.79E-09	0.2142	0.113	0.01577	7.78E-13	17:44261613:T:TCC
17_44261753_T_C	17	44261753	C	0.2121	-0.0462	0.0076	1.29E-09	0.2147	0.1146	0.01579	3.97E-13	17:44261753:T:C
17_44262203_CTTTTTT_C	17	44262203	C	0.2114	-0.046	0.0077	2.10E-09	0.2137	0.1126	0.0158	1.04E-12	17:44262203:CTTTTTT:C
17_44262403_C_T	17	44262403	T	0.2114	-0.047	0.0076	6.48E-10	0.2138	0.1124	0.01579	1.09E-12	17:44262403:C:T
17_44262418_G_A	17	44262418	A	0.2114	-0.047	0.0076	6.49E-10	0.2138	0.1124	0.01579	1.09E-12	17:44262418:G:A
17_44262581_A_C	17	44262581	C	0.1711	-0.0507	0.0088	1.04E-08	0.1725	0.1153	0.01804	1.64E-10	17:44262581:A:C
17_44262582_C_A	17	44262582	A	0.1711	-0.0507	0.0088	1.04E-08	0.1725	0.1153	0.01804	1.64E-10	17:44262582:C:A
17_44262758_C_T	17	44262758	T	0.1827	-0.0555	0.0083	2.89E-11	0.1785	0.1124	0.01695	3.29E-11	17:44262758:C:T
17_44263022_C_CAT	17	44263022	CAT	0.2108	-0.0465	0.0077	1.49E-09	0.2135	0.1124	0.01582	1.21E-12	17:44263022:C:CAT
17_44263341_GA_G	17	44263341	G	0.2158	-0.0453	0.0076	2.96E-09	0.216	0.1119	0.01571	1.04E-12	17:44263341:GA:G
17_44263479_T_C	17	44263479	C	0.2114	-0.0471	0.0076	6.21E-10	0.2138	0.1125	0.01579	1.07E-12	17:44263479:T:C
17_44263725_G_T	17	44263725	T	0.1965	-0.0478	0.008	2.52E-09	0.1938	0.113	0.01648	6.98E-12	17:44263725:G:T
17_44263729_C_G	17	44263729	G	0.2114	-0.047	0.0076	6.83E-10	0.2138	0.1124	0.01579	1.09E-12	17:44263729:C:G
17_44263923_T_C	17	44263923	C	0.2011	-0.0522	0.0079	4.10E-11	0.1991	0.1153	0.01609	7.78E-13	17:44263923:T:C
17_44263955_A_G	17	44263955	G	0.2011	-0.0522	0.0079	4.11E-11	0.1991	0.1153	0.01609	7.79E-13	17:44263955:A:G
17_44263965_T_C	17	44263965	C	0.2114	-0.047	0.0076	6.75E-10	0.2138	0.1124	0.01579	1.09E-12	17:44263965:T:C
17_44264045_T_C	17	44264045	C	0.2114	-0.047	0.0076	6.97E-10	0.2138	0.1123	0.01579	1.16E-12	17:44264045:T:C
17_44264269_GT_G	17	44264269	G	0.2361	-0.0452	0.0076	2.61E-09	0.2336	0.1109	0.01561	1.20E-12	17:44264269:GT:G
17_44264717_A_C	17	44264717	C	0.2114	-0.0469	0.0076	7.13E-10	0.2138	0.1124	0.01579	1.10E-12	17:44264717:A:C
17_44264943_T_C	17	44264943	C	0.2113	-0.0468	0.0076	8.20E-10	0.2138	0.1151	0.01579	3.12E-13	17:44264943:T:C
17_44265192_AT_A	17	44265192	A	0.2123	-0.0449	0.0077	4.86E-09	0.2147	0.1124	0.01577	1.03E-12	17:44265192:AT:A
17_44265328_A_G	17	44265328	G	0.2123	-0.0466	0.0076	9.15E-10	0.2141	0.1132	0.01579	7.59E-13	17:44265328:A:G
17_44265477_G_C	17	44265477	C	0.2013	-0.0518	0.0079	5.51E-11	0.1996	0.1139	0.01608	1.40E-12	17:44265477:G:C
17_44265702_A_T	17	44265702	T	0.2111	-0.0466	0.0076	9.03E-10	0.2138	0.1125	0.01579	1.08E-12	17:44265702:A:T
17_44265839_C_T	17	44265839	T	0.4001	-0.0252	0.0063	0.00007292	0.3836	0.07906	0.01343	3.89E-09	rs2532240:44265839:C:T
17_44266022_A_G	17	44266022	G	0.2125	-0.0461	0.0076	1.33E-09	0.2142	0.1128	0.01579	9.09E-13	17:44266022:A:G
17_44266227_T_C	17	44266227	C	0.2114	-0.0467	0.0076	8.93E-10	0.2139	0.1118	0.01579	1.45E-12	rs2532239:44266227:T:C
17_44266290_G_C	17	44266290	C	0.2126	-0.0461	0.0076	1.42E-09	0.215	0.1123	0.01579	1.13E-12	rs2696569:44266290:G:C
17_44266342_T_C	17	44266342	C	0.2114	-0.0467	0.0076	8.81E-10	0.2138	0.1117	0.01579	1.53E-12	rs2696568:44266342:T:C
17_44266531_G_A	17	44266531	A	0.2114	-0.0467	0.0076	8.85E-10	0.2138	0.1117	0.01579	1.51E-12	rs2696566:44266531:G:A

17_44266692_C_A	17	44266692	A	0.1928	-0.0504	0.0081	4.09E-10	0.1877	0.1111	0.0164	1.28E-11	17:44266692:C:A
17_44266972_A_G	17	44266972	G	0.2114	-0.0467	0.0076	8.97E-10	0.2138	0.1118	0.01579	1.46E-12	17:44266972:A:G
17_44266975_G_A	17	44266975	A	0.2017	-0.0516	0.0079	6.84E-11	0.1997	0.114	0.01608	1.36E-12	17:44266975:G:A
17_44267164_C_T	17	44267164	T	0.2121	-0.0466	0.0076	9.54E-10	0.2152	0.1118	0.01579	1.45E-12	17:44267164:C:T
17_44267170_G_T	17	44267170	T	0.2121	-0.0466	0.0076	9.54E-10	0.2152	0.1118	0.01579	1.45E-12	17:44267170:G:T
17_44267227_A_G	17	44267227	G	0.2121	-0.0466	0.0076	9.56E-10	0.2152	0.1118	0.01579	1.44E-12	17:44267227:A:G
17_44267617_A_G	17	44267617	G	0.2137	-0.047	0.0076	7.56E-10	0.2192	0.1094	0.01584	4.82E-12	17:44267617:A:G
17_44267801_A_AT	17	44267801	AT	0.1906	-0.0505	0.0082	7.44E-10	0.1865	0.1119	0.01662	1.68E-11	rs141166507:44267801:A:AT
17_44267863_G_A	17	44267863	A	0.2111	-0.0473	0.0076	5.16E-10	0.2144	0.1127	0.0158	9.60E-13	17:44267863:G:A
17_44267904_T_C	17	44267904	C	0.2124	-0.0462	0.0076	1.27E-09	0.2149	0.1145	0.01579	4.16E-13	17:44267904:T:C
17_44268488_C_T	17	44268488	T	0.2115	-0.0467	0.0076	8.77E-10	0.214	0.112	0.01579	1.32E-12	rs2141298:44268488:C:T
17_44268697_A_C	17	44268697	C	0.193	-0.0503	0.0081	4.35E-10	0.1894	0.1115	0.0164	1.07E-11	17:44268697:A:C
17_44269217_G_C	17	44269217	C	0.1927	-0.0502	0.0081	4.58E-10	0.1893	0.1126	0.01642	7.00E-12	17:44269217:G:C
17_44269421_C_T	17	44269421	T	0.1912	-0.0506	0.0081	4.54E-10	0.188	0.1107	0.01652	2.11E-11	17:44269421:C:T
17_44269442_A_C	17	44269442	C	0.1976	-0.0528	0.008	4.22E-11	0.197	0.1165	0.0163	8.69E-13	17:44269442:A:C
17_44269493_T_C	17	44269493	C	0.1985	-0.0528	0.008	3.77E-11	0.1964	0.1163	0.01624	8.14E-13	17:44269493:T:C
17_44269510_A_G	17	44269510	G	0.193	-0.0502	0.0081	4.47E-10	0.1894	0.1115	0.0164	1.06E-11	17:44269510:A:G
17_44269546_C_T	17	44269546	T	0.212	-0.0468	0.0076	7.87E-10	0.214	0.1121	0.0158	1.28E-12	17:44269546:C:T
17_44269676_T_TAA	17	44269676	TAA	0.2068	-0.0463	0.0078	2.86E-09	0.2061	0.1124	0.016	2.17E-12	17:44269676:T:TAA
17_44269726_G_A	17	44269726	A	0.2011	-0.0517	0.0079	6.46E-11	0.1995	0.1139	0.01608	1.41E-12	rs2696635:44269726:G:A
17_44269836_CAAGAG_C	17	44269836	C	0.1921	-0.0497	0.0081	9.82E-10	0.1889	0.1116	0.01643	1.11E-11	s141752007:44269836:CAAGAG:C
17_44269922_T_C	17	44269922	C	0.1929	-0.0503	0.0081	4.32E-10	0.1894	0.1117	0.0164	9.81E-12	rs62060947:44269922:T:C
17_44269964_T_A	17	44269964	A	0.2113	-0.0465	0.0076	1.06E-09	0.2143	0.1117	0.0158	1.56E-12	rs11079733:44269964:T:A
17_44270059_A_T	17	44270059	T	0.212	-0.0468	0.0076	7.75E-10	0.2144	0.113	0.01579	8.32E-13	rs2696633:44270059:A:T
17_44270153_CAGG_C	17	44270153	C	0.188	-0.0459	0.0082	2.50E-08	0.1836	0.1112	0.01682	3.88E-11	rs143625699:44270153:CAGG:C
17_44270708_AGCGGTGGC	17	44270708	A	0.2	-0.0443	0.0079	1.89E-08	0.2	0.1092	0.01625	1.86E-11	17:44270708:AGCGGTGGCG:A
17_44270809_A_G	17	44270809	G	0.2111	-0.0468	0.0076	8.30E-10	0.2138	0.1124	0.0158	1.14E-12	rs113417378:44270809:A:G
17_44271152_G_A	17	44271152	A	0.2127	-0.0459	0.0076	1.69E-09	0.215	0.1113	0.01581	1.93E-12	17:44271152:G:A
17_44271430_A_G	17	44271430	G	0.211	-0.0469	0.0076	7.65E-10	0.2137	0.1126	0.0158	1.04E-12	17:44271430:A:G
17_44271512_G_C	17	44271512	C	0.1927	-0.0505	0.0081	3.61E-10	0.1893	0.112	0.0164	8.41E-12	17:44271512:G:C
17_44272000_G_A	17	44272000	A	0.209	-0.0482	0.0077	3.35E-10	0.2112	0.1136	0.01587	8.08E-13	17:44272000:G:A
17_44272266_A_G	17	44272266	G	0.2112	-0.0471	0.0076	6.37E-10	0.2138	0.1126	0.0158	1.03E-12	17:44272266:A:G
17_44272552_C_T	17	44272552	T	0.2111	-0.0467	0.0076	9.04E-10	0.2149	0.1127	0.0158	9.59E-13	17:44272552:C:T
17_44272679_G_C	17	44272679	C	0.2118	-0.046	0.0076	1.56E-09	0.2144	0.1124	0.01579	1.06E-12	17:44272679:G:C
17_44272928_C_A	17	44272928	A	0.2109	-0.0466	0.0076	9.76E-10	0.2141	0.112	0.0158	1.33E-12	17:44272928:C:A
17_44273218_C_T	17	44273218	T	0.211	-0.0468	0.0076	7.96E-10	0.2142	0.113	0.0158	8.57E-13	rs2532233:44273218:C:T
17_44273264_G_A	17	44273264	A	0.2109	-0.0469	0.0076	7.45E-10	0.2138	0.1128	0.0158	9.52E-13	17:44273264:G:A
17_44273398_C_T	17	44273398	T	0.1921	-0.0508	0.0081	3.20E-10	0.1883	0.1132	0.01642	5.32E-12	rs62060952:44273398:C:T
17_44273448_C_A	17	44273448	A	0.2105	-0.0471	0.0076	6.56E-10	0.2135	0.1124	0.01581	1.17E-12	17:44273448:C:A
17_44273653_T_G	17	44273653	G	0.1898	-0.0517	0.0081	2.22E-10	0.1841	0.1125	0.01653	1.01E-11	17:44273653:T:G
17_44273664_A_G	17	44273664	G	0.1898	-0.0517	0.0081	2.22E-10	0.1841	0.1125	0.01653	1.01E-11	17:44273664:A:G
17_44273889_C_T	17	44273889	T	0.1923	-0.0492	0.0081	1.07E-09	0.1882	0.1122	0.01638	7.41E-12	17:44273889:C:T
17_44273919_A_G	17	44273919	G	0.1908	-0.0511	0.0081	2.80E-10	0.1864	0.1121	0.0165	1.10E-11	17:44273919:A:G
17_44274451_G_C	17	44274451	C	0.2008	-0.052	0.0079	4.65E-11	0.1992	0.1143	0.01608	1.17E-12	17:44274451:G:C
17_44274560_T_C	17	44274560	C	0.211	-0.0468	0.0076	7.90E-10	0.2167	0.1123	0.0158	1.20E-12	17:44274560:T:C
17_44274766_T_C	17	44274766	C	0.2109	-0.0468	0.0076	8.44E-10	0.2137	0.113	0.0158	8.58E-13	17:44274766:T:C
17_44274838_G_A	17	44274838	A	0.2	-0.0524	0.0079	3.83E-11	0.1978	0.1151	0.01612	9.57E-13	17:44274838:G:A
17_44274933_C_G	17	44274933	G	0.1922	-0.0507	0.0081	3.30E-10	0.1886	0.1129	0.01641	6.06E-12	17:44274933:C:G
17_44274985_C_A	17	44274985	A	0.2108	-0.0469	0.0076	7.53E-10	0.2134	0.1126	0.0158	1.02E-12	17:44274985:C:A
17_44275035_T_G	17	44275035	G	0.2108	-0.0469	0.0076	7.52E-10	0.2134	0.1126	0.0158	1.02E-12	17:44275035:T:G
17_44275172_A_ACT	17	44275172	ACT	0.2113	-0.0458	0.0077	2.44E-09	0.214	0.112	0.0158	1.35E-12	17:44275172:A:ACT
17_44275230_G_T	17	44275230	T	0.1991	-0.0518	0.008	7.40E-11	0.1977	0.1141	0.01617	1.74E-12	17:44275230:G:T
17_44275619_A_G	17	44275619	G	0.2136	-0.0462	0.0076	1.13E-09	0.2159	0.1096	0.01578	3.71E-12	17:44275619:A:G
17_44275649_CTAT_C	17	44275649	C	0.2113	-0.0457	0.0077	2.63E-09	0.214	0.1125	0.0158	1.07E-12	17:44275649:CTAT:C
17_44276013_G_A	17	44276013	A	0.2108	-0.0469	0.0076	7.30E-10	0.2134	0.1126	0.0158	1.03E-12	17:44276013:G:A

17_44276330_T_C	17	44276330	C	0.2112	-0.0467	0.0076	8.43E-10	0.214	0.1126	0.0158	1.04E-12	17:44276330:T:C
17_44276431_T_TAGAA	17	44276431	TAGAA	0.2109	-0.046	0.0077	2.21E-09	0.2134	0.1126	0.0158	1.03E-12	17:44276431:T:TAGAA
17_44276479_T_G	17	44276479	G	0.1919	-0.0509	0.0081	2.86E-10	0.1884	0.1125	0.01643	7.52E-12	17:44276479:T:G
17_44276578_T_C	17	44276578	C	0.2122	-0.0476	0.0076	3.94E-10	0.2145	0.1123	0.01575	1.02E-12	17:44276578:T:C
17_44276618_A_G	17	44276618	G	0.2122	-0.0476	0.0076	3.91E-10	0.2145	0.1123	0.01575	1.02E-12	17:44276618:A:G
17_44276821_G_A	17	44276821	A	0.2133	-0.0464	0.0076	1.01E-09	0.2154	0.1092	0.01577	4.48E-12	17:44276821:G:A
17_44277168_ATTTAC_A	17	44277168	A	0.1903	-0.0495	0.0082	1.66E-09	0.1869	0.1087	0.01657	5.41E-11	s141184610:44277168:ATTTAC:A
17_44277265_A_C	17	44277265	C	0.2126	-0.0465	0.0076	1.04E-09	0.214	0.1135	0.01579	6.45E-13	rs2532229:44277265:A:C
17_44277404_T_TACACACA	17	44277404	TACACACACACAC	0.1434	-0.0483	0.0101	1.59E-06	0.142	0.123	0.0209	4.01E-09	17:44277404:T:TACACACACACAC
17_44277476_C_CTTTAG	17	44277476	CTTTAG	0.2159	-0.0451	0.0076	3.21E-09	0.2167	0.1132	0.01568	5.17E-13	s147317628:44277476:C:CTTTAG
17_44277691_T_C	17	44277691	C	0.2112	-0.0473	0.0076	5.34E-10	0.2137	0.1127	0.01579	9.47E-13	17:44277691:T:C
17_44277707_A_G	17	44277707	G	0.1916	-0.0513	0.0081	2.22E-10	0.1871	0.114	0.01646	4.30E-12	17:44277707:A:G
17_44277818_A_G	17	44277818	G	0.2112	-0.0471	0.0076	6.05E-10	0.2147	0.1125	0.0158	1.09E-12	17:44277818:A:G
17_44277825_C_T	17	44277825	T	0.2006	-0.0521	0.0079	4.36E-11	0.1989	0.1144	0.01608	1.15E-12	17:44277825:C:T
17_44277867_G_A	17	44277867	A	0.2114	-0.0469	0.0076	7.49E-10	0.2142	0.1124	0.01579	1.10E-12	17:44277867:G:A
17_44277923_G_A	17	44277923	A	0.2113	-0.0469	0.0076	7.63E-10	0.2142	0.1125	0.01579	1.03E-12	17:44277923:G:A
17_44278110_AAT_A	17	44278110	A	0.2411	-0.0378	0.0076	7.15E-07	0.2435	0.1091	0.01572	3.84E-12	rs66498281:44278110:AAT:A
17_44278661_G_A	17	44278661	A	0.2006	-0.0522	0.0079	4.23E-11	0.1989	0.1144	0.01608	1.15E-12	17:44278661:G:A
17_44278742_A_G	17	44278742	G	0.2108	-0.0472	0.0076	5.95E-10	0.2134	0.1128	0.0158	9.40E-13	rs17664048:44278742:A:G
17_44279101_A_G	17	44279101	G	0.2108	-0.0472	0.0076	5.90E-10	0.2134	0.1128	0.0158	9.35E-13	rs1918786:44279101:A:G
17_44279252_A_G	17	44279252	G	0.2108	-0.0472	0.0076	5.88E-10	0.2134	0.1128	0.0158	9.33E-13	rs1918787:44279252:A:G
17_44279371_TCAAA_T	17	44279371	T	0.2109	-0.0462	0.0077	1.81E-09	0.2134	0.1128	0.0158	9.32E-13	17:44279371:TCAAA:T
17_44279557_TA_T	17	44279557	T	0.2118	-0.0462	0.0077	1.74E-09	0.2145	0.1121	0.0158	1.27E-12	17:44279557:TA:T
17_44279760_G_A	17	44279760	A	0.2108	-0.0472	0.0076	5.91E-10	0.2134	0.1128	0.0158	9.43E-13	17:44279760:G:A
17_44279803_T_G	17	44279803	G	0.2001	-0.0525	0.0079	3.58E-11	0.1983	0.114	0.01612	1.52E-12	17:44279803:T:G
17_44280188_T_A	17	44280188	A	0.2116	-0.0475	0.0076	4.37E-10	0.2136	0.1143	0.01579	4.61E-13	17:44280188:T:A
17_44280523_A_G	17	44280523	G	0.2108	-0.0472	0.0076	5.75E-10	0.2134	0.1128	0.0158	9.24E-13	17:44280523:A:G
17_44280598_TC_T	17	44280598	T	0.1922	-0.0499	0.0081	8.63E-10	0.1882	0.1133	0.01643	5.26E-12	rs139293294:44280598:TC:T
17_44280697_T_C	17	44280697	C	0.2009	-0.0521	0.0079	4.54E-11	0.1993	0.1154	0.0161	7.74E-13	17:44280697:T:C
17_44280902_G_C	17	44280902	C	0.2108	-0.0472	0.0076	5.77E-10	0.2134	0.1128	0.0158	9.26E-13	17:44280902:G:C
17_44281159_G_GA	17	44281159	GA	0.1903	-0.05	0.0082	1.06E-09	0.1852	0.1148	0.01654	3.84E-12	rs148606226:44281159:G:GA
17_44281308_G_A	17	44281308	A	0.2007	-0.0524	0.0079	3.40E-11	0.199	0.1144	0.01608	1.12E-12	17:44281308:G:A
17_44281452_A_G	17	44281452	G	0.2121	-0.0475	0.0076	4.48E-10	0.2145	0.1126	0.01581	1.06E-12	17:44281452:A:G
17_44281588_T_C	17	44281588	C	0.2108	-0.0472	0.0076	5.81E-10	0.2134	0.1128	0.0158	9.29E-13	17:44281588:T:C
17_44281633_G_A	17	44281633	A	0.2006	-0.0522	0.0079	4.01E-11	0.1989	0.1144	0.01608	1.16E-12	17:44281633:G:A
17_44281722_T_C	17	44281722	C	0.2108	-0.0472	0.0076	5.82E-10	0.2134	0.1128	0.0158	9.30E-13	17:44281722:T:C
17_44281821_A_C	17	44281821	C	0.1922	-0.0509	0.0081	2.84E-10	0.1886	0.113	0.01641	5.92E-12	17:44281821:A:C
17_44281964_T_C	17	44281964	C	0.192	-0.0505	0.0081	3.96E-10	0.1884	0.1132	0.01642	5.41E-12	17:44281964:T:C
17_44282007_T_C	17	44282007	C	0.2108	-0.0472	0.0076	5.83E-10	0.2134	0.1128	0.0158	9.32E-13	17:44282007:T:C
17_44282472_T_C	17	44282472	C	0.1995	-0.0521	0.0079	5.22E-11	0.1983	0.1164	0.01614	5.52E-13	17:44282472:T:C
17_44282519_T_TA	17	44282519	TA	0.1921	-0.05	0.0081	8.06E-10	0.1884	0.1127	0.01643	7.01E-12	rs139098505:44282519:T:TA
17_44282744_G_C	17	44282744	C	0.2108	-0.0472	0.0076	5.88E-10	0.2134	0.1128	0.0158	9.37E-13	17:44282744:G:C
17_44282892_T_C	17	44282892	C	0.2117	-0.0475	0.0076	4.45E-10	0.2145	0.112	0.01579	1.33E-12	17:44282892:T:C
17_44282979_G_A	17	44282979	A	0.1925	-0.0506	0.0081	3.33E-10	0.189	0.1119	0.0164	8.79E-12	17:44282979:G:A
17_44283022_A_G	17	44283022	G	0.2136	-0.0455	0.0076	2.31E-09	0.2172	0.1124	0.01581	1.13E-12	17:44283022:A:G
17_44283139_C_A	17	44283139	A	0.2115	-0.0468	0.0076	8.24E-10	0.2151	0.112	0.0158	1.35E-12	17:44283139:C:A
17_44283479_T_C	17	44283479	C	0.2121	-0.0461	0.0076	1.40E-09	0.2158	0.1104	0.0158	2.78E-12	17:44283479:T:C
17_44283571_C_T	17	44283571	T	0.2005	-0.0524	0.0079	3.47E-11	0.1989	0.1145	0.01609	1.11E-12	17:44283571:C:T
17_44283761_A_T	17	44283761	T	0.2119	-0.0461	0.0076	1.43E-09	0.2141	0.1131	0.0158	7.95E-13	17:44283761:A:T
17_44283858_G_A	17	44283858	A	0.1857	-0.0589	0.0083	1.22E-12	0.1861	0.1154	0.01685	7.57E-12	17:44283858:G:A
17_44284057_C_T	17	44284057	T	0.2132	-0.0469	0.0076	6.92E-10	0.2162	0.111	0.01578	1.98E-12	17:44284057:C:T
17_44284420_C_T	17	44284420	T	0.2142	-0.0468	0.0076	8.79E-10	0.2165	0.112	0.01582	1.46E-12	17:44284420:C:T
17_44284542_G_A	17	44284542	A	0.2123	-0.0474	0.0076	4.68E-10	0.2155	0.1115	0.0158	1.71E-12	17:44284542:G:A
17_44284641_T_G	17	44284641	G	0.2117	-0.0466	0.0076	1.02E-09	0.2135	0.1109	0.01581	2.32E-12	rs2668668:44284641:T:G
17_44284734_G_C	17	44284734	C	0.2144	-0.0467	0.0076	8.80E-10	0.217	0.1108	0.0158	2.32E-12	17:44284734:G:C

17_44284877_AAAAAAAAA	17	44284877	A	0.2202	-0.0431	0.0077	1.93E-08	0.2277	0.1121	0.0158	1.29E-12	3412:44284877:AAAAAAAAAAAAAAG:A
17_44284962_A_AG	17	44284962	AG	0.2102	-0.0462	0.0077	1.97E-09	0.2118	0.1126	0.01583	1.15E-12	rs34221112:44284962:A:AG
17_44285142_G_C	17	44285142	C	0.2178	-0.046	0.0076	1.33E-09	0.2215	0.1052	0.01574	2.28E-11	17:44285142:G:C
17_44285436_C_T	17	44285436	T	0.1925	-0.0506	0.0081	3.50E-10	0.189	0.1119	0.0164	8.69E-12	17:44285436:C:T
17_44285460_G_GA	17	44285460	GA	0.2163	-0.046	0.0077	2.15E-09	0.2187	0.1127	0.01581	1.02E-12	17:44285460:G:GA
17_44285467_A_G	17	44285467	G	0.2168	-0.0473	0.0076	5.62E-10	0.2194	0.1117	0.01581	1.60E-12	17:44285467:A:G
17_44285475_C_CA	17	44285475	CA	0.2009	-0.0439	0.0081	6.62E-08	0.1958	0.1125	0.01667	1.53E-11	17:44285475:C:CA
17_44285531_G_A	17	44285531	A	0.2108	-0.0471	0.0076	6.14E-10	0.2136	0.1127	0.0158	9.88E-13	17:44285531:G:A
17_44285683_T_C	17	44285683	C	0.1925	-0.0506	0.0081	3.46E-10	0.189	0.1119	0.0164	8.69E-12	17:44285683:T:C
17_44285952_T_C	17	44285952	C	0.2121	-0.0458	0.0076	1.84E-09	0.2157	0.1118	0.01579	1.48E-12	rs2532423:44285952:T:C
17_44285982_CAA_C	17	44285982	C	0.2185	-0.0433	0.0077	1.78E-08	0.2226	0.1096	0.01582	4.27E-12	rs149187563:44285982:CAA:C
17_44286089_G_A	17	44286089	A	0.2131	-0.0466	0.0076	9.38E-10	0.2168	0.1119	0.0158	1.40E-12	17:44286089:G:A
17_44286128_A_G	17	44286128	G	0.2123	-0.0463	0.0076	1.24E-09	0.2161	0.1116	0.0158	1.61E-12	17:44286128:A:G
17_44286198_G_A	17	44286198	A	0.2142	-0.0467	0.0076	8.67E-10	0.2195	0.1093	0.01575	3.88E-12	17:44286198:G:A
17_44286218_CA_C	17	44286218	C	0.2627	-0.0394	0.0078	4.99E-07	0.2591	0.1018	0.01611	2.63E-10	17:44286218:CA:C
17_44286972_A_C	17	44286972	C	0.2002	-0.0525	0.0079	3.39E-11	0.1989	0.1145	0.01609	1.12E-12	17:44286972:A:C
17_44287006_T_G	17	44287006	G	0.1903	-0.0519	0.0081	1.56E-10	0.1874	0.1132	0.01651	7.21E-12	17:44287006:T:G
17_44287310_A_G	17	44287310	G	0.211	-0.0473	0.0076	5.27E-10	0.2143	0.1125	0.0158	1.05E-12	17:44287310:A:G
17_44287373_G_C	17	44287373	C	0.1919	-0.0507	0.0081	3.50E-10	0.1884	0.1131	0.01645	6.20E-12	17:44287373:G:C
17_44287390_A_G	17	44287390	G	0.2012	-0.0522	0.0079	4.10E-11	0.1995	0.1146	0.01608	9.99E-13	17:44287390:A:G
17_44287709_A_AG	17	44287709	AG	0.1919	-0.0497	0.0081	1.01E-09	0.1882	0.1128	0.01647	7.36E-12	rs140712254:44287709:A:AG
17_44288114_TA_T	17	44288114	T	0.2111	-0.046	0.0077	2.14E-09	0.2139	0.1129	0.0158	8.76E-13	17:44288114:TA:T
17_44288156_T_C	17	44288156	C	0.2118	-0.0465	0.0076	1.01E-09	0.2149	0.1134	0.0158	7.16E-13	rs2668653:44288156:T:C
17_44288281_C_T	17	44288281	T	0.1927	-0.0503	0.0081	4.23E-10	0.1889	0.1103	0.01637	1.56E-11	rs2532419:44288281:C:T
17_44288284_G_A	17	44288284	A	0.1996	-0.053	0.008	2.57E-11	0.197	0.1173	0.01617	4.02E-13	rs2732628:44288284:G:A
17_44288579_T_C	17	44288579	C	0.211	-0.0469	0.0076	7.28E-10	0.2139	0.113	0.0158	8.53E-13	rs2532418:44288579:T:C
17_44288640_A_G	17	44288640	G	0.2111	-0.0467	0.0076	8.57E-10	0.2142	0.1129	0.0158	8.94E-13	rs2668645:44288640:A:G
17_44288672_G_A	17	44288672	A	0.2111	-0.0467	0.0076	8.57E-10	0.2142	0.1129	0.0158	8.98E-13	rs34898647:44288672:G:A
17_44288702_G_T	17	44288702	T	0.2007	-0.0524	0.0079	3.51E-11	0.1993	0.1142	0.01608	1.24E-12	rs2696445:44288702:G:T
17_44289101_A_G	17	44289101	G	0.2112	-0.0466	0.0076	9.51E-10	0.2148	0.1123	0.0158	1.15E-12	rs2732629:44289101:A:G
17_44289150_A_C	17	44289150	C	0.2116	-0.0462	0.0076	1.30E-09	0.2151	0.113	0.0158	8.63E-13	rs2732630:44289150:A:C
17_44289220_C_T	17	44289220	T	0.2116	-0.0462	0.0076	1.33E-09	0.2151	0.1132	0.0158	7.85E-13	rs2532417:44289220:C:T
17_44289232_G_T	17	44289232	T	0.2123	-0.0467	0.0076	8.02E-10	0.2164	0.1116	0.01579	1.59E-12	rs2732631:44289232:G:T
17_44289291_A_C	17	44289291	C	0.2129	-0.0467	0.0076	7.95E-10	0.216	0.1133	0.01578	7.03E-13	rs2532416:44289291:A:C
17_44289628_A_C	17	44289628	C	0.2114	-0.0476	0.0076	4.09E-10	0.2148	0.1122	0.0158	1.24E-12	rs2668670:44289628:A:C
17_44289832_A_G	17	44289832	G	0.3978	-0.0256	0.0064	0.00005795	0.3805	0.07941	0.01344	3.50E-09	rs2696466:44289832:A:G
17_44290047_G_A	17	44290047	A	0.2131	-0.0472	0.0076	5.74E-10	0.2153	0.1133	0.01579	7.20E-13	rs2668665:44290047:G:A
17_44290759_T_C	17	44290759	C	0.2107	-0.0472	0.0076	5.94E-10	0.2136	0.1123	0.0158	1.15E-12	rs2668662:44290759:T:C
17_44290849_T_A	17	44290849	A	0.2107	-0.0472	0.0076	5.93E-10	0.2136	0.1123	0.0158	1.15E-12	rs76475191:44290849:T:A
17_44290850_T_A	17	44290850	A	0.2077	-0.0488	0.0077	2.43E-10	0.2092	0.1127	0.01589	1.34E-12	rs78826239:44290850:T:A
17_44290910_A_G	17	44290910	G	0.2107	-0.0471	0.0076	6.11E-10	0.2136	0.1124	0.0158	1.13E-12	rs79861768:44290910:A:G
17_44291365_C_T	17	44291365	T	0.2108	-0.047	0.0076	6.48E-10	0.2137	0.112	0.0158	1.32E-12	rs2732606:44291365:C:T
17_44291381_A_G	17	44291381	G	0.2109	-0.0472	0.0076	5.77E-10	0.2138	0.1122	0.0158	1.23E-12	rs2732605:44291381:A:G
17_44291479_G_A	17	44291479	A	0.2109	-0.0469	0.0076	7.09E-10	0.2137	0.1119	0.01579	1.37E-12	rs2732601:44291479:G:A
17_44291734_T_A	17	44291734	A	0.1922	-0.0509	0.0081	2.74E-10	0.1889	0.1116	0.01641	1.02E-11	rs2957296:44291734:T:A
17_44291820_A_G	17	44291820	G	0.2107	-0.0472	0.0076	5.51E-10	0.2136	0.1123	0.0158	1.19E-12	rs2696610:44291820:A:G
17_44292021_C_CAAA	17	44292021	CAAA	0.2101	-0.0461	0.0077	2.31E-09	0.2124	0.1125	0.01586	1.31E-12	17:44292021:C:CAAA
17_44292126_T_C	17	44292126	C	0.2108	-0.0475	0.0076	4.53E-10	0.2138	0.113	0.0158	8.82E-13	rs2668695:44292126:T:C
17_44292319_T_C	17	44292319	C	0.2108	-0.0471	0.0076	6.37E-10	0.2139	0.1121	0.0158	1.31E-12	rs2668694:44292319:T:C
17_44293020_G_A	17	44293020	A	0.2111	-0.0474	0.0076	4.76E-10	0.2137	0.1136	0.0158	6.30E-13	rs2668692:44293020:G:A
17_44293205_A_G	17	44293205	G	0.2161	-0.0463	0.0076	9.50E-10	0.2166	0.1127	0.01569	6.92E-13	rs2696609:44293205:A:G
17_44293546_C_T	17	44293546	T	0.1916	-0.0511	0.0081	2.93E-10	0.187	0.1132	0.01649	6.82E-12	rs2668691:44293546:C:T
17_44293671_A_G	17	44293671	G	0.2006	-0.0521	0.0079	5.17E-11	0.199	0.1134	0.01613	2.06E-12	rs2696608:44293671:A:G
17_44293963_T_A	17	44293963	A	0.2115	-0.0475	0.0076	4.49E-10	0.2137	0.1127	0.0158	9.86E-13	rs2458204:44293963:T:A
17_44294105_C_T	17	44294105	T	0.2019	-0.0526	0.0079	3.01E-11	0.1997	0.1145	0.0161	1.13E-12	rs2532414:44294105:C:T

17_44294786_A_G	17	44294786	G	0.211	-0.0473	0.0076	5.21E-10	0.2135	0.1122	0.0158	1.26E-12	rs2266497:44294786:A:G
17_44294983_C_A	17	44294983	A	0.211	-0.0473	0.0076	5.19E-10	0.2135	0.1122	0.0158	1.27E-12	rs2532413:44294983:C:A
17_44295157_A_G	17	44295157	G	0.2111	-0.0473	0.0076	5.21E-10	0.2135	0.1122	0.0158	1.23E-12	17:44295157:A:G
17_44295695_A_G	17	44295695	G	0.201	-0.0527	0.0079	2.77E-11	0.1991	0.1137	0.01609	1.56E-12	rs2532412:44295695:A:G
17_44295795_G_A	17	44295795	A	0.201	-0.0527	0.0079	2.77E-11	0.1991	0.1137	0.01609	1.57E-12	rs2942186:44295795:G:A
17_44296097_C_T	17	44296097	T	0.2001	-0.0523	0.0079	4.30E-11	0.1981	0.1136	0.01613	1.95E-12	rs113146341:44296097:C:T
17_44296179_G_C	17	44296179	C	0.2009	-0.0528	0.0079	2.65E-11	0.1989	0.1135	0.01609	1.71E-12	rs77294312:44296179:G:C
17_44296224_C_T	17	44296224	T	0.1912	-0.0494	0.0081	1.03E-09	0.1879	0.1111	0.01649	1.63E-11	rs2429449:44296224:C:T
17_44296230_T_A	17	44296230	A	0.2113	-0.0472	0.0076	5.92E-10	0.2139	0.1121	0.0158	1.26E-12	rs78358711:44296230:T:A
17_44296251_T_C	17	44296251	C	0.2113	-0.0474	0.0076	4.86E-10	0.2136	0.1116	0.0158	1.63E-12	17:44296251:T:C
17_44296355_G_A	17	44296355	A	0.2007	-0.0529	0.0079	2.33E-11	0.1989	0.1137	0.01611	1.72E-12	rs2942187:44296355:G:A
17_44296522_T_C	17	44296522	C	0.211	-0.0476	0.0076	4.39E-10	0.2133	0.1124	0.01581	1.19E-12	rs111314258:44296522:T:C
17_44296523_G_A	17	44296523	A	0.2109	-0.0476	0.0076	4.29E-10	0.2131	0.1124	0.01582	1.20E-12	rs144416125:44296523:G:A
17_44296720_AT_A	17	44296720	A	0.0918	-0.0662	0.0133	6.79E-07	0.09007	0.1559	0.02722	1.03E-08	17:44296720:AT:A
17_44296845_A_C	17	44296845	C	0.2158	-0.0453	0.0076	2.58E-09	0.2168	0.1135	0.01576	6.00E-13	17:44296845:A:C
17_44296846_G_A	17	44296846	A	0.2158	-0.0453	0.0076	2.58E-09	0.2168	0.1135	0.01576	6.00E-13	17:44296846:G:A
17_44297148_G_A	17	44297148	A	0.2151	-0.0461	0.0076	1.43E-09	0.2175	0.1151	0.01578	3.05E-13	17:44297148:G:A
17_44297459_G_A	17	44297459	A	0.1805	-0.0505	0.0086	4.44E-09	0.1741	0.1135	0.0176	1.13E-10	rs75543806:44297459:G:A
17_44298102_G_A	17	44298102	A	0.2114	-0.0477	0.0076	4.01E-10	0.2156	0.1116	0.0158	1.62E-12	17:44298102:G:A
17_44298178_A_G	17	44298178	G	0.2111	-0.0474	0.0076	4.95E-10	0.2135	0.1118	0.0158	1.46E-12	17:44298178:A:G
17_44298209_T_C	17	44298209	C	0.2111	-0.0474	0.0076	5.12E-10	0.2135	0.1118	0.0158	1.47E-12	17:44298209:T:C
17_44298279_C_T	17	44298279	T	0.2116	-0.0473	0.0076	5.37E-10	0.2139	0.1117	0.0158	1.53E-12	17:44298279:C:T
17_44298631_A_G	17	44298631	G	0.1775	-0.0534	0.0086	4.74E-10	0.1801	0.1085	0.01781	1.10E-09	rs117662214:44298631:A:G
17_44299864_AC_A	17	44299864	AC	0.2643	-0.0347	0.0072	1.26E-06	0.2607	0.0958	0.01479	9.47E-11	rs201443147:44299864:AC:A
17_44300067_A_G	17	44300067	G	0.2013	-0.0526	0.0079	3.14E-11	0.1987	0.114	0.0161	1.46E-12	rs147642589:44300067:A:G
17_44301546_T_C	17	44301546	C	0.2112	-0.0474	0.0076	5.05E-10	0.2135	0.1119	0.0158	1.42E-12	rs145848989:44301546:T:C
17_44301840_T_C	17	44301840	C	0.2133	-0.0474	0.0078	1.12E-09	0.2142	0.1107	0.01615	7.21E-12	rs142920272:44301840:T:C
17_44302752_G_A	17	44302752	A	0.2013	-0.0525	0.0079	3.22E-11	0.1986	0.1141	0.0161	1.40E-12	17:44302752:G:A
17_44302881_C_T	17	44302881	T	0.2125	-0.0476	0.0076	4.31E-10	0.2144	0.1123	0.01581	1.21E-12	17:44302881:C:T
17_44302904_T_C	17	44302904	C	0.2013	-0.0526	0.0079	3.04E-11	0.1987	0.114	0.0161	1.42E-12	17:44302904:T:C
17_44303525_G_A	17	44303525	A	0.2109	-0.0473	0.0076	5.84E-10	0.2131	0.112	0.01581	1.42E-12	rs368557302:44303525:G:A
17_44303564_C_T	17	44303564	T	0.1987	-0.0449	0.0079	1.44E-08	0.2	0.1099	0.01646	2.37E-11	17:44303564:C:T
17_44303606_AG_A	17	44303606	A	0.2112	-0.0464	0.0077	1.61E-09	0.2132	0.1119	0.0158	1.41E-12	rs139203747:44303606:AG:A
17_44303668_G_T	17	44303668	T	0.2112	-0.0474	0.0076	5.13E-10	0.2132	0.1119	0.0158	1.44E-12	rs371411506:44303668:G:T
17_44304130_C_G	17	44304130	G	0.2085	-0.0467	0.0077	1.31E-09	0.2092	0.1127	0.01593	1.51E-12	17:44304130:C:G
17_44304203_T_C	17	44304203	C	0.2111	-0.0473	0.0076	5.42E-10	0.2132	0.1119	0.0158	1.42E-12	17:44304203:T:C
17_44304298_T_A	17	44304298	A	0.2111	-0.0473	0.0076	5.42E-10	0.2132	0.1119	0.0158	1.42E-12	17:44304298:T:A
17_44304490_T_C	17	44304490	C	0.2113	-0.0476	0.0076	4.43E-10	0.2133	0.1114	0.0158	1.81E-12	17:44304490:T:C
17_44304740_A_T	17	44304740	T	0.2113	-0.0476	0.0076	4.41E-10	0.2133	0.1114	0.0158	1.81E-12	17:44304740:A:T
17_44304884_C_T	17	44304884	T	0.2407	-0.0478	0.0076	3.51E-10	0.2425	0.1079	0.0158	8.37E-12	17:44304884:C:T
17_44304910_G_C	17	44304910	C	0.2114	-0.0473	0.0076	5.52E-10	0.2133	0.1105	0.0158	2.67E-12	rs148992948:44304910:G:C
17_44305026_G_A	17	44305026	A	0.2131	-0.048	0.0076	3.19E-10	0.2161	0.1091	0.01577	4.47E-12	17:44305026:G:A
17_44305199_T_C	17	44305199	C	0.2119	-0.0479	0.0076	3.50E-10	0.2134	0.1113	0.01582	1.97E-12	17:44305199:T:C
17_44305252_G_A	17	44305252	A	0.2113	-0.0476	0.0076	4.41E-10	0.2133	0.1114	0.0158	1.81E-12	17:44305252:G:A
17_44305689_A_G	17	44305689	G	0.1824	-0.0501	0.0084	2.58E-09	0.1865	0.1191	0.01743	8.30E-12	17:44305689:A:G
17_44305817_T_C	17	44305817	C	0.1809	-0.0504	0.0085	2.64E-09	0.185	0.1178	0.01756	1.93E-11	rs140256385:44305817:T:C
17_44306628_G_GAA	17	44306628	GAA	0.1359	-0.0584	0.0105	2.87E-08	0.1296	0.133	0.02162	7.77E-10	rs199726619:44306628:G:GAA
17_44307193_C_T	17	44307193	T	0.1969	-0.0493	0.008	7.03E-10	0.1981	0.112	0.01654	1.27E-11	rs2532395:44307193:C:T
17_44308053_A_G	17	44308053	G	0.1573	-0.0519	0.0094	3.32E-08	0.1582	0.1336	0.01954	8.01E-12	rs138985755:44308053:A:G
17_44309250_T_TA	17	44309250	TA	0.1949	-0.046	0.0081	1.40E-08	0.1897	0.113	0.01653	8.17E-12	rs199632045:44309250:T:TA
17_44309255_C_A	17	44309255	A	0.1946	-0.0469	0.0081	5.66E-09	0.1897	0.113	0.01653	8.18E-12	17:44309255:C:A
17_44309856_G_A	17	44309856	A	0.2111	-0.0479	0.0076	3.65E-10	0.2129	0.1108	0.01583	2.58E-12	rs146200535:44309856:G:A
17_44310101_A_G	17	44310101	G	0.2145	-0.0486	0.0076	1.98E-10	0.2157	0.1101	0.01581	3.33E-12	17:44310101:A:G
17_44310164_T_C	17	44310164	C	0.2111	-0.0478	0.0076	3.76E-10	0.2129	0.1108	0.01583	2.56E-12	17:44310164:T:C
17_44310234_T_C	17	44310234	C	0.2111	-0.0478	0.0076	3.71E-10	0.2128	0.1108	0.01583	2.57E-12	17:44310234:T:C

17_44310961_A_AT	17	44310961	AT	0.2084	-0.0483	0.0079	1.04E-09	0.2046	0.1113	0.01612	5.04E-12	17:44310961:A:AT
17_44311099_G_A	17	44311099	A	0.2037	-0.0462	0.0078	3.43E-09	0.2045	0.1145	0.01617	1.45E-12	17:44311099:G:A
17_44311107_G_C	17	44311107	C	0.2037	-0.0462	0.0078	3.43E-09	0.2045	0.1145	0.01617	1.45E-12	17:44311107:G:C
17_44311200_T_C	17	44311200	C	0.1971	-0.0486	0.008	1.17E-09	0.1988	0.11	0.01651	2.75E-11	rs373392968:44311200:T:C
17_44311529_G_C	17	44311529	C	0.1906	-0.0509	0.0081	3.67E-10	0.1858	0.1089	0.01655	4.77E-11	17:44311529:G:C
17_44312911_G_T	17	44312911	T	0.2009	-0.0525	0.0079	3.57E-11	0.1974	0.1134	0.01611	1.90E-12	17:44312911:G:T
17_44313224_A_G	17	44313224	G	0.1912	-0.0509	0.0081	3.57E-10	0.1876	0.1127	0.0165	8.47E-12	rs148033495:44313224:A:G
17_44313522_G_T	17	44313522	T	0.2069	-0.0475	0.0077	7.94E-10	0.2054	0.1129	0.01596	1.54E-12	rs118064774:44313522:G:T
17_44313757_G_A	17	44313757	A	0.2112	-0.0475	0.0076	4.91E-10	0.2132	0.1119	0.0158	1.44E-12	17:44313757:G:A
17_44313950_C_A	17	44313950	A	0.2112	-0.0475	0.0076	4.92E-10	0.2132	0.1119	0.0158	1.44E-12	17:44313950:C:A
17_44314066_A_G	17	44314066	G	0.2112	-0.0475	0.0076	4.91E-10	0.2132	0.1119	0.0158	1.44E-12	17:44314066:A:G
17_44314148_T_A	17	44314148	A	0.1927	-0.0511	0.0081	2.36E-10	0.1886	0.1104	0.01641	1.76E-11	rs111535660:44314148:T:A
17_44314179_G_A	17	44314179	A	0.2111	-0.0475	0.0076	5.03E-10	0.2132	0.1114	0.01581	1.81E-12	rs112493812:44314179:G:A
17_44314217_A_G	17	44314217	G	0.2107	-0.047	0.0076	7.31E-10	0.2114	0.1119	0.01582	1.51E-12	rs113343439:44314217:A:G
17_44314261_C_T	17	44314261	T	0.2107	-0.047	0.0076	7.84E-10	0.2114	0.1119	0.01582	1.54E-12	rs113138968:44314261:C:T
17_44314342_T_C	17	44314342	C	0.2106	-0.047	0.0076	7.66E-10	0.2113	0.1117	0.01582	1.64E-12	17:44314342:T:C
17_44315803_A_C	17	44315803	C	0.2033	-0.049	0.0078	4.10E-10	0.2061	0.11	0.01616	9.96E-12	rs2696673:44315803:A:C
17_44315946_TTA_T	17	44315946	T	0.1822	-0.049	0.0085	6.98E-09	0.1786	0.1142	0.01705	2.11E-11	rs149148270:44315946:TTA:T
17_44315987_G_A	17	44315987	A	0.1822	-0.0503	0.0084	2.25E-09	0.1788	0.1143	0.01703	1.95E-11	17:44315987:G:A
17_44316076_G_T	17	44316076	T	0.2112	-0.0474	0.0076	5.14E-10	0.2133	0.1116	0.0158	1.63E-12	rs55653937:44316076:G:T
17_44316280_T_C	17	44316280	C	0.2112	-0.0474	0.0076	5.16E-10	0.2138	0.1121	0.0158	1.29E-12	rs55744103:44316280:T:C
17_44316389_G_A	17	44316389	A	0.2112	-0.0475	0.0076	4.81E-10	0.2138	0.1121	0.0158	1.29E-12	17:44316389:G:A
17_44316449_A_C	17	44316449	C	0.2117	-0.0477	0.0076	4.20E-10	0.2142	0.1116	0.0158	1.65E-12	rs62073098:44316449:A:C
17_44316491_G_C	17	44316491	C	0.1901	-0.0493	0.0081	1.46E-09	0.1846	0.1134	0.01655	7.41E-12	rs62073099:44316491:G:C
17_44316509_G_C	17	44316509	C	0.1957	-0.0507	0.008	2.76E-10	0.1957	0.1131	0.0164	5.26E-12	rs149753849:44316509:G:C
17_44316878_CA_C	17	44316878	C	0.2114	-0.0465	0.0077	1.47E-09	0.2138	0.1121	0.0158	1.29E-12	rs141716100:44316878:CA:C
17_44316888_A_G	17	44316888	G	0.2112	-0.0474	0.0076	5.15E-10	0.2138	0.1121	0.0158	1.29E-12	17:44316888:A:G
17_44317103_T_C	17	44317103	C	0.2112	-0.0474	0.0076	5.27E-10	0.214	0.1121	0.0158	1.33E-12	17:44317103:T:C
17_44317210_C_A	17	44317210	A	0.2116	-0.0471	0.0076	6.89E-10	0.2144	0.1111	0.0158	2.05E-12	17:44317210:C:A
17_44318184_A_G	17	44318184	G	0.2132	-0.0479	0.0076	3.00E-10	0.215	0.1118	0.01578	1.37E-12	17:44318184:A:G
17_44318575_T_G	17	44318575	G	0.2129	-0.0472	0.0076	6.10E-10	0.2183	0.111	0.0158	2.09E-12	rs3110331:44318575:T:G
17_44318663_G_A	17	44318663	A	0.213	-0.048	0.0076	3.05E-10	0.2179	0.1104	0.0158	2.75E-12	17:44318663:G:A
17_44318665_T_C	17	44318665	C	0.1965	-0.0506	0.008	2.65E-10	0.1969	0.1117	0.01636	8.74E-12	17:44318665:T:C
17_44318863_T_C	17	44318863	C	0.2209	-0.0472	0.0076	4.70E-10	0.2233	0.1119	0.01568	9.79E-13	17:44318863:T:C
17_44319167_G_A	17	44319167	A	0.2119	-0.048	0.0076	3.30E-10	0.2149	0.1121	0.01582	1.38E-12	rs2696607:44319167:G:A
17_44319366_C_T	17	44319366	T	0.2124	-0.0472	0.0076	5.98E-10	0.215	0.109	0.01573	4.10E-12	17:44319366:C:T
17_44319369_T_C	17	44319369	C	0.2124	-0.0472	0.0076	6.00E-10	0.215	0.109	0.01573	4.10E-12	17:44319369:T:C
17_44321478_A_G	17	44321478	G	0.1834	-0.0489	0.0084	6.99E-09	0.1848	0.1171	0.01754	2.45E-11	17:44321478:A:G
17_44321527_C_T	17	44321527	T	0.2111	-0.0474	0.0076	5.55E-10	0.2139	0.112	0.01582	1.45E-12	17:44321527:C:T
17_44322577_G_C	17	44322577	C	0.2015	-0.0479	0.0079	1.28E-09	0.2025	0.1138	0.01629	2.91E-12	rs372745970:44322577:G:C
17_44322922_A_G	17	44322922	G	0.2123	-0.0486	0.0076	2.07E-10	0.2148	0.1125	0.01582	1.13E-12	17:44322922:A:G
17_44323425_C_T	17	44323425	T	0.2179	-0.0482	0.0076	2.12E-10	0.2194	0.1088	0.01574	4.65E-12	rs141633411:44323425:C:T
17_44324048_A_G	17	44324048	G	0.2064	-0.0527	0.0078	1.93E-11	0.2071	0.1116	0.01603	3.44E-12	17:44324048:A:G
17_44324185_A_G	17	44324185	G	0.2213	-0.0474	0.0076	4.59E-10	0.2252	0.1064	0.01576	1.47E-11	17:44324185:A:G
17_44324257_G_T	17	44324257	T	0.2195	-0.0472	0.0076	5.38E-10	0.2234	0.1068	0.01574	1.17E-11	17:44324257:G:T
17_44324539_T_C	17	44324539	T	0.2191	-0.0471	0.0076	5.25E-10	0.2191	0.1132	0.01567	5.03E-13	rs2668639:44324539:T:C
17_44324572_A_G	17	44324572	G	0.2183	-0.0453	0.0076	2.68E-09	0.2225	0.1116	0.01578	1.49E-12	17:44324572:A:G
17_44325593_TAA_T	17	44325593	T	0.2162	-0.0462	0.0077	1.66E-09	0.22	0.1086	0.01576	5.49E-12	rs142380704:44325593:TAA:T
17_44325635_C_G	17	44325635	C	0.2205	-0.0475	0.0076	5.29E-10	0.2251	0.1131	0.01585	9.49E-13	17:44325635:C:G
17_44325782_CCT_C	17	44325782	C	0.1967	-0.0497	0.0081	7.24E-10	0.1968	0.1118	0.01636	8.37E-12	rs201746845:44325782:CCT:C
17_44326063_T_G	17	44326063	G	0.1969	-0.051	0.008	2.07E-10	0.1973	0.111	0.01636	1.15E-11	rs143628920:44326063:T:G
17_44326105_G_C	17	44326105	C	0.2115	-0.0477	0.0076	3.97E-10	0.2141	0.1118	0.0158	1.51E-12	rs191247549:44326105:G:C
17_44326245_A_G	17	44326245	G	0.1965	-0.0505	0.008	2.95E-10	0.1968	0.1118	0.01636	8.28E-12	17:44326245:A:G
17_44326396_T_C	17	44326396	C	0.1965	-0.0505	0.008	2.94E-10	0.1968	0.1118	0.01636	8.29E-12	17:44326396:T:C
17_44326509_G_A	17	44326509	A	0.1982	-0.0514	0.008	1.21E-10	0.1991	0.1104	0.01629	1.21E-11	17:44326509:G:A

17_44326619_A_G	17	44326619	G	0.2243	-0.0447	0.0076	3.69E-09	0.2316	0.1023	0.01572	7.57E-11	17:44326619:A:G
17_44326712_T_C	17	44326712	C	0.1842	-0.0517	0.0083	5.26E-10	0.1795	0.1115	0.01694	4.60E-11	17:44326712:T:C
17_44326845_A_G	17	44326845	G	0.2267	-0.0493	0.0076	8.52E-11	0.2331	0.1064	0.0157	1.21E-11	17:44326845:A:G
17_44326864_A_G	17	44326864	G	0.2254	-0.0495	0.0076	6.93E-11	0.2317	0.1064	0.0157	1.22E-11	17:44326864:A:G
17_44327070_G_A	17	44327070	A	0.2222	-0.0468	0.0076	7.78E-10	0.23	0.1049	0.01571	2.50E-11	17:44327070:G:A
17_44327082_G_T	17	44327082	T	0.197	-0.0508	0.008	2.20E-10	0.1974	0.112	0.01634	7.38E-12	17:44327082:G:T
17_44327370_C_A	17	44327370	A	0.1971	-0.0509	0.008	2.18E-10	0.1977	0.1122	0.01634	6.72E-12	17:44327370:C:A
17_44327438_C_G	17	44327438	G	0.2236	-0.0483	0.0076	2.01E-10	0.23	0.1096	0.0157	2.95E-12	17:44327438:C:G
17_44327482_G_A	17	44327482	A	0.2243	-0.0481	0.0076	2.39E-10	0.2304	0.1101	0.01569	2.21E-12	17:44327482:G:A
17_44327642_AC_A	17	44327642	A	0.2146	-0.0468	0.0077	1.13E-09	0.2171	0.1114	0.01579	1.72E-12	17:44327642:AC:A
17_44327712_C_T	17	44327712	T	0.2156	-0.0483	0.0076	2.37E-10	0.2176	0.1112	0.01579	1.87E-12	17:44327712:C:T
17_44327958_C_G	17	44327958	G	0.1965	-0.0501	0.008	4.27E-10	0.1956	0.1124	0.01634	5.92E-12	17:44327958:C:G
17_44328260_TCTTCCTCTT	17	44328260	T	0.196	-0.0495	0.0081	8.80E-10	0.1944	0.1123	0.01639	7.19E-12	91353:44328260:TCTTCCTCTTCCTCTC:T
17_44328668_A_G	17	44328668	G	0.1965	-0.0499	0.008	5.03E-10	0.1956	0.1124	0.01634	6.12E-12	17:44328668:A:G
17_44328871_A_G	17	44328871	G	0.183	-0.0529	0.0084	3.69E-10	0.1818	0.1307	0.0174	5.74E-14	17:44328871:A:G
17_44328919_T_C	17	44328919	C	0.1816	-0.0535	0.0085	2.84E-10	0.1794	0.1302	0.01746	8.89E-14	rs374470873:44328919:T:C
17_44328921_T_G	17	44328921	G	0.1816	-0.0535	0.0085	2.84E-10	0.1794	0.1302	0.01746	8.89E-14	rs377762376:44328921:T:G
17_44329636_T_C	17	44329636	C	0.2081	-0.0478	0.0077	5.61E-10	0.2092	0.1155	0.01596	4.53E-13	rs2243967:44329636:T:C
17_44330105_A_G	17	44330105	G	0.1955	-0.0489	0.0081	1.37E-09	0.1932	0.122	0.01675	3.27E-13	rs79641193:44330105:A:G
17_44330106_T_C	17	44330106	C	0.1955	-0.0489	0.0081	1.37E-09	0.1932	0.122	0.01675	3.27E-13	rs76147580:44330106:T:C
17_44330398_A_G	17	44330398	G	0.1594	-0.0526	0.0093	1.44E-08	0.1627	0.1207	0.01926	3.62E-10	rs192799606:44330398:A:G
17_44330410_G_A	17	44330410	A	0.1593	-0.0526	0.0093	1.45E-08	0.1626	0.1213	0.01926	3.03E-10	rs182821552:44330410:G:A
17_44330438_A_G	17	44330438	G	0.1593	-0.0526	0.0093	1.43E-08	0.1626	0.1213	0.01926	3.03E-10	17:44330438:A:G
17_44331074_A_AGCTTCG	17	44331074	AGCTTCGGCTCG	0.0729	-0.0676	0.0151	7.19E-06	0.07279	0.1721	0.03119	3.42E-08	17:44331074:A:AGCTTCGGCTCG
17_44331214_T_C	17	44331214	C	0.2091	-0.049	0.0077	2.40E-10	0.2084	0.113	0.01587	1.09E-12	17:44331214:T:C
17_44331297_G_T	17	44331297	T	0.2107	-0.0485	0.0077	2.41E-10	0.2123	0.1101	0.01587	4.00E-12	17:44331297:G:T
17_44331803_A_ATTTT	17	44331803	ATTTT	0.2119	-0.0467	0.0077	1.25E-09	0.2143	0.11	0.01581	3.48E-12	rs200422537:44331803:A:ATTTT
17_44332093_G_A	***17***	***44332093***	***A***	***0.4373***	***0.0159***	***0.0065***	***0.0137***	***0.4569***	***-0.07424***	***0.01361***	***4.88E-08***	***rs11655181:44332093:G:A***
17_44332200_GT_G	17	44332200	G	0.2002	-0.0467	0.008	5.02E-09	0.1953	0.1121	0.01627	5.65E-12	rs373294137:44332200:GT:G
17_44332351_A_G	17	44332351	G	0.2146	-0.0482	0.0076	2.56E-10	0.2173	0.1088	0.01577	5.32E-12	rs2950015:44332351:A:G
17_44332429_C_T	17	44332429	T	0.2128	-0.0479	0.0076	3.42E-10	0.2149	0.1095	0.01579	4.04E-12	rs2732625:44332429:C:T
17_44332793_G_A	17	44332793	A	0.2523	-0.0392	0.0073	8.81E-08	0.2489	0.09782	0.01507	8.63E-11	rs71375338:44332793:G:A
17_44332970_A_G	17	44332970	G	0.2115	-0.0483	0.0076	2.57E-10	0.2142	0.111	0.0158	2.12E-12	rs2532364:44332970:A:G
17_44333121_G_A	17	44333121	A	0.2115	-0.0483	0.0076	2.56E-10	0.2142	0.111	0.01581	2.17E-12	rs62073155:44333121:G:A
17_44333293_A_G	17	44333293	G	0.2115	-0.0483	0.0076	2.59E-10	0.2142	0.111	0.01581	2.15E-12	rs190796367:44333293:A:G
17_44333331_A_G	17	44333331	G	0.2102	-0.0473	0.0077	7.16E-10	0.212	0.1117	0.01588	1.94E-12	rs150592114:44333331:A:G
17_44333412_G_A	17	44333412	A	0.209	-0.0494	0.0077	1.42E-10	0.2099	0.1109	0.01593	3.33E-12	rs111920741:44333412:G:A
17_44333423_G_T	17	44333423	T	0.2094	-0.0497	0.0077	1.03E-10	0.2109	0.1109	0.01591	3.16E-12	rs2532363:44333423:G:T
17_44333499_G_T	17	44333499	T	0.2096	-0.0481	0.0077	3.89E-10	0.2107	0.1139	0.01592	8.43E-13	rs2532362:44333499:G:T
17_44333532_C_G	17	44333532	G	0.2111	-0.0483	0.0076	2.66E-10	0.214	0.1107	0.01582	2.59E-12	rs113343751:44333532:C:G
17_44333568_T_C	17	44333568	C	0.2109	-0.0483	0.0077	2.79E-10	0.2139	0.1107	0.01583	2.72E-12	rs62073156:44333568:T:C
17_44333889_T_C	17	44333889	C	0.1884	-0.0499	0.0083	1.88E-09	0.19	0.12	0.01726	3.60E-12	rs2696422:44333889:T:C
17_44333890_G_A	17	44333890	A	0.1884	-0.0498	0.0083	1.99E-09	0.19	0.12	0.01726	3.63E-12	rs2696423:44333890:G:A
17_44334052_G_A	17	44334052	A	0.2119	-0.0482	0.0076	2.75E-10	0.2142	0.1109	0.01581	2.31E-12	rs62073157:44334052:G:A
17_44334288_C_G	17	44334288	G	0.2129	-0.0477	0.0076	4.27E-10	0.214	0.1133	0.0158	7.50E-13	17:44334288:C:G
17_44334419_C_T	17	44334419	T	0.212	-0.0482	0.0076	2.82E-10	0.2143	0.1109	0.01581	2.30E-12	17:44334419:C:T
17_44334768_A_G	17	44334768	G	0.2119	-0.0482	0.0076	2.81E-10	0.2143	0.111	0.01581	2.20E-12	rs62074562:44334768:A:G
17_44335274_G_A	17	44335274	A	0.2032	-0.0503	0.0079	1.80E-10	0.2021	0.1149	0.01609	9.29E-13	rs2696429:44335274:G:A
17_44335579_G_A	17	44335579	A	0.1953	-0.0484	0.0081	1.83E-09	0.1949	0.1116	0.01643	1.10E-11	rs139077859:44335579:G:A
17_44335635_G_A	17	44335635	A	0.2173	-0.0451	0.0076	3.11E-09	0.2216	0.1068	0.0158	1.36E-11	rs147431626:44335635:G:A
17_44335752_T_C	17	44335752	C	0.2118	-0.0481	0.0076	3.04E-10	0.2142	0.1113	0.01582	1.96E-12	rs76155390:44335752:T:C
17_44335806_A_C	17	44335806	C	0.2036	-0.0501	0.0079	2.04E-10	0.2023	0.1139	0.01607	1.38E-12	17:44335806:A:C
17_44335818_A_G	17	44335818	G	0.2118	-0.0481	0.0076	3.08E-10	0.2142	0.1113	0.01582	1.95E-12	17:44335818:A:G
17_44335865_A_G	17	44335865	G	0.2032	-0.0501	0.0079	1.98E-10	0.2021	0.1138	0.01609	1.55E-12	17:44335865:A:G
17_44335895_CAT_C	17	44335895	C	0.1954	-0.049	0.0081	1.47E-09	0.1959	0.111	0.01649	1.63E-11	rs72485539:44335895:CAT:C

17_44336237_C_T	17	44336237	T	0.2136	-0.048	0.0076	3.44E-10	0.2162	0.1102	0.01582	3.20E-12	17:44336237:C:T
17_44336594_G_A	17	44336594	G	0.2119	-0.0478	0.0076	4.12E-10	0.2146	0.1126	0.01582	1.12E-12	rs2957321:44336594:G:A
17_44336619_AGGG_A	17	44336619	AGGG	0.212	-0.047	0.0077	1.02E-09	0.2146	0.1126	0.01582	1.12E-12	rs143555493:44336619:AGGG:A
17_44336651_T_C	17	44336651	C	0.309	-0.0344	0.0069	7.01E-07	0.313	0.08466	0.01437	3.84E-09	rs2458203:44336651:T:C
17_44336976_C_T	17	44336976	C	0.1942	-0.0496	0.0081	1.07E-09	0.1911	0.1133	0.0166	8.90E-12	rs2469937:44336976:C:T
17_44336997_C_G	17	44336997	G	0.386	-0.0241	0.0066	0.0002272	0.3755	0.0759	0.0138	3.80E-08	17:44336997:C:G
17_44337429_G_C	17	44337429	C	0.2124	-0.0487	0.0076	1.85E-10	0.2158	0.1116	0.01582	1.74E-12	17:44337429:G:C
17_44337512_A_T	17	44337512	A	0.3995	-0.0334	0.0071	2.81E-06	0.4141	0.08388	0.01485	1.63E-08	17:44337512:A:T
17_44337524_A_T	17	44337524	A	0.3933	-0.0337	0.0071	2.07E-06	0.407	0.08584	0.0148	6.62E-09	17:44337524:A:T
17_44337903_C_G	17	44337903	G	0.2039	-0.0501	0.0078	1.71E-10	0.2054	0.1122	0.01626	5.28E-12	rs112305366:44337903:C:G
17_44337986_CTTTTTTT_C	17	44337986	C	0.211	-0.0464	0.0077	1.71E-09	0.2132	0.1127	0.01583	1.08E-12	17:44337986:CTTTTTTT:C
17_44338279_G_C	17	44338279	C	0.2267	-0.045	0.0076	3.49E-09	0.2327	0.1067	0.01579	1.42E-11	rs2696430:44338279:G:C
17_44338280_T_A	17	44338280	A	0.1956	-0.0484	0.008	1.66E-09	0.1964	0.1123	0.01643	8.02E-12	rs375807182:44338280:T:A
17_44338285_C_T	17	44338285	T	0.1959	-0.0485	0.008	1.51E-09	0.197	0.1128	0.01642	6.29E-12	rs369196070:44338285:C:T
17_44338404_G_A	17	44338404	A	0.1956	-0.0485	0.008	1.51E-09	0.1964	0.1124	0.01643	7.81E-12	17:44338404:G:A
17_44338422_G_A	17	44338422	A	0.1956	-0.0485	0.008	1.51E-09	0.1964	0.1124	0.01643	7.81E-12	17:44338422:G:A
17_44338433_T_A	17	44338433	A	0.1956	-0.0485	0.008	1.51E-09	0.1964	0.1124	0.01643	7.80E-12	rs2950656:44338433:T:A
17_44338503_C_A	17	44338503	A	0.2293	-0.0425	0.0076	2.31E-08	0.2351	0.1065	0.01576	1.39E-11	17:44338503:C:A
17_44338534_C_T	17	44338534	T	0.2287	-0.043	0.0076	1.59E-08	0.2341	0.1067	0.01577	1.31E-11	17:44338534:C:T
17_44338536_T_C	17	44338536	C	0.2292	-0.0428	0.0076	1.82E-08	0.2347	0.1061	0.01577	1.75E-11	17:44338536:T:C
17_44338594_G_A	17	44338594	A	0.22	-0.046	0.0076	1.67E-09	0.2258	0.1079	0.01578	7.95E-12	rs113313727:44338594:G:A
17_44338640_TATC_T	17	44338640	T	0.2014	-0.049	0.008	8.61E-10	0.1998	0.115	0.01618	1.16E-12	rs141650602:44338640:TATC:T
17_44338694_G_A	17	44338694	A	0.2228	-0.0458	0.0076	1.99E-09	0.2312	0.1071	0.01583	1.30E-11	17:44338694:G:A
17_44338735_C_T	17	44338735	T	0.2251	-0.0446	0.0076	5.04E-09	0.2331	0.1065	0.01583	1.76E-11	17:44338735:C:T
17_44338782_AT_A	17	44338782	A	0.199	-0.0476	0.008	2.93E-09	0.1948	0.1145	0.01637	2.63E-12	rs34081316:44338782:AT:A
17_44338869_C_T	17	44338869	T	0.1826	-0.0519	0.0085	8.60E-10	0.1829	0.1154	0.01729	2.46E-11	17:44338869:C:T
17_44338966_A_C	17	44338966	C	0.2248	-0.0455	0.0076	2.43E-09	0.2285	0.114	0.01579	5.19E-13	17:44338966:A:C
17_44338967_T_C	17	44338967	C	0.2249	-0.0456	0.0076	2.15E-09	0.2286	0.1138	0.01579	5.71E-13	17:44338967:T:C
17_44339003_G_T	17	44339003	T	0.2238	-0.0465	0.0076	1.16E-09	0.2275	0.113	0.01582	9.25E-13	17:44339003:G:T
17_44339109_AAAAAAAG_	17	44339109	A	0.2123	-0.0461	0.0077	1.81E-09	0.2138	0.1112	0.01572	1.52E-12	01657714:44339109:AAAAAAAG:A
17_44339153_A_G	17	44339153	G	0.1958	-0.0486	0.008	1.44E-09	0.197	0.1123	0.01642	7.95E-12	17:44339153:A:G
17_44339174_C_T	17	44339174	T	0.1958	-0.0486	0.008	1.44E-09	0.197	0.1123	0.01642	7.94E-12	17:44339174:C:T
17_44339354_T_C	17	44339354	C	0.1956	-0.0485	0.008	1.53E-09	0.1966	0.1125	0.01642	7.43E-12	rs113178301:44339354:T:C
17_44339375_A_G	17	44339375	G	0.1956	-0.0485	0.008	1.53E-09	0.1966	0.1125	0.01642	7.43E-12	rs80290584:44339375:A:G
17_44339408_C_T	17	44339408	T	0.2163	-0.048	0.0076	3.28E-10	0.2192	0.1123	0.01582	1.25E-12	rs2732685:44339408:C:T
17_44339473_A_G	17	44339473	G	0.2149	-0.0477	0.0076	4.53E-10	0.2172	0.1131	0.01583	9.22E-13	rs2532349:44339473:A:G
17_44339513_A_C	17	44339513	C	0.1956	-0.0485	0.008	1.55E-09	0.1966	0.1125	0.01643	7.41E-12	rs34046424:44339513:A:C
17_44339607_C_T	17	44339607	T	0.1986	-0.0479	0.008	1.85E-09	0.1955	0.1138	0.01634	3.20E-12	rs77917260:44339607:C:T
17_44339608_A_G	17	44339608	G	0.1983	-0.0483	0.008	1.76E-09	0.1987	0.1134	0.01642	4.88E-12	rs79947689:44339608:A:G
17_44339651_T_C	17	44339651	C	0.1979	-0.0482	0.008	1.98E-09	0.1982	0.1135	0.01643	4.89E-12	rs36036607:44339651:T:C
17_44339665_C_G	17	44339665	G	0.1979	-0.0482	0.008	1.98E-09	0.1982	0.1135	0.01643	4.89E-12	rs2732683:44339665:C:G
17_44339675_T_C	17	44339675	C	0.1979	-0.0482	0.008	1.98E-09	0.1982	0.1135	0.01643	4.88E-12	rs2732682:44339675:T:C
17_44339712_T_G	17	44339712	G	0.1956	-0.0486	0.008	1.48E-09	0.1966	0.1125	0.01643	7.38E-12	rs2668687:44339712:T:G
17_44339744_TC_T	17	44339744	T	0.1832	-0.0481	0.0084	1.18E-08	0.1793	0.1129	0.01727	6.35E-11	17:44339744:TC:T
17_44339747_TC_T	17	44339747	T	0.1832	-0.0481	0.0084	1.18E-08	0.1793	0.1129	0.01727	6.35E-11	rs67404079:44339747:TC:T
17_44339966_T_A	17	44339966	A	0.1952	-0.0488	0.008	1.36E-09	0.196	0.1121	0.01646	9.81E-12	17:44339966:T:A
17_44340021_C_T	17	44340021	T	0.1955	-0.0485	0.008	1.51E-09	0.1966	0.1125	0.01643	7.34E-12	17:44340021:C:T
17_44340151_T_C	17	44340151	C	0.2135	-0.0467	0.0077	1.05E-09	0.2178	0.1117	0.01585	1.86E-12	17:44340151:T:C
17_44340153_GAA_G	17	44340153	G	0.2108	-0.0463	0.0077	1.85E-09	0.2131	0.1132	0.01584	8.95E-13	rs372228208:44340153:GAA:G
17_44340253_A_G	17	44340253	G	0.2132	-0.0481	0.0076	2.93E-10	0.2178	0.1099	0.01575	2.95E-12	17:44340253:A:G
17_44340328_A_C	17	44340328	C	0.2125	-0.0475	0.0077	5.43E-10	0.2154	0.1118	0.01584	1.67E-12	17:44340328:A:C
17_44340506_C_G	17	44340506	G	0.2128	-0.0483	0.0076	2.70E-10	0.2175	0.1123	0.01584	1.33E-12	17:44340506:C:G
17_44340525_A_C	17	44340525	C	0.2133	-0.0481	0.0076	3.13E-10	0.2178	0.1125	0.01583	1.20E-12	17:44340525:A:C
17_44340880_G_GCA	17	44340880	GCA	0.1719	-0.052	0.0088	4.24E-09	0.1712	0.1128	0.01813	4.88E-10	17:44340880:G:GCA
17_44340942_T_C	17	44340942	C	0.2118	-0.0472	0.0077	6.97E-10	0.217	0.113	0.01585	1.01E-12	17:44340942:T:C

17_44341412_G_<CN3>	17	44341412	<CN3>	0.2022	-0.0435	0.0079	3.73E-08	0.2065	0.1093	0.01625	1.77E-11	17:44341412:G:<CN3>:44366497
17_44341609_T_C	17	44341609	C	0.1952	-0.0485	0.008	1.60E-09	0.1956	0.1121	0.01643	8.82E-12	17:44341609:T:C
17_44341627_G_T	17	44341627	T	0.1952	-0.0485	0.008	1.60E-09	0.1956	0.1121	0.01643	8.82E-12	17:44341627:G:T
17_44341868_CA_C	17	44341868	C	0.2113	-0.0463	0.0077	1.81E-09	0.2139	0.1125	0.01585	1.24E-12	rs143191191:44341868:CA:C
17_44341870_A_C	17	44341870	C	0.1937	-0.0489	0.0081	1.50E-09	0.1947	0.1121	0.01655	1.25E-11	17:44341870:A:C
17_44342123_G_C	17	44342123	C	0.3148	-0.0338	0.0069	9.82E-07	0.3208	0.08794	0.01433	8.41E-10	rs2732677:44342123:G:C
17_44342327_T_G	17	44342327	G	0.2142	-0.0474	0.0077	6.10E-10	0.2181	0.1126	0.01584	1.17E-12	17:44342327:T:G
17_44342378_G_A	***17***	***44342378***	***A***	***0.4431***	***0.0154***	***0.0065***	***0.01719***	***0.464***	***-0.07517***	***0.01361***	***3.36E-08***	***rs79061491:44342378:G:A***
17_44342404_A_C	17	44342404	C	0.1956	-0.0478	0.008	2.70E-09	0.1973	0.1134	0.01642	4.99E-12	17:44342404:A:C
17_44342461_A_AGCTT	17	44342461	AGCTT	0.1955	-0.0476	0.0081	3.77E-09	0.1966	0.1126	0.01643	7.29E-12	rs147456794:44342461:A:AGCTT
17_44342482_GT_G	17	44342482	G	0.1872	-0.0483	0.0083	6.82E-09	0.1886	0.1167	0.01698	6.26E-12	rs112528980:44342482:GT:G
17_44342513_T_C	17	44342513	C	0.1953	-0.0483	0.008	1.81E-09	0.1966	0.1126	0.01643	7.30E-12	rs2668713:44342513:T:C
17_44342563_A_G	17	44342563	G	0.1953	-0.0483	0.008	1.78E-09	0.1966	0.1126	0.01643	7.30E-12	rs2429440:44342563:A:G
17_44342994_C_T	17	44342994	T	0.2142	-0.0463	0.0076	1.39E-09	0.2172	0.1094	0.01586	5.09E-12	rs62071573:44342994:C:T
17_44343004_C_T	17	44343004	T	0.1908	-0.05	0.0082	9.14E-10	0.1907	0.1151	0.0167	5.44E-12	rs2950706:44343004:C:T
17_44343084_T_G	17	44343084	G	0.1952	-0.0483	0.008	1.84E-09	0.1965	0.1125	0.01643	7.31E-12	17:44343084:T:G
17_44343121_A_G	17	44343121	G	0.2121	-0.047	0.0077	8.45E-10	0.2136	0.1133	0.01587	9.35E-13	17:44343121:A:G
17_44343125_C_T	17	44343125	T	0.2119	-0.0474	0.0076	5.72E-10	0.2154	0.1124	0.0158	1.15E-12	17:44343125:C:T
17_44343192_G_A	17	44343192	A	0.1938	-0.0475	0.0081	3.91E-09	0.1957	0.1128	0.01651	8.34E-12	17:44343192:G:A
17_44343282_G_A	17	44343282	A	0.2195	-0.0461	0.0076	1.67E-09	0.2259	0.1098	0.01583	3.94E-12	17:44343282:G:A
17_44343291_C_G	17	44343291	G	0.2195	-0.0461	0.0076	1.67E-09	0.2259	0.1098	0.01583	3.94E-12	17:44343291:C:G
17_44343304_T_A	17	44343304	A	0.2196	-0.0461	0.0076	1.66E-09	0.2259	0.1101	0.01583	3.44E-12	17:44343304:T:A
17_44343370_C_G	17	44343370	C	0.3163	-0.0328	0.0069	2.21E-06	0.3212	0.08956	0.01433	4.13E-10	rs2696694:44343370:C:G
17_44343371_G_A	17	44343371	A	0.2139	-0.0464	0.0076	1.24E-09	0.2195	0.114	0.01581	5.57E-13	17:44343371:G:A
17_44343392_G_A	17	44343392	A	0.1952	-0.0482	0.008	1.96E-09	0.1965	0.1125	0.01643	7.31E-12	17:44343392:G:A
17_44343719_C_T	17	44343719	T	0.2129	-0.0467	0.0076	1.03E-09	0.2155	0.1141	0.0158	5.03E-13	17:44343719:C:T
17_44343930_A_G	17	44343930	G	0.2124	-0.0464	0.0076	1.21E-09	0.2176	0.1128	0.01579	9.01E-13	17:44343930:A:G
17_44344097_G_C	17	44344097	C	0.2158	-0.0452	0.0076	3.24E-09	0.2192	0.1141	0.01579	5.07E-13	rs2532343:44344097:G:C
17_44344178_T_G	17	44344178	G	0.2175	-0.0456	0.0076	2.36E-09	0.2222	0.1124	0.0158	1.15E-12	17:44344178:T:G
17_44344219_C_T	17	44344219	T	0.2004	-0.0452	0.008	1.30E-08	0.1952	0.1144	0.01627	2.02E-12	17:44344219:C:T
17_44344222_C_G	17	44344222	G	0.2004	-0.0452	0.008	1.30E-08	0.1952	0.1144	0.01627	2.02E-12	17:44344222:C:G
17_44344300_G_T	17	44344300	T	0.2199	-0.0446	0.0076	5.27E-09	0.2252	0.1112	0.01578	1.84E-12	17:44344300:G:T
17_44344376_G_A	17	44344376	A	0.2154	-0.0434	0.0077	1.88E-08	0.2239	0.1088	0.01604	1.17E-11	rs112534607:44344376:G:A
17_44344377_C_T	17	44344377	T	0.1444	-0.0532	0.0101	1.48E-07	0.1489	0.1229	0.02123	7.11E-09	rs144129607:44344377:C:T
17_44344409_A_C	17	44344409	C	0.2141	-0.0435	0.0077	1.91E-08	0.2227	0.1087	0.01605	1.24E-11	rs111413387:44344409:A:C
17_44344456_T_C	17	44344456	C	0.2138	-0.0432	0.0077	2.40E-08	0.2224	0.109	0.01605	1.12E-11	17:44344456:T:C
17_44344541_C_A	17	44344541	A	0.1919	-0.0481	0.0081	2.68E-09	0.1901	0.1107	0.01647	1.80E-11	rs111854089:44344541:C:A
17_44344552_C_T	17	44344552	T	0.191	-0.046	0.0081	1.53E-08	0.1869	0.1095	0.01672	5.83E-11	rs113830390:44344552:C:T
17_44344595_G_T	17	44344595	T	0.1921	-0.0482	0.0081	2.41E-09	0.1904	0.1105	0.01646	1.93E-11	rs117995241:44344595:G:T
17_44344596_C_A	17	44344596	A	0.1921	-0.0482	0.0081	2.42E-09	0.1904	0.1105	0.01646	1.93E-11	rs117629202:44344596:C:A
17_44344737_GGCTGGTGA	17	44344737	G	0.1921	-0.0474	0.0081	5.26E-09	0.1901	0.1107	0.01647	1.81E-11	39917:44344737:GGCTGGTGACCCT:G
17_44344810_T_G	17	44344810	G	0.2052	-0.0464	0.0078	2.26E-09	0.2108	0.1101	0.0161	8.07E-12	rs2732649:44344810:T:G
17_44344822_G_A	17	44344822	A	0.1919	-0.0481	0.0081	2.71E-09	0.1901	0.1107	0.01647	1.81E-11	rs76934998:44344822:G:A
17_44344858_A_G	17	44344858	G	0.1919	-0.0481	0.0081	2.72E-09	0.1901	0.1107	0.01647	1.82E-11	rs74358353:44344858:A:G
17_44344926_A_G	17	44344926	G	0.1919	-0.0481	0.0081	2.72E-09	0.1901	0.1107	0.01647	1.82E-11	rs74652075:44344926:A:G
17_44344970_T_C	17	44344970	C	0.1919	-0.0481	0.0081	2.73E-09	0.1901	0.1107	0.01647	1.82E-11	rs77568881:44344970:T:C
17_44344988_C_G	17	44344988	G	0.2051	-0.0461	0.0078	2.71E-09	0.2109	0.1112	0.01609	4.93E-12	rs2732650:44344988:C:G
17_44345047_A_ACT	17	44345047	ACT	0.2052	-0.0453	0.0078	6.39E-09	0.211	0.1103	0.0161	7.36E-12	rs138875687:44345047:A:ACT
17_44345063_C_T	17	44345063	T	0.1912	-0.0459	0.0081	1.61E-08	0.1872	0.1101	0.01671	4.47E-11	rs2732651:44345063:C:T
17_44345090_C_A	17	44345090	A	0.1919	-0.0481	0.0081	2.73E-09	0.1901	0.1107	0.01647	1.83E-11	rs2668719:44345090:C:A
17_44345114_C_T	17	44345114	T	0.1919	-0.0481	0.0081	2.72E-09	0.1901	0.1107	0.01647	1.83E-11	rs2732652:44345114:C:T
17_44345653_A_G	17	44345653	G	0.2054	-0.046	0.0078	2.95E-09	0.2117	0.1102	0.0161	7.74E-12	rs2532340:44345653:A:G
17_44345668_A_G	17	44345668	G	0.1925	-0.0477	0.0081	4.18E-09	0.1952	0.1123	0.0166	1.33E-11	rs2532339:44345668:A:G
17_44346039_A_G	17	44346039	G	0.1924	-0.0495	0.0081	9.75E-10	0.1931	0.1131	0.01656	8.34E-12	17:44346039:A:G
17_44346393_C_G	17	44346393	G	0.1949	-0.0482	0.008	1.92E-09	0.1968	0.1131	0.01643	5.75E-12	rs2696561:44346393:C:G

17_44346405_C_T	17	44346405	T	0.188	-0.0473	0.0082	9.17E-09	0.1828	0.1085	0.0169	1.40E-10	rs2732654:44346405:C:T
17_44346407_G_C	17	44346407	C	0.188	-0.0473	0.0082	9.17E-09	0.1828	0.1084	0.0169	1.40E-10	rs2732655:44346407:G:C
17_44346589_G_A	17	44346589	A	0.192	-0.048	0.0081	2.91E-09	0.1902	0.1109	0.01648	1.72E-11	rs77488920:44346589:G:A
17_44346610_A_G	17	44346610	G	0.1919	-0.0482	0.0081	2.57E-09	0.19	0.111	0.01648	1.67E-11	17:44346610:A:G
17_44346666_G_A	17	44346666	A	0.1919	-0.0482	0.0081	2.57E-09	0.19	0.1109	0.01648	1.70E-11	17:44346666:G:A
17_44346674_T_C	17	44346674	C	0.2009	-0.0463	0.0078	3.09E-09	0.2029	0.108	0.01618	2.46E-11	rs2696559:44346674:T:C
17_44346690_C_G	17	44346690	G	0.1919	-0.0482	0.0081	2.57E-09	0.19	0.1109	0.01648	1.72E-11	17:44346690:C:G
17_44346751_T_G	17	44346751	G	0.1919	-0.0482	0.0081	2.56E-09	0.19	0.1108	0.01648	1.75E-11	17:44346751:T:G
17_44346829_C_T	17	44346829	T	0.1919	-0.0482	0.0081	2.55E-09	0.19	0.1108	0.01648	1.80E-11	rs62071576:44346829:C:T
17_44346951_T_A	17	44346951	A	0.3105	-0.0323	0.007	4.25E-06	0.3167	0.08476	0.01454	5.56E-09	rs2696558:44346951:T:A
17_44346962_C_T	17	44346962	T	0.1921	-0.0481	0.0081	2.68E-09	0.1902	0.1108	0.01649	1.80E-11	rs2458216:44346962:C:T
17_44347097_A_G	17	44347097	G	0.1921	-0.0482	0.0081	2.61E-09	0.1901	0.1107	0.01649	1.91E-11	17:44347097:A:G
17_44347109_A_G	17	44347109	G	0.1921	-0.0482	0.0081	2.59E-09	0.1901	0.1107	0.01649	1.93E-11	17:44347109:A:G
17_44347165_T_C	17	44347165	C	0.1847	-0.0438	0.0083	1.57E-07	0.19	0.1118	0.01727	9.74E-11	17:44347165:T:C
17_44347218_C_A	17	44347218	A	0.2047	-0.046	0.0078	3.01E-09	0.2103	0.1107	0.01611	6.29E-12	17:44347218:C:A
17_44347557_G_A	17	44347557	A	0.1918	-0.0483	0.0081	2.37E-09	0.1898	0.1104	0.01649	2.14E-11	17:44347557:G:A
17_44347561_T_C	17	44347561	C	0.1918	-0.0483	0.0081	2.37E-09	0.1898	0.1104	0.01649	2.14E-11	17:44347561:T:C
17_44347638_C_T	17	44347638	T	0.2081	-0.0459	0.0077	3.11E-09	0.2146	0.1099	0.01608	8.04E-12	17:44347638:C:T
17_44347727_A_T	17	44347727	T	0.1919	-0.0484	0.0081	2.06E-09	0.1901	0.1108	0.01648	1.75E-11	17:44347727:A:T
17_44347931_TTAACTCAG	17	44347931	T	0.1615	-0.0479	0.0092	1.89E-07	0.1616	0.1307	0.01873	3.04E-12	17:44347931:TTAACTCAGGCA:T
17_44348013_A_G	17	44348013	G	0.1918	-0.0483	0.0081	2.38E-09	0.1898	0.1104	0.01649	2.14E-11	17:44348013:A:G
17_44348221_A_G	17	44348221	G	0.2072	-0.0468	0.0078	1.60E-09	0.2135	0.1109	0.01611	5.78E-12	17:44348221:A:G
17_44348265_G_C	17	44348265	C	0.2069	-0.0454	0.0078	4.63E-09	0.2132	0.1103	0.01609	7.09E-12	rs2429438:44348265:G:C
17_44348298_A_G	17	44348298	G	0.1929	-0.0479	0.0081	2.87E-09	0.1904	0.1107	0.01648	1.81E-11	rs2950694:44348298:A:G
17_44348356_T_A	17	44348356	A	0.1918	-0.0483	0.0081	2.38E-09	0.1898	0.1104	0.01649	2.14E-11	rs2950693:44348356:T:A
17_44348370_A_G	17	44348370	G	0.2069	-0.0458	0.0077	3.45E-09	0.2141	0.1095	0.01609	1.01E-11	rs2696555:44348370:A:G
17_44348387_A_G	17	44348387	G	0.1918	-0.0483	0.0081	2.38E-09	0.1898	0.1104	0.01649	2.14E-11	rs2950692:44348387:A:G
17_44348535_T_TTTCTTTT	17	44348535	TTTCTTTTCTTTTC	0.1985	-0.045	0.0079	1.34E-08	0.1991	0.1078	0.01629	3.55E-11	17:44348535:T:TTTCTTTTCTTTTC
17_44348548_T_TC	17	44348548	TC	0.1985	-0.045	0.0079	1.34E-08	0.1991	0.1078	0.01629	3.55E-11	17:44348548:T:TC
17_44348593_A_G	17	44348593	G	0.2054	-0.046	0.0078	3.02E-09	0.2113	0.1099	0.01611	8.85E-12	rs2732713:44348593:A:G
17_44348616_C_T	17	44348616	T	0.1918	-0.0483	0.0081	2.38E-09	0.1898	0.1104	0.01649	2.14E-11	rs113056783:44348616:C:T
17_44348634_T_C	17	44348634	C	0.1909	-0.0462	0.0081	1.46E-08	0.1866	0.109	0.01673	7.15E-11	rs112665297:44348634:T:C
17_44348753_T_C	17	44348753	C	0.1908	-0.0461	0.0081	1.48E-08	0.1865	0.1086	0.01673	8.33E-11	17:44348753:T:C
17_44348768_A_G	17	44348768	G	0.1918	-0.0483	0.0081	2.38E-09	0.1898	0.1104	0.01649	2.14E-11	rs2950691:44348768:A:G
17_44348825_C_G	17	44348825	G	0.1918	-0.0484	0.0081	2.26E-09	0.1898	0.1104	0.01649	2.11E-11	rs2942175:44348825:C:G
17_44348848_G_A	17	44348848	A	0.1918	-0.0484	0.0081	2.26E-09	0.1898	0.1104	0.01649	2.11E-11	rs2942176:44348848:G:A
17_44348932_T_G	17	44348932	G	0.2085	-0.0454	0.0077	4.28E-09	0.2152	0.1061	0.01608	4.19E-11	rs2732712:44348932:T:G
17_44348963_TAG_T	17	44348963	T	0.192	-0.0478	0.0081	4.09E-09	0.1898	0.1104	0.01649	2.11E-11	rs67667485:44348963:TAG:T
17_44348987_G_A	17	44348987	A	0.1918	-0.0484	0.0081	2.27E-09	0.1898	0.1104	0.01649	2.11E-11	rs2942177:44348987:G:A
17_44349031_A_AGATTAC	17	44349031	AGATTAC	0.1427	-0.0539	0.01	7.84E-08	0.1405	0.1344	0.02052	5.81E-11	17:44349031:A:AGATTAC
17_44349079_C_A	17	44349079	A	0.1918	-0.0483	0.0081	2.39E-09	0.1898	0.1104	0.01649	2.14E-11	rs75257416:44349079:C:A
17_44349080_C_G	17	44349080	G	0.1918	-0.0483	0.0081	2.39E-09	0.1898	0.1104	0.01649	2.14E-11	rs78570732:44349080:C:G
17_44349136_CT_C	17	44349136	C	0.1909	-0.0454	0.0082	2.82E-08	0.1864	0.1087	0.01673	8.16E-11	rs67962447:44349136:CT:C
17_44349150_CAG_C	17	44349150	C	0.1922	-0.0474	0.0081	5.57E-09	0.1898	0.1105	0.01649	2.09E-11	rs67912164:44349150:CAG:C
17_44349167_G_A	17	44349167	A	0.1907	-0.0461	0.0081	1.54E-08	0.1863	0.1089	0.01674	7.82E-11	rs62071595:44349167:G:A
17_44349169_T_C	17	44349169	C	0.1907	-0.0461	0.0081	1.54E-08	0.1863	0.1089	0.01674	7.82E-11	rs62071596:44349169:T:C
17_44349234_C_T	17	44349234	T	0.1867	-0.0465	0.0083	2.24E-08	0.1904	0.1097	0.01715	1.58E-10	rs2696551:44349234:C:T
17_44349283_T_C	17	44349283	C	0.1921	-0.0479	0.0081	3.15E-09	0.1898	0.1105	0.01649	2.09E-11	rs2469944:44349283:T:C
17_44349290_C_G	17	44349290	G	0.1867	-0.0466	0.0083	2.03E-08	0.1905	0.1098	0.01715	1.55E-10	rs2696550:44349290:C:G
17_44349347_C_G	17	44349347	G	0.1921	-0.048	0.0081	3.10E-09	0.1898	0.1105	0.01649	2.09E-11	rs2469943:44349347:C:G
17_44349372_C_A	17	44349372	A	0.1861	-0.0461	0.0083	3.08E-08	0.1895	0.1135	0.01724	4.74E-11	rs2696549:44349372:C:A
17_44349380_C_G	17	44349380	G	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	17:44349380:C:G
17_44349736_C_T	17	44349736	T	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	rs2262140:44349736:C:T
17_44349744_A_G	17	44349744	G	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	rs2469941:44349744:A:G
17_44349761_A_AT	17	44349761	AT	0.1922	-0.0474	0.0081	5.40E-09	0.1898	0.1105	0.01649	2.09E-11	17:44349761:A:AT

17_44349867_G_A	17	44349867	A	0.2054	-0.0465	0.0078	2.01E-09	0.2111	0.11	0.01612	8.82E-12	rs2532330:44349867:G:A
17_44349899_G_A	17	44349899	A	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	rs2261016:44349899:G:A
17_44350090_G_A	17	44350090	A	0.2085	-0.0471	0.0078	1.29E-09	0.2156	0.1093	0.01611	1.18E-11	rs2532329:44350090:G:A
17_44350125_C_T	17	44350125	T	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	rs2668611:44350125:C:T
17_44350203_A_G	17	44350203	G	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	17:44350203:A:G
17_44350217_A_G	17	44350217	G	0.1921	-0.048	0.0081	3.05E-09	0.1898	0.1105	0.01649	2.09E-11	17:44350217:A:G
17_44350293_A_G	17	44350293	G	0.1874	-0.0455	0.0083	4.54E-08	0.1916	0.1129	0.01718	5.07E-11	rs2732711:44350293:A:G
17_44350296_ACC_A	17	44350296	A	0.1901	-0.0456	0.0082	2.84E-08	0.1851	0.111	0.01676	3.52E-11	rs66475798:44350296:ACC:A
17_44350310_G_A	17	44350310	A	0.1921	-0.048	0.0081	3.06E-09	0.1898	0.1105	0.01649	2.09E-11	rs2668614:44350310:G:A
17_44350387_A_G	17	44350387	G	0.1905	-0.0459	0.0082	1.79E-08	0.1857	0.1102	0.01673	4.44E-11	rs62071597:44350387:A:G
17_44350395_G_C	17	44350395	C	0.1894	-0.0459	0.0082	2.61E-08	0.1936	0.1105	0.01705	9.23E-11	rs2696547:44350395:G:C
17_44350460_A_G	17	44350460	G	0.1921	-0.048	0.0081	3.07E-09	0.1898	0.1105	0.01649	2.09E-11	17:44350460:A:G
17_44350511_A_G	17	44350511	G	0.1921	-0.048	0.0081	3.07E-09	0.1898	0.1105	0.01649	2.09E-11	rs2262144:44350511:A:G
17_44350527_T_A	17	44350527	A	0.1921	-0.048	0.0081	3.07E-09	0.1898	0.1105	0.01649	2.09E-11	rs2732710:44350527:T:A
17_44350662_G_C	17	44350662	C	0.1921	-0.048	0.0081	3.07E-09	0.1898	0.1105	0.01649	2.09E-11	17:44350662:G:C
17_44350919_A_C	17	44350919	C	0.2064	-0.0452	0.0078	5.71E-09	0.2125	0.1096	0.01611	1.02E-11	17:44350919:A:C
17_44351007_T_C	17	44351007	C	0.1921	-0.048	0.0081	3.08E-09	0.1898	0.1105	0.01649	2.09E-11	17:44351007:T:C
17_44351087_T_C	17	44351087	C	0.1899	-0.0454	0.0082	2.87E-08	0.1933	0.1132	0.01693	2.32E-11	17:44351087:T:C
17_44351249_C_A	17	44351249	A	0.1921	-0.048	0.0081	3.08E-09	0.1898	0.1105	0.01649	2.09E-11	17:44351249:C:A
17_44351285_A_G	17	44351285	G	0.2055	-0.0461	0.0078	2.87E-09	0.2107	0.1088	0.0161	1.38E-11	17:44351285:A:G
17_44351298_G_A	17	44351298	A	0.1894	-0.0457	0.0082	2.58E-08	0.1934	0.1154	0.01695	1.00E-11	17:44351298:G:A
17_44351387_C_T	17	44351387	T	0.2065	-0.0457	0.0078	3.95E-09	0.2123	0.1086	0.01611	1.56E-11	rs2732708:44351387:C:T
17_44351452_T_C	17	44351452	C	0.1924	-0.0478	0.0081	3.53E-09	0.1901	0.1105	0.01649	2.04E-11	17:44351452:T:C
17_44351533_A_G	17	44351533	G	0.208	-0.0452	0.0078	5.69E-09	0.2141	0.1098	0.0161	9.35E-12	rs2696542:44351533:A:G
17_44351578_T_C	17	44351578	C	0.1921	-0.048	0.0081	3.06E-09	0.1897	0.1106	0.01649	2.01E-11	17:44351578:T:C
17_44351600_C_T	17	44351600	T	0.1902	-0.0452	0.0082	3.26E-08	0.1939	0.1139	0.01691	1.65E-11	rs2732707:44351600:C:T
17_44351686_C_T	17	44351686	T	0.2071	-0.0463	0.0077	2.29E-09	0.2122	0.1094	0.01608	1.02E-11	rs2732706:44351686:C:T
17_44351731_T_G	17	44351731	G	0.1921	-0.048	0.0081	3.06E-09	0.1897	0.1106	0.01649	2.02E-11	rs2469940:44351731:T:G
17_44351739_G_A	17	44351739	A	0.1921	-0.048	0.0081	3.06E-09	0.1897	0.1106	0.01649	2.02E-11	rs2469939:44351739:G:A
17_44351743_G_A	17	44351743	A	0.1904	-0.0456	0.0082	2.44E-08	0.194	0.1123	0.01688	2.83E-11	rs2696541:44351743:G:A
17_44351858_T_G	17	44351858	G	0.1921	-0.048	0.0081	3.06E-09	0.1897	0.1106	0.01649	2.02E-11	17:44351858:T:G
17_44351929_T_G	17	44351929	G	0.2055	-0.046	0.0078	3.19E-09	0.212	0.1105	0.01612	7.14E-12	rs2732705:44351929:T:G
17_44352131_G_T	17	44352131	T	0.2094	-0.046	0.0078	3.05E-09	0.2224	0.1089	0.01611	1.35E-11	rs2668622:44352131:G:T
17_44352149_CTTTT_C	17	44352149	C	0.2027	-0.0458	0.0078	5.14E-09	0.2053	0.1055	0.01606	5.08E-11	17:44352149:CTTTT:C
17_44352361_C_T	17	44352361	T	0.2073	-0.0456	0.0078	4.07E-09	0.2147	0.1087	0.01612	1.50E-11	17:44352361:C:T
17_44352432_AT_A	17	44352432	A	0.1837	-0.0443	0.0084	1.41E-07	0.1876	0.1151	0.01736	3.27E-11	17:44352432:AT:A
17_44352621_A_G	17	44352621	G	0.2056	-0.0461	0.0078	2.96E-09	0.2134	0.1105	0.01611	7.07E-12	17:44352621:A:G
17_44352633_GT_G	17	44352633	G	0.205	-0.0452	0.0078	7.00E-09	0.2112	0.1106	0.01612	6.83E-12	17:44352633:GT:G
17_44352639_G_A	17	44352639	A	0.2057	-0.0462	0.0078	2.69E-09	0.2118	0.11	0.01611	8.79E-12	17:44352639:G:A
17_44352872_A_G	17	44352872	G	0.2052	-0.0458	0.0078	3.70E-09	0.2111	0.1086	0.01611	1.61E-11	17:44352872:A:G
17_44352970_C_A	17	44352970	A	0.192	-0.0478	0.0081	3.67E-09	0.1898	0.1107	0.01649	1.95E-11	17:44352970:C:A
17_44353114_T_C	17	44353114	C	0.192	-0.0478	0.0081	3.68E-09	0.1898	0.1106	0.01649	1.95E-11	rs2732704:44353114:T:C
17_44353175_T_C	17	44353175	C	0.192	-0.0478	0.0081	3.68E-09	0.1898	0.1106	0.01649	1.95E-11	rs2668626:44353175:T:C
17_44353206_T_C	17	44353206	C	0.192	-0.0478	0.0081	3.68E-09	0.1898	0.1106	0.01649	1.95E-11	rs2458217:44353206:T:C
17_44353260_AT_A	17	44353260	A	0.2018	-0.0452	0.0078	7.96E-09	0.2021	0.1058	0.01606	4.58E-11	17:44353260:AT:A
17_44353262_T_C	17	44353262	C	0.2016	-0.0459	0.0078	3.81E-09	0.2021	0.1058	0.01606	4.58E-11	17:44353262:T:C
17_44353318_G_A	17	44353318	A	0.1921	-0.048	0.0081	3.17E-09	0.19	0.1108	0.01649	1.87E-11	17:44353318:G:A
17_44353320_G_A	17	44353320	A	0.192	-0.0478	0.0081	3.67E-09	0.1898	0.1106	0.01649	1.95E-11	17:44353320:G:A
17_44353343_G_A	17	44353343	A	0.192	-0.0478	0.0081	3.67E-09	0.1898	0.1106	0.01649	1.95E-11	17:44353343:G:A
17_44353344_C_A	17	44353344	A	0.192	-0.0478	0.0081	3.67E-09	0.1898	0.1106	0.01649	1.95E-11	17:44353344:C:A
17_44353414_A_G	17	44353414	G	0.2061	-0.0455	0.0078	4.73E-09	0.2137	0.1112	0.01611	5.20E-12	rs36050210:44353414:A:G
17_44353505_C_T	17	44353505	T	0.1921	-0.0475	0.0081	4.31E-09	0.19	0.1102	0.01648	2.22E-11	17:44353505:C:T
17_44353693_T_C	17	44353693	C	0.2101	-0.0462	0.0077	2.40E-09	0.2178	0.1061	0.01609	4.32E-11	rs2668627:44353693:T:C
17_44353728_T_G	17	44353728	G	0.2079	-0.0466	0.0078	1.97E-09	0.2164	0.1094	0.01612	1.13E-11	17:44353728:T:G
17_44353885_G_A	17	44353885	A	0.2041	-0.0463	0.0078	2.68E-09	0.2139	0.1099	0.01612	9.18E-12	17:44353885:G:A

17_44354103_A_G	17	44354103	G	0.2065	-0.0458	0.0078	3.52E-09	0.2155	0.1104	0.0161	6.96E-12	17:44354103:A:G
17_44354231_A_G	17	44354231	G	0.206	-0.0461	0.0078	3.13E-09	0.2148	0.1074	0.01614	2.88E-11	17:44354231:A:G
17_44354530_T_A	17	44354530	A	0.1913	-0.0482	0.0081	3.09E-09	0.1898	0.1105	0.01654	2.39E-11	17:44354530:T:A
17_44354549_C_G	17	44354549	G	0.2131	-0.0462	0.0078	2.48E-09	0.2245	0.1048	0.01611	7.77E-11	17:44354549:C:G
17_44354569_TA_T	17	44354569	T	0.1701	-0.0508	0.0088	9.36E-09	0.1655	0.1232	0.01796	7.02E-12	rs139718809:44354569:TA:T
17_44354587_A_G	17	44354587	G	0.1917	-0.0479	0.0081	3.44E-09	0.1905	0.1105	0.01653	2.29E-11	17:44354587:A:G
17_44354904_T_C	17	44354904	T	0.1599	-0.0595	0.0093	1.42E-10	0.1549	0.1111	0.01891	4.20E-09	rs2732699:44354904:T:C
17_44355130_A_G	17	44355130	G	0.1947	-0.0482	0.0081	2.47E-09	0.1966	0.1119	0.01649	1.17E-11	rs2696535:44355130:A:G
17_44355138_G_A	17	44355138	A	0.1859	-0.0473	0.0083	1.08E-08	0.183	0.1137	0.01685	1.54E-11	17:44355138:G:A
17_44355162_A_G	17	44355162	G	0.2007	-0.0463	0.0079	4.46E-09	0.2054	0.1084	0.01633	3.18E-11	rs112758891:44355162:A:G
17_44355173_T_C	17	44355173	C	0.1837	-0.0463	0.0083	2.75E-08	0.1778	0.1114	0.01707	6.66E-11	rs111446248:44355173:T:C
17_44355284_G_A	17	44355284	A	0.1899	-0.0474	0.0082	6.27E-09	0.1866	0.1112	0.01659	2.04E-11	rs112243618:44355284:G:A
17_44355303_T_C	17	44355303	C	0.204	-0.0463	0.0078	2.85E-09	0.2103	0.1095	0.01617	1.26E-11	rs112082260:44355303:T:C
17_44355304_G_T	17	44355304	T	0.1901	-0.0467	0.0082	1.19E-08	0.1949	0.1114	0.01689	4.25E-11	rs371894855:44355304:G:T
17_44355315_AT_A	17	44355315	A	0.2041	-0.0456	0.0078	5.80E-09	0.2103	0.1095	0.01617	1.27E-11	17:44355315:AT:A
17_44355343_T_C	17	44355343	C	0.2051	-0.0458	0.0078	4.26E-09	0.2118	0.1094	0.01615	1.25E-11	rs2696533:44355343:T:C
17_44355376_G_A	17	44355376	A	0.1903	-0.0477	0.0081	4.78E-09	0.1873	0.1115	0.01658	1.71E-11	17:44355376:G:A
17_44355516_T_C	17	44355516	C	0.1894	-0.0488	0.0082	2.43E-09	0.186	0.1108	0.01663	2.67E-11	17:44355516:T:C
17_44355532_G_A	17	44355532	A	0.1894	-0.0488	0.0082	2.48E-09	0.186	0.1107	0.01663	2.81E-11	17:44355532:G:A
17_44355602_A_G	17	44355602	G	0.2029	-0.0463	0.0078	3.26E-09	0.2084	0.1103	0.0162	9.91E-12	rs2696532:44355602:A:G
17_44355634_C_A	17	44355634	A	0.1101	-0.0554	0.012	3.79E-06	0.1037	0.1355	0.02449	3.14E-08	rs2696531:44355634:C:A
17_44355714_A_G	17	44355714	G	0.2044	-0.0465	0.0078	2.26E-09	0.2097	0.1101	0.01612	8.36E-12	rs2696530:44355714:A:G
17_44355726_T_A	17	44355726	A	0.2046	-0.0458	0.0078	3.76E-09	0.2095	0.1097	0.01612	1.01E-11	rs74807476:44355726:T:A
17_44355750_C_T	17	44355750	T	0.2038	-0.0464	0.0078	2.71E-09	0.2102	0.1094	0.01618	1.37E-11	rs113677423:44355750:C:T
17_44356098_A_C	17	44356098	C	0.1947	-0.0481	0.0081	2.59E-09	0.1966	0.1119	0.01649	1.17E-11	17:44356098:A:C
17_44356320_C_T	17	44356320	T	0.1938	-0.0478	0.0081	3.56E-09	0.1949	0.1104	0.01654	2.43E-11	rs2696528:44356320:C:T
17_44356394_T_G	17	44356394	G	0.1854	-0.0488	0.0083	4.63E-09	0.1828	0.1119	0.0169	3.58E-11	17:44356394:T:G
17_44356410_T_C	17	44356410	C	0.1854	-0.0488	0.0083	4.63E-09	0.1828	0.1119	0.0169	3.58E-11	rs74390346:44356410:T:C
17_44356433_G_T	17	44356433	T	0.1938	-0.0484	0.0081	2.37E-09	0.1953	0.1112	0.01652	1.67E-11	rs2696527:44356433:G:T
17_44356436_T_C	17	44356436	C	0.1855	-0.0489	0.0083	3.94E-09	0.183	0.1112	0.01684	4.10E-11	rs76167437:44356436:T:C
17_44356637_C_T	17	44356637	T	0.1944	-0.0481	0.0081	2.72E-09	0.1963	0.1117	0.01651	1.31E-11	rs2696525:44356637:C:T
17_44356682_G_A	17	44356682	A	0.1945	-0.0481	0.0081	2.56E-09	0.1964	0.112	0.0165	1.12E-11	17:44356682:G:A
17_44356694_T_C	17	44356694	C	0.1901	-0.048	0.0082	3.89E-09	0.1872	0.1116	0.01659	1.71E-11	rs111912558:44356694:T:C
17_44356746_T_C	17	44356746	C	0.1904	-0.0476	0.0081	5.20E-09	0.1875	0.1111	0.01657	1.95E-11	rs113896715:44356746:T:C
17_44356770_G_A	17	44356770	A	0.1946	-0.0481	0.0081	2.62E-09	0.1966	0.1119	0.01649	1.14E-11	17:44356770:G:A
17_44356793_A_G	17	44356793	G	0.2039	-0.0463	0.0078	2.88E-09	0.2102	0.1095	0.01617	1.27E-11	rs2696524:44356793:A:G
17_44356890_T_C	17	44356890	C	0.204	-0.0462	0.0078	3.13E-09	0.2103	0.1095	0.01617	1.26E-11	rs2696522:44356890:T:C
17_44356949_T_C	17	44356949	C	0.204	-0.0462	0.0078	3.19E-09	0.2103	0.1095	0.01617	1.26E-11	17:44356949:T:C
17_44357172_C_T	17	44357172	T	0.1902	-0.0475	0.0082	5.61E-09	0.1873	0.1111	0.01659	2.10E-11	rs113130019:44357172:C:T
17_44357198_G_A	17	44357198	A	0.1904	-0.0476	0.0081	5.25E-09	0.1875	0.1111	0.01657	1.96E-11	rs80296410:44357198:G:A
17_44357297_G_T	17	44357297	T	0.204	-0.0462	0.0078	3.14E-09	0.2103	0.1094	0.01617	1.30E-11	17:44357297:G:T
17_44357351_T_C	17	44357351	C	0.204	-0.0462	0.0078	3.14E-09	0.2103	0.1094	0.01617	1.30E-11	rs17665188:44357351:T:C
17_44357360_G_A	17	44357360	A	0.1903	-0.0477	0.0082	5.05E-09	0.1874	0.1107	0.01658	2.46E-11	rs75033119:44357360:G:A
17_44357392_C_A	17	44357392	A	0.195	-0.0484	0.0081	2.01E-09	0.1967	0.1112	0.01649	1.52E-11	rs112254607:44357392:C:A
17_44357412_TC_T	17	44357412	T	0.2044	-0.0458	0.0078	5.02E-09	0.2104	0.1088	0.01617	1.71E-11	17:44357412:TC:T
17_44357453_G_T	17	44357453	T	0.2044	-0.0464	0.0078	2.67E-09	0.2104	0.1088	0.01617	1.71E-11	rs74839514:44357453:G:T
17_44357562_C_T	17	44357562	T	0.1903	-0.0474	0.0082	6.15E-09	0.1873	0.1108	0.01657	2.27E-11	rs112750270:44357562:C:T
17_44357654_C_T	17	44357654	T	0.1718	-0.0494	0.0088	1.94E-08	0.1647	0.1206	0.01805	2.34E-11	17:44357654:C:T
17_44357655_G_C	17	44357655	C	0.1718	-0.0494	0.0088	1.92E-08	0.1647	0.1206	0.01805	2.34E-11	17:44357655:G:C
17_44357777_C_T	17	44357777	T	0.2044	-0.0465	0.0078	2.52E-09	0.2104	0.1088	0.01617	1.72E-11	17:44357777:C:T
17_44357796_C_T	17	44357796	T	0.1893	-0.048	0.0082	4.54E-09	0.1855	0.1117	0.01664	1.88E-11	17:44357796:C:T
17_44357885_T_G	17	44357885	G	0.1941	-0.0481	0.0081	2.74E-09	0.1901	0.1134	0.01654	7.12E-12	rs2696518:44357885:T:G
17_44358107_G_T	17	44358107	T	0.2061	-0.0454	0.0078	6.00E-09	0.211	0.1075	0.01617	2.89E-11	rs2696516:44358107:G:T
17_44358109_A_T	17	44358109	T	0.2061	-0.0454	0.0078	6.00E-09	0.211	0.1075	0.01617	2.89E-11	rs2696515:44358109:A:T
17_44358146_G_A	17	44358146	A	0.1959	-0.0484	0.0081	1.91E-09	0.1975	0.1118	0.01647	1.13E-11	17:44358146:G:A

17_44358347_TAG_T	17	44358347	T	0.1828	-0.0455	0.0084	6.75E-08	0.1809	0.113	0.01712	4.08E-11	rs149535063:44358347:TAG:T
17_44358428_G_A	17	44358428	A	0.2035	-0.046	0.0078	3.92E-09	0.2081	0.1093	0.0162	1.51E-11	rs2532322:44358428:G:A
17_44358561_G_A	17	44358561	A	0.2075	-0.0472	0.0077	1.05E-09	0.2101	0.1156	0.01597	4.50E-13	17:44358561:G:A
17_44358562_C_T	17	44358562	T	0.2075	-0.0472	0.0077	1.05E-09	0.2101	0.1156	0.01597	4.50E-13	17:44358562:C:T
17_44358721_C_T	17	44358721	T	0.1319	-0.056	0.0106	1.15E-07	0.1342	0.1216	0.02211	3.76E-08	17:44358721:C:T
17_44358811_G_A	17	44358811	A	0.1836	-0.0445	0.0084	1.06E-07	0.1785	0.1096	0.01717	1.71E-10	17:44358811:G:A
17_44358812_G_A	17	44358812	A	0.1836	-0.0445	0.0084	1.06E-07	0.1785	0.1096	0.01717	1.71E-10	rs374242426:44358812:G:A
17_44359499_C_T	17	44359499	T	0.2045	-0.046	0.0078	3.79E-09	0.2106	0.1089	0.01617	1.61E-11	rs79523636:44359499:C:T
17_44359663_G_T	17	44359663	T	0.1957	-0.0482	0.0081	2.16E-09	0.1983	0.1109	0.01647	1.67E-11	rs36123991:44359663:G:T
17_44359779_G_T	17	44359779	T	0.209	-0.0437	0.0078	2.05E-08	0.2139	0.1075	0.01615	2.76E-11	rs192856660:44359779:G:T
17_44359783_G_T	17	44359783	T	0.2045	-0.0454	0.0078	6.79E-09	0.2079	0.1075	0.01619	3.18E-11	rs184837332:44359783:G:T
17_44360071_A_C	17	44360071	C	0.1913	-0.048	0.0081	3.69E-09	0.1897	0.1105	0.01654	2.42E-11	17:44360071:A:C
17_44360154_AAG_A	17	44360154	A	0.1448	-0.0487	0.01	1.05E-06	0.1416	0.1329	0.02024	5.17E-11	rs200019631:44360154:AAG:A
17_44360168_C_G	17	44360168	G	0.1913	-0.048	0.0081	3.69E-09	0.1897	0.1105	0.01655	2.41E-11	17:44360168:C:G
17_44360349_A_G	17	44360349	G	0.2008	-0.046	0.0079	4.59E-09	0.2035	0.1093	0.01623	1.68E-11	rs373695612:44360349:A:G
17_44360580_C_G	17	44360580	G	0.1952	-0.0486	0.0081	1.77E-09	0.1968	0.1112	0.01649	1.54E-11	17:44360580:C:G
17_44360760_C_T	17	44360760	T	0.1904	-0.0475	0.0082	5.66E-09	0.1874	0.111	0.01657	2.11E-11	17:44360760:C:T
17_44360941_T_C	17	44360941	C	0.1917	-0.0471	0.0082	7.63E-09	0.1936	0.113	0.01665	1.15E-11	17:44360941:T:C
17_44361007_T_G	17	44361007	G	0.1975	-0.0471	0.008	3.92E-09	0.1998	0.1115	0.01641	1.10E-11	17:44361007:T:G
17_44361075_C_G	17	44361075	G	0.2083	-0.0461	0.0078	3.16E-09	0.218	0.1036	0.01614	1.38E-10	17:44361075:C:G
17_44361129_G_A	17	44361129	A	0.1912	-0.0479	0.0081	3.85E-09	0.1897	0.1105	0.01655	2.42E-11	17:44361129:G:A
17_44361147_A_G	17	44361147	G	0.1912	-0.0479	0.0081	3.85E-09	0.1897	0.1105	0.01655	2.42E-11	17:44361147:A:G
17_44361337_G_T	17	44361337	T	0.2069	-0.047	0.0078	1.62E-09	0.213	0.1052	0.01616	7.61E-11	17:44361337:G:T
17_44361383_T_C	17	44361383	C	0.201	-0.0476	0.0079	1.81E-09	0.2051	0.1099	0.01626	1.39E-11	rs2458218:44361383:T:C
17_44361861_T_G	17	44361861	G	0.1917	-0.0465	0.0081	1.01E-08	0.1893	0.1116	0.01652	1.41E-11	17:44361861:T:G
17_44361869_G_C	17	44361869	C	0.1917	-0.0465	0.0081	9.95E-09	0.1893	0.1116	0.01652	1.41E-11	17:44361869:G:C
17_44362355_A_G	17	44362355	G	0.2004	-0.0461	0.0079	4.45E-09	0.2034	0.1083	0.01623	2.53E-11	17:44362355:A:G
17_44362552_C_T	17	44362552	T	0.2057	-0.046	0.0078	3.55E-09	0.2167	0.109	0.01615	1.49E-11	17:44362552:C:T
17_44362633_G_T	17	44362633	T	0.2004	-0.0461	0.0079	5.94E-09	0.205	0.1102	0.01634	1.50E-11	17:44362633:G:T
17_44362865_A_C	17	44362865	C	0.2051	-0.0462	0.0078	3.11E-09	0.212	0.1089	0.01615	1.54E-11	17:44362865:A:C
17_44363632_A_C	17	44363632	C	0.191	-0.0458	0.0082	1.89E-08	0.1869	0.1097	0.01673	5.49E-11	17:44363632:A:C
17_44363885_G_T	17	44363885	T	0.1963	-0.0486	0.0081	1.61E-09	0.1976	0.1093	0.01639	2.58E-11	17:44363885:G:T
17_44363929_C_T	17	44363929	T	0.2084	-0.0464	0.0078	2.74E-09	0.2135	0.1061	0.01609	4.26E-11	17:44363929:C:T
17_44364019_GA_G	17	44364019	G	0.2084	-0.0451	0.0078	7.58E-09	0.2146	0.1056	0.01607	5.12E-11	17:44364019:GA:G
17_44364056_T_C	17	44364056	C	0.1919	-0.0478	0.0081	4.08E-09	0.1899	0.1082	0.01647	5.04E-11	17:44364056:T:C
17_44364209_C_T	17	44364209	T	0.1917	-0.0479	0.0081	4.02E-09	0.1897	0.1085	0.01648	4.71E-11	17:44364209:C:T
17_44364298_G_C	17	44364298	C	0.1919	-0.0478	0.0081	4.09E-09	0.1899	0.1082	0.01647	5.04E-11	17:44364298:G:C
17_44364335_G_A	17	44364335	A	0.1685	-0.0492	0.0089	3.14E-08	0.1682	0.1067	0.01812	3.93E-09	17:44364335:G:A
17_44364481_C_G	17	44364481	G	0.1784	-0.0509	0.0085	2.55E-09	0.1776	0.1122	0.01734	9.57E-11	17:44364481:C:G
17_44364519_C_G	17	44364519	G	0.212	-0.0439	0.0078	1.62E-08	0.2184	0.104	0.01606	9.49E-11	17:44364519:C:G
17_44364538_G_C	17	44364538	C	0.1919	-0.0478	0.0081	4.09E-09	0.1899	0.1082	0.01647	5.04E-11	17:44364538:G:C
17_44364584_C_T	17	44364584	T	0.1901	-0.0489	0.0082	2.91E-09	0.1928	0.112	0.01676	2.35E-11	17:44364584:C:T
17_44364649_C_T	17	44364649	T	0.207	-0.0463	0.0078	2.68E-09	0.2128	0.1074	0.01607	2.36E-11	17:44364649:C:T
17_44364699_C_T	17	44364699	T	0.207	-0.0459	0.0078	3.85E-09	0.2124	0.1075	0.01607	2.27E-11	17:44364699:C:T
17_44364829_A_C	17	44364829	C	0.2074	-0.0459	0.0078	3.83E-09	0.213	0.1064	0.01609	3.77E-11	rs2732613:44364829:A:C
17_44364864_C_T	17	44364864	T	0.2053	-0.046	0.0078	3.46E-09	0.211	0.1062	0.01608	3.97E-11	rs2696495:44364864:C:T
17_44364958_G_A	17	44364958	A	0.1919	-0.0478	0.0081	4.10E-09	0.1899	0.1082	0.01647	5.04E-11	17:44364958:G:A
17_44365000_C_G	17	44365000	G	0.2046	-0.0465	0.0078	2.59E-09	0.21	0.1057	0.0161	5.07E-11	rs2696494:44365000:C:G
17_44365050_G_A	17	44365050	A	0.206	-0.0462	0.0078	3.10E-09	0.2114	0.106	0.01608	4.40E-11	17:44365050:G:A
17_44365369_T_C	17	44365369	C	0.2023	-0.0461	0.0078	4.00E-09	0.2055	0.1073	0.01614	2.94E-11	17:44365369:T:C
17_44365374_C_T	17	44365374	T	0.2023	-0.0461	0.0078	4.00E-09	0.2055	0.1073	0.01614	2.94E-11	17:44365374:C:T
17_44365487_A_C	17	44365487	C	0.195	-0.0482	0.0081	2.46E-09	0.1954	0.1093	0.01643	2.90E-11	17:44365487:A:C
17_44365897_C_T	17	44365897	T	0.1964	-0.0482	0.0081	2.19E-09	0.1973	0.1095	0.0164	2.37E-11	17:44365897:C:T
17_44365980_A_T	17	44365980	T	0.2205	-0.0442	0.0077	1.07E-08	0.2295	0.1019	0.01598	1.81E-10	17:44365980:A:T
17_44365981_A_T	17	44365981	T	0.2147	-0.0448	0.0078	7.87E-09	0.222	0.105	0.01601	5.59E-11	17:44365981:A:T

17_44366315_T_C	17	44366315	C	0.2062	-0.0463	0.0078	2.92E-09	0.2119	0.1063	0.01609	3.99E-11	17:44366315:T:C
17_44366410_T_C	17	44366410	C	0.2061	-0.0461	0.0078	3.48E-09	0.2109	0.1074	0.01609	2.51E-11	17:44366410:T:C
17_44366624_C_CTA	17	44366624	CTA	0.1268	-0.0624	0.0108	8.79E-09	0.1203	0.1167	0.0221	1.28E-07	17:44366624:C:CTA
17_44366665_C_T	17	44366665	T	0.2062	-0.046	0.0078	3.76E-09	0.213	0.1074	0.01608	2.41E-11	17:44366665:C:T
17_44367288_G_C	17	44367288	C	0.2065	-0.0462	0.0078	3.11E-09	0.2114	0.108	0.01607	1.81E-11	17:44367288:G:C
17_44367296_G_A	17	44367296	A	0.1956	-0.0482	0.0081	2.46E-09	0.1969	0.1088	0.01642	3.41E-11	17:44367296:G:A
17_44367453_G_C	17	44367453	C	0.205	-0.0459	0.0078	4.03E-09	0.2116	0.1067	0.0161	3.33E-11	17:44367453:G:C
17_44367588_TG_T	17	44367588	T	0.1978	-0.0467	0.008	5.00E-09	0.1988	0.1099	0.01636	1.89E-11	17:44367588:TG:T
17_44367939_G_A	17	44367939	A	0.2011	-0.0473	0.0079	2.11E-09	0.2059	0.1047	0.01629	1.31E-10	17:44367939:G:A
17_44368055_G_C	17	44368055	C	0.2037	-0.0456	0.0078	5.44E-09	0.2098	0.1057	0.01613	5.77E-11	17:44368055:G:C
17_44368212_C_A	17	44368212	A	0.1919	-0.0478	0.0081	4.02E-09	0.1899	0.1083	0.01647	4.80E-11	rs2957297:44368212:C:A
17_44368266_T_TA	17	44368266	TA	0.202	-0.0452	0.0079	9.88E-09	0.2051	0.1102	0.01624	1.13E-11	17:44368266:T:TA
17_44368404_C_T	17	44368404	T	0.2043	-0.0462	0.0078	3.26E-09	0.2084	0.1075	0.01611	2.48E-11	17:44368404:C:T
17_44368431_C_T	17	44368431	T	0.2043	-0.0468	0.0078	2.33E-09	0.2079	0.1069	0.01612	3.33E-11	rs62073178:44368431:C:T
17_44368926_C_A	17	44368926	A	0.2276	-0.0411	0.0077	8.28E-08	0.2287	0.09644	0.01588	1.25E-09	rs2532424:44368926:C:A
17_44368946_A_C	17	44368946	C	0.2024	-0.0435	0.008	5.64E-08	0.2033	0.1049	0.01633	1.36E-10	17:44368946:A:C
17_44369214_A_C	17	44369214	C	0.2041	-0.046	0.0078	4.24E-09	0.2128	0.1048	0.01612	8.07E-11	17:44369214:A:C
17_44369224_A_G	17	44369224	G	0.2041	-0.0459	0.0078	4.34E-09	0.213	0.1047	0.01612	8.23E-11	17:44369224:A:G
17_44369320_C_T	17	44369320	T	0.2036	-0.0464	0.0078	3.34E-09	0.2128	0.1046	0.01617	9.98E-11	17:44369320:C:T
17_44369585_C_A	17	44369585	A	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369585:C:A
17_44369590_T_C	17	44369590	C	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369590:T:C
17_44369591_G_A	17	44369591	A	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369591:G:A
17_44369595_A_G	17	44369595	G	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369595:A:G
17_44369596_A_G	17	44369596	G	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369596:A:G
17_44369605_T_G	17	44369605	G	0.2154	-0.0456	0.0086	1.15E-07	0.2289	0.1095	0.018	1.17E-09	17:44369605:T:G
17_44374710_A_G	17	44374710	A	0.2663	-0.0364	0.0077	2.14E-06	0.2818	0.1004	0.01583	2.25E-10	rs201223330:44374710:A:G
17_44388912_G_C	17	44388912	C	0.2055	-0.044	0.0087	3.73E-07	0.2108	0.1112	0.01792	5.48E-10	rs372454544:44388912:G:C
17_44393298_T_TC	17	44393298	TC	0.195	-0.0443	0.008	3.22E-08	0.1926	0.1063	0.01641	9.25E-11	17:44393298:T:TC
17_44408004_A_C	17	44408004	C	0.1648	-0.0481	0.0091	1.09E-07	0.169	0.1264	0.01875	1.59E-11	17:44408004:A:C
17_44408485_T_C	17	44408485	C	0.1272	-0.0495	0.0108	4.51E-06	0.1276	0.1304	0.02201	3.14E-09	17:44408485:T:C
17_44412076_A_G	17	44412076	G	0.2006	-0.0442	0.0079	1.93E-08	0.2004	0.1068	0.01625	4.93E-11	rs369158541:44412076:A:G
17_44412252_C_T	17	44412252	C	0.2837	-0.0342	0.0076	7.10E-06	0.3027	0.0943	0.01576	2.19E-09	rs140997625:44412252:C:T
17_44458840_C_CT	17	44458840	CT	0.1538	-0.0482	0.0095	4.14E-07	0.1497	0.121	0.01968	7.72E-10	17:44458840:C:CT
17_44459139_TA_T	17	44459139	T	0.1868	-0.0452	0.0082	4.14E-08	0.1814	0.11	0.01684	6.56E-11	17:44459139:TA:T
17_44477277_C_T	17	44477277	T	0.2195	-0.0435	0.0082	1.15E-07	0.2299	0.09706	0.01707	1.30E-08	rs142948617:44477277:C:T
17_44482245_AAAAT_A	17	44482245	A	0.3647	-0.0386	0.0074	1.85E-07	0.3681	0.09229	0.01528	1.56E-09	rs376997656:44482245:AAAAT:A
17_44487793_G_C	17	44487793	C	0.2104	-0.0452	0.0077	4.58E-09	0.2119	0.1141	0.01593	8.07E-13	17:44487793:G:C
17_44487794_A_T	17	44487794	T	0.2104	-0.0452	0.0077	4.58E-09	0.2119	0.1141	0.01593	8.07E-13	17:44487794:A:T
17_44499795_T_C	17	44499795	C	0.2909	-0.0393	0.0077	3.92E-07	0.306	0.08861	0.01616	4.15E-08	rs145487105:44499795:T:C
17_44500095_A_G	17	44500095	G	0.2909	-0.0393	0.0077	3.97E-07	0.306	0.08863	0.01616	4.13E-08	rs149197001:44500095:A:G
17_44514788_C_T	17	44514788	T	0.2468	-0.0456	0.0082	2.43E-08	0.2603	0.09159	0.01706	7.91E-08	rs142045106:44514788:C:T
17_44517766_T_A	17	44517766	A	0.2377	-0.047	0.0083	1.34E-08	0.2507	0.09775	0.01714	1.17E-08	17:44517766:T:A
17_44527102_T_C	17	44527102	C	0.2816	-0.0369	0.0079	3.11E-06	0.2959	0.09495	0.01651	8.89E-09	rs138033946:44527102:T:C
17_44563656_G_A	17	44563656	A	0.2833	-0.0392	0.0078	5.51E-07	0.2972	0.08946	0.01634	4.34E-08	rs375876675:44563656:G:A
17_44568241_CT_C	17	44568241	C	0.2137	-0.046	0.0078	3.86E-09	0.2162	0.1122	0.01606	2.82E-12	17:44568241:CT:C
17_44574285_A_G	17	44574285	G	0.2558	-0.0448	0.0083	6.30E-08	0.2558	0.1036	0.01714	1.48E-09	17:44574285:A:G
17_44574701_ATTTG_A	17	44574701	A	0.186	-0.0457	0.0088	1.88E-07	0.1868	0.1158	0.01794	1.06E-10	rs200194382:44574701:ATTTG:A
17_44582284_T_G	17	44582284	G	0.2547	-0.0392	0.0077	3.75E-07	0.2675	0.0881	0.01598	3.52E-08	rs145711463:44582284:T:G
17_44611782_T_C	17	44611782	C	0.1862	-0.0471	0.0087	5.29E-08	0.1907	0.1194	0.01777	1.80E-11	rs369234167:44611782:T:C
17_44617964_TA_T	17	44617964	T	0.1498	-0.0487	0.0097	5.36E-07	0.1446	0.1181	0.01981	2.48E-09	17:44617964:TA:T
17_44625866_A_C	17	44625866	C	0.2039	-0.0432	0.0082	1.24E-07	0.214	0.1142	0.01691	1.44E-11	rs199913382:44625866:A:C
17_44630070_G_GA	17	44630070	GA	0.1951	-0.045	0.008	2.19E-08	0.194	0.1037	0.01654	3.65E-10	rs201101030:44630070:G:GA
17_44633053_C_A	17	44633053	C	0.2274	-0.0368	0.0077	1.89E-06	0.2241	0.1112	0.01588	2.56E-12	rs202076405:44633053:C:A
17_44633053_C_T	17	44633053	T	0.1944	-0.0472	0.0081	5.30E-09	0.1921	0.1146	0.01658	4.85E-12	rs202076405:44633053:C:T
17_44633530_G_C	17	44633530	G	0.4227	-0.0218	0.0072	0.002532	0.4264	0.09048	0.01512	2.19E-09	rs142967716:44633530:G:C

17_44679414_G_T	17	44679414	G	0.3978	-0.0228	0.0074	0.002046	0.3976	0.09104	0.01558	5.14E-09	rs138981448:44679414:G:T
17_44690708_G_A	17	44690708	A	0.1816	-0.0413	0.0085	1.24E-06	0.1851	0.1164	0.01774	5.36E-11	rs140288713:44690708:G:A
17_44699851_G_A	17	44699851	A	0.1932	-0.0401	0.0081	7.24E-07	0.1919	0.1118	0.01678	2.72E-11	rs116956554:44699851:G:A
17_44705517_C_CA	17	44705517	C	0.2173	-0.0338	0.0078	0.0000162	0.217	0.1006	0.01624	6.03E-10	rs151062946:44705517:C:CA
17_44708736_A_T	17	44708736	T	0.2216	-0.0339	0.0077	0.00001072	0.2192	0.1029	0.01606	1.48E-10	rs369268849:44708736:A:T
17_44734604_CAAGTGTA_(	17	44734604	C	0.1971	-0.042	0.008	1.59E-07	0.1949	0.1061	0.01647	1.17E-10	17:44734604:CAAGTGTA:C
17_44736722_CCCTT_C	17	44736722	CCCTT	0.2239	-0.0344	0.0076	6.01E-06	0.2249	0.0985	0.01579	4.38E-10	rs145281367:44736722:CCCTT:C
17_44753350_A_G	17	44753350	A	0.258	-0.033	0.0077	0.00001741	0.2566	0.091	0.01607	1.49E-08	rs117300236:44753350:A:G
17_44753643_G_T	17	44753643	G	0.2414	-0.0331	0.0073	6.26E-06	0.2438	0.09605	0.0153	3.40E-10	rs374952396:44753643:G:T
17_44753645_C_G	17	44753645	C	0.2414	-0.0331	0.0073	6.26E-06	0.2438	0.09605	0.0153	3.40E-10	rs369332489:44753645:C:G
17_44755729_A_C	17	44755729	C	0.1984	-0.0409	0.0078	1.76E-07	0.1964	0.1093	0.01626	1.81E-11	rs141783865:44755729:A:C
17_44757058_C_CA	17	44757058	CA	0.2215	-0.0436	0.0082	8.97E-08	0.2151	0.09921	0.01679	3.47E-09	17:44757058:C:CA
17_44759766_G_A	17	44759766	A	0.1408	-0.0562	0.01	1.96E-08	0.1411	0.1478	0.02089	1.53E-12	17:44759766:G:A
17_44762252_A_G	17	44762252	G	0.1991	-0.0403	0.0078	2.41E-07	0.1967	0.1081	0.01621	2.60E-11	17:44762252:A:G
17_44762589_G_A	17	44762589	A	0.231	-0.0327	0.0074	9.02E-06	0.2292	0.09868	0.0154	1.46E-10	rs77819282:44762589:G:A
17_44764775_A_C	17	44764775	C	0.2014	-0.0361	0.008	6.31E-06	0.1974	0.09893	0.01669	3.05E-09	rs199460:44764775:A:C
17_44773783_A_G	17	44773783	A	0.2033	-0.0383	0.0077	7.19E-07	0.2006	0.1065	0.0161	3.62E-11	17:44773783:A:G
17_44781030_G_C	17	44781030	C	0.1919	-0.0414	0.008	2.31E-07	0.1872	0.1072	0.01653	8.88E-11	17:44781030:G:C
17_44781143_C_A	17	44781143	C	0.234	-0.0312	0.0073	0.00002069	0.2322	0.09578	0.0153	3.86E-10	17:44781143:C:A
17_44782224_A_AGT	17	44782224	AGT	0.1938	-0.0421	0.0082	2.36E-07	0.1909	0.1093	0.01665	5.26E-11	rs146122400:44782224:A:AGT
17_44786336_T_A	17	44786336	A	0.2316	-0.0328	0.0073	7.91E-06	0.2298	0.09742	0.01533	2.09E-10	rs199437:44786336:T:A
17_44787312_C_T	17	44787312	T	0.2003	-0.0405	0.0078	1.74E-07	0.1974	0.1083	0.01614	1.96E-11	rs1378358:44787312:C:T
17_44787313_G_C	17	44787313	C	0.2001	-0.0401	0.0078	2.30E-07	0.1973	0.1081	0.01614	2.09E-11	rs538628:44787313:G:C
17_44788310_G_A	17	44788310	A	0.2316	-0.0327	0.0073	8.27E-06	0.2298	0.09792	0.01533	1.68E-10	rs183211:44788310:G:A
17_44789285_A_G	17	44789285	G	0.2316	-0.0326	0.0073	8.46E-06	0.2298	0.09717	0.01533	2.32E-10	rs199436:44789285:A:G
17_44790203_A_G	17	44790203	G	0.2002	-0.0399	0.0078	2.63E-07	0.1973	0.1076	0.01614	2.59E-11	rs169201:44790203:A:G
17_44791643_G_A	17	44791643	A	0.2316	-0.0327	0.0073	8.20E-06	0.2299	0.0975	0.01533	2.02E-10	rs199438:44791643:G:A
17_44793503_A_G	17	44793503	G	0.2001	-0.0401	0.0078	2.26E-07	0.1974	0.108	0.01614	2.20E-11	rs199439:44793503:A:G
17_44793627_C_CT	17	44793627	C	0.2988	-0.0332	0.0073	5.62E-06	0.2963	0.1079	0.01521	1.31E-12	rs56755526:44793627:C:CT
17_44795234_A_G	17	44795234	G	0.2317	-0.0326	0.0073	8.56E-06	0.23	0.09795	0.01533	1.66E-10	rs142167:44795234:A:G
17_44795469_C_T	17	44795469	T	0.2	-0.0403	0.0078	2.07E-07	0.1973	0.1084	0.01615	1.94E-11	rs199457:44795469:C:T
17_44797919_C_T	17	44797919	T	0.2001	-0.0407	0.0078	1.54E-07	0.1974	0.1083	0.01615	1.94E-11	rs199456:44797919:C:T
17_44799216_C_T	17	44799216	C	0.234	-0.0312	0.0073	0.00001934	0.2325	0.09604	0.01529	3.32E-10	rs199455:44799216:C:T
17_44800046_G_A	17	44800046	G	0.2689	-0.0274	0.007	0.00008646	0.2646	0.09365	0.01464	1.57E-10	rs7224296:44800046:G:A
17_44800110_G_A	17	44800110	G	0.2333	-0.0313	0.0073	0.00001857	0.2316	0.09523	0.0153	4.90E-10	rs199454:44800110:G:A
17_44800946_C_T	17	44800946	T	0.2321	-0.0328	0.0073	7.48E-06	0.2305	0.09764	0.01533	1.89E-10	rs199453:44800946:C:T
17_44801340_C_T	17	44801340	T	0.2311	-0.0321	0.0073	0.00001232	0.2298	0.09731	0.01534	2.25E-10	rs199452:44801340:C:T
17_44801784_G_A	17	44801784	A	0.199	-0.0401	0.0078	2.43E-07	0.1969	0.1094	0.01618	1.36E-11	rs199451:44801784:G:A
17_44808342_C_CA	17	44808342	C	0.2331	-0.0312	0.0074	0.0000239	0.2315	0.09454	0.01531	6.65E-10	rs34162554:44808342:C:CA
17_44808902_G_A	17	44808902	A	0.2311	-0.0326	0.0073	8.93E-06	0.2299	0.09712	0.01534	2.47E-10	rs199449:44808902:G:A
17_44809001_A_G	17	44809001	G	0.1997	-0.0397	0.0078	3.03E-07	0.1973	0.1071	0.01615	3.31E-11	rs199448:44809001:A:G
17_44812188_C_T	17	44812188	T	0.1997	-0.0398	0.0078	3.01E-07	0.1974	0.1072	0.01615	3.15E-11	rs199447:44812188:C:T
17_44813169_G_A	17	44813169	G	0.2329	-0.0309	0.0073	0.00002466	0.2316	0.09454	0.01531	6.69E-10	rs199446:44813169:G:A
17_44817408_C_T	17	44817408	T	0.1999	-0.0395	0.0078	3.44E-07	0.1976	0.107	0.01615	3.39E-11	rs199445:44817408:C:T
17_44818276_T_C	17	44818276	C	0.2314	-0.0323	0.0073	0.00001041	0.2301	0.09664	0.01534	2.98E-10	rs199444:44818276:T:C
17_44818954_C_CA	17	44818954	CA	0.2016	-0.0388	0.0078	7.72E-07	0.1991	0.1063	0.01617	4.82E-11	rs113562005:44818954:C:CA
17_44819565_C_T	17	44819565	T	0.1999	-0.0386	0.0078	6.36E-07	0.1976	0.1073	0.01614	3.02E-11	rs199443:44819565:C:T
17_44820122_G_A	17	44820122	A	0.2311	-0.0325	0.0073	9.48E-06	0.2301	0.09742	0.01534	2.17E-10	rs199442:44820122:G:A
17_44820425_T_C	17	44820425	T	0.2329	-0.0309	0.0073	0.00002421	0.2317	0.09445	0.01531	6.91E-10	rs199536:44820425:T:C
17_44821987_G_GA	17	44821987	GA	0.1969	-0.0386	0.0079	1.09E-06	0.1951	0.1101	0.01633	1.58E-11	rs111404933:44821987:G:GA
17_44822662_A_G	17	44822662	G	0.1999	-0.039	0.0078	4.92E-07	0.1976	0.1079	0.01614	2.36E-11	rs199535:44822662:A:G
17_44824213_T_G	17	44824213	G	0.1998	-0.039	0.0078	4.86E-07	0.1975	0.1075	0.01615	2.84E-11	rs199534:44824213:T:G
17_44826056_C_G	17	44826056	G	0.2007	-0.039	0.0078	4.73E-07	0.1995	0.1127	0.01614	2.92E-12	rs9896243:44826056:C:G
17_44828931_G_A	17	44828931	A	0.2001	-0.038	0.0078	9.63E-07	0.1982	0.1072	0.01614	3.02E-11	rs199533:44828931:G:A
17_44830414_T_C	17	44830414	C	0.2331	-0.0333	0.0073	5.31E-06	0.2313	0.09896	0.01533	1.07E-10	rs199531:44830414:T:C

17_44835367_G_GA	17	44835367	GA	0.2029	-0.0377	0.0079	1.64E-06	0.2034	0.1067	0.01618	4.20E-11	rs201825860:44835367:G:GA
17_44836302_T_C	17	44836302	T	0.2698	-0.0264	0.007	0.000158	0.2659	0.09202	0.01467	3.52E-10	rs9912530:44836302:T:C
17_44836653_G_A	17	44836653	G	0.2344	-0.0306	0.0073	0.00002856	0.2333	0.09453	0.01531	6.58E-10	rs199530:44836653:G:A
17_44837217_A_C	17	44837217	C	0.2191	-0.0362	0.0075	1.50E-06	0.215	0.103	0.0156	4.12E-11	rs199529:44837217:A:C
17_44843136_C_T	17	44843136	T	0.2007	-0.0399	0.0078	2.69E-07	0.2002	0.1044	0.01615	1.01E-10	rs199528:44843136:C:T
17_44843667_G_A	17	44843667	G	0.2372	-0.0327	0.0073	7.63E-06	0.2374	0.0899	0.01527	3.91E-09	rs199527:44843667:G:A
17_44847707_C_G	17	44847707	C	0.2167	-0.0365	0.0075	1.25E-06	0.218	0.09454	0.01577	2.01E-09	rs199526:44847707:C:G
17_44847834_T_G	17	44847834	G	0.2007	-0.04	0.0078	2.58E-07	0.2002	0.1043	0.01614	1.07E-10	rs199525:44847834:T:G
17_44848438_G_T	17	44848438	G	0.235	-0.0331	0.0073	6.18E-06	0.2356	0.09082	0.01528	2.78E-09	rs199524:44848438:G:T
17_44848517_C_A	17	44848517	C	0.235	-0.0331	0.0073	6.01E-06	0.2354	0.09105	0.01528	2.53E-09	rs199523:44848517:C:A
17_44853456_G_C	17	44853456	G	0.2348	-0.0335	0.0073	5.01E-06	0.2381	0.09114	0.01528	2.48E-09	rs199521:44853456:G:C
17_44853872_G_A	17	44853872	G	0.2347	-0.034	0.0073	3.34E-06	0.2358	0.09045	0.01527	3.14E-09	rs199520:44853872:G:A
17_44853924_G_A	17	44853924	G	0.2347	-0.0341	0.0073	3.09E-06	0.2358	0.09038	0.01527	3.24E-09	rs199519:44853924:G:A
17_44854580_A_C	17	44854580	A	0.2347	-0.0342	0.0073	2.97E-06	0.2358	0.09084	0.01527	2.70E-09	rs199518:44854580:A:C
17_44854587_A_G	17	44854587	A	0.2346	-0.034	0.0073	3.39E-06	0.2358	0.09035	0.01527	3.30E-09	rs199517:44854587:A:G
17_44856485_C_T	17	44856485	C	0.2017	-0.0398	0.0077	2.65E-07	0.2012	0.1045	0.01609	8.31E-11	rs199516:44856485:C:T
17_44856641_G_C	17	44856641	G	0.2015	-0.0397	0.0077	2.98E-07	0.2009	0.1042	0.01609	9.47E-11	rs199515:44856641:G:C
17_44856881_G_A	17	44856881	G	0.2014	-0.0395	0.0077	3.41E-07	0.2006	0.1036	0.01609	1.21E-10	rs199514:44856881:G:A
17_44856932_A_G	17	44856932	A	0.2014	-0.0396	0.0077	3.19E-07	0.2003	0.1037	0.0161	1.16E-10	rs199513:44856932:A:G
17_44857126_CT_C	17	44857126	CT	0.1997	-0.0396	0.0079	4.53E-07	0.1989	0.1054	0.01617	7.19E-11	rs372432390:44857126:CT:C
17_44857352_T_C	17	44857352	T	0.2015	-0.0396	0.0077	3.23E-07	0.2011	0.1039	0.0161	1.06E-10	rs199512:44857352:T:C
17_44857929_A_C	17	44857929	A	0.2015	-0.0396	0.0077	3.08E-07	0.2011	0.104	0.0161	1.03E-10	rs199510:44857929:A:C
17_44858598_CA_C	17	44858598	CA	0.2568	-0.0398	0.0078	3.64E-07	0.2576	0.09158	0.01616	1.45E-08	rs376907784:44858598:CA:C
17_44858728_G_A	17	44858728	G	0.2015	-0.0397	0.0077	2.90E-07	0.2011	0.1041	0.0161	9.99E-11	rs199509:44858728:G:A
17_44858838_C_G	17	44858838	C	0.2328	-0.0356	0.0074	1.34E-06	0.2326	0.09437	0.01537	8.31E-10	rs199508:44858838:C:G
17_44858855_A_G	17	44858855	A	0.2015	-0.0398	0.0077	2.85E-07	0.2011	0.1042	0.0161	9.89E-11	rs199507:44858855:A:G
17_44859031_A_G	17	44859031	A	0.2007	-0.0391	0.0078	4.75E-07	0.2003	0.1054	0.01612	6.14E-11	rs199506:44859031:A:G
17_44859144_C_T	17	44859144	C	0.2011	-0.0399	0.0077	2.54E-07	0.2008	0.1042	0.01611	9.83E-11	rs415430:44859144:C:T
17_44859148_T_C	17	44859148	T	0.2011	-0.0398	0.0077	2.77E-07	0.2008	0.1042	0.0161	9.77E-11	rs430685:44859148:T:C
17_44859410_A_G	17	44859410	A	0.2012	-0.0399	0.0077	2.54E-07	0.2008	0.1044	0.01611	9.08E-11	rs199505:44859410:A:G
17_44859715_T_C	17	44859715	T	0.2012	-0.0399	0.0077	2.63E-07	0.2008	0.1044	0.01611	9.16E-11	rs70602:44859715:T:C
17_44860021_C_T	17	44860021	T	0.1999	-0.0414	0.0078	1.02E-07	0.1996	0.1054	0.01615	6.67E-11	rs70600:44860021:C:T
17_44861003_C_T	17	44861003	C	0.2023	-0.0392	0.0077	4.11E-07	0.2016	0.1058	0.01607	4.55E-11	rs199504:44861003:C:T
17_44862162_G_A	17	44862162	A	0.1997	-0.0411	0.0078	1.30E-07	0.1996	0.1054	0.01618	7.29E-11	rs199503:44862162:G:A
17_44862347_G_A	17	44862347	A	0.2105	-0.0414	0.0077	7.46E-08	0.2117	0.09393	0.01609	5.25E-09	rs199502:44862347:G:A
17_44862613_A_G	17	44862613	A	0.2294	-0.0351	0.0074	2.12E-06	0.2306	0.09417	0.01546	1.12E-09	rs199501:44862613:A:G
17_44863133_T_C	17	44863133	C	0.2362	-0.034	0.0074	3.75E-06	0.2332	0.09726	0.01529	1.99E-10	rs916888:44863133:T:C
17_44865439_T_G	17	44865439	G	0.2458	-0.0395	0.0072	4.13E-08	0.2429	0.08706	0.01507	7.54E-09	rs2074404:44865439:T:G
17_44865498_C_T	17	44865498	T	0.1881	-0.0427	0.0081	1.46E-07	0.1903	0.09971	0.01694	3.94E-09	rs199499:44865498:C:T
17_44865603_T_C	17	44865603	C	0.2094	-0.0433	0.0077	2.23E-08	0.2112	0.09446	0.01636	7.69E-09	rs199498:44865603:T:C

a. All the variants with *P* < 5E-8 between 42,836,399 and 44,910,520 of the chromosome 17 were extracted from the OCAC (OCAC overall invasive meta-analysis) and BCAC (OncoArray-iCOGS-GWAS meta-analysis) latest meta-analysis datasets.

b. Online Supplementary Material

c. The GWAS index variants were highlighted in yellow (rs12942666 at chr17:43499839 and rs17631303 at chr17:43516402 for epithelial ovarian cancer risk, See Table S3 for references; rs2532263 at chr17:44252468 for breast cancer risk, PMID: 29059683).

Supplementary Table S8. Association results between minor alleles of 467 variants incorportated in the cross tissue gene expression prediction model for the gene of *CRHR1* .[a]

SNP	CHR	pos	Effect Allele (minor allele)	Reference Allele	Effect Allele Frequency	weight (beta)_Expression	Beta_BCAC_GWAS	SE_BCAC_GWAS	*P* _BCAC_GWAS	Beta_OCAC_GWAS	SE_OCAC_GWAS	*P* _OCAC_GWAS
rs8069296	17	42935059	**C**	T	0.2073	0.08109601	0.0018	0.0081	0.8233	0.02221	0.01729	0.199
rs9911406	***17***	***43003906***	***G***	***C***	***0.07995***	***-0.01505708***	***0.0211***	***0.0116***	***0.06855***	***0.006445***	***0.02427***	***0.7906***
rs9890538	***17***	***43003907***	***G***	***T***	***0.07995***	***-0.01370979***	***0.0211***	***0.0116***	***0.06858***	***0.006445***	***0.02427***	***0.7906***
rs962888	17	43059071	**A**	G	0.2927	0.03466586	0.0092	0.007	0.1884	-0.001942	0.0149	0.8963
rs12449792	17	43302259	**T**	C	0.4607	0.002005022	-0.0126	0.0065	0.05328	0.03239	0.01345	0.01601
rs7216796	17	43392208	**G**	A	0.481	0.03613696	-0.0005	0.0062	0.936	0.01884	0.01323	0.1543
rs4328483	17	43401540	**T**	G	0.416	0.005209526	-0.0066	0.0063	0.2993	0.02129	0.01348	0.1142
rs4792814	17	43403005	**T**	C	0.416	0.005889683	-0.0059	0.0063	0.3519	0.02053	0.01344	0.1267
rs17686238	17	43417273	**T**	G	0.1043	0.015773	-0.026	0.0102	0.01115	0.08744	0.02096	0.00003018
rs241030	17	43734503	**G**	A	0.2249	0.000574556	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241027	17	43735478	**G**	A	0.2249	0.003009953	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241026	17	43735555	**A**	G	0.2249	0.003439532	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241023	17	43737040	**A**	G	0.2249	0.003527698	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241022	17	43737730	**C**	T	0.2249	0.003564193	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241021	17	43738627	**G**	T	0.2249	0.003587661	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs241020	17	43738676	**A**	C	0.2249	0.003601846	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17760577	17	43741452	**T**	C	0.2249	0.00360663	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17760631	17	43743045	**C**	T	0.2249	0.00038636	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs1635299	***17***	***43743079***	***T***	***C***	***0.1355***	***-0.0641243***	***0.0216***	***0.0087***	***0.0136***	***-0.07006***	***0.01879***	***0.0001927***
rs17687462	17	43744990	**T**	C	0.2249	2.38E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17760733	17	43746276	**T**	G	0.2249	6.94E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687504	17	43746721	**G**	A	0.2249	6.86E-08	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687534	17	43749579	**C**	T	0.2249	5.42E-09	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687571	17	43750010	**A**	G	0.2249	3.87E-10	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687625	17	43750238	**G**	A	0.2249	0.0000672	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687667	17	43754099	**A**	G	0.2249	0.000395059	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687740	17	43756376	**C**	G	0.2249	0.000612715	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs757502	17	43756506	**T**	C	0.2249	0.000779563	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs757501	17	43756685	**G**	A	0.2249	0.000936337	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs757500	17	43756833	**A**	C	0.2249	0.001090586	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17761046	17	43758382	**C**	T	0.2249	0.001239211	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687838	17	43759048	**C**	T	0.2249	0.001377642	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17687849	17	43759719	**G**	A	0.2249	0.001502744	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17761100	17	43760389	**G**	A	0.2249	0.001613501	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17761124	17	43760516	**T**	A	0.2249	0.001710754	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2049515	17	43761856	**T**	C	0.2249	0.001796537	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2158474	17	43761939	**C**	G	0.2249	0.001873374	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17761207	17	43762255	**C**	T	0.2249	0.001943714	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688002	17	43762594	**T**	A	0.2249	0.002009578	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2040846	17	43762846	**G**	A	0.2249	0.002072382	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs4486953	17	43763007	**C**	T	0.2249	0.002132924	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688032	17	43763202	**A**	G	0.2249	0.002191457	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688056	17	43763241	**T**	C	0.2249	0.002247828	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688068	17	43763935	**G**	A	0.2249	0.002301641	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688090	17	43764987	**A**	G	0.2249	0.002352411	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17761387	17	43765450	**A**	G	0.2249	0.002399699	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688205	17	43766352	**C**	G	0.2249	0.002443204	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688296	17	43767815	**T**	C	0.2249	0.002482814	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688391	17	43772109	**A**	C	0.2249	0.002518615	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688410	17	43772251	**T**	C	0.2249	0.002550862	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688434	17	43772540	**A**	G	0.2249	0.002579939	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17688452	17	43773085	**A**	G	0.2249	0.000964326	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs10491144	17	43773124	**C**	A	0.2249	0.000784689	Reaching GWAS significance in either BCAC or OCAC, See Table S7					

rs10491143	17	43773248	**T**	A	0.2249	0.000716198	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688534	17	43773877	**T**	A	0.2249	0.000618966	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17761838	17	43774959	**C**	T	0.2249	0.000532065	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150141	17	43775145	**A**	G	0.2249	0.000486767	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150610	17	43775479	**C**	T	0.2249	0.000490508	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150547	17	43775546	**G**	A	0.2249	0.00053515	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688682	17	43775929	**G**	C	0.2249	0.000605137	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150454	17	43776061	**T**	C	0.2249	0.000683702	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150464	17	43776371	**T**	C	0.2249	0.000757238	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17761985	17	43776787	**T**	C	0.2249	0.000817561	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688767	17	43777542	**G**	A	0.2249	0.000862155	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688773	17	43777710	**C**	T	0.2249	0.000892979	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762073	17	43777745	**A**	C	0.2249	0.000914667	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688875	17	43778406	**G**	A	0.2249	0.000932752	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762165	17	43778602	**T**	C	0.2249	0.000952302	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688922	17	43779351	**A**	G	0.2249	0.000977101	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17688944	17	43779419	**A**	T	0.2249	0.00100934	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1526128	17	43779624	**T**	C	0.2249	0.001049671	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1526129	17	43779657	**C**	T	0.2249	0.0010975	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762308	17	43780948	**C**	T	0.2249	0.0000598	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs968028	17	43781105	**G**	A	0.2249	3.26E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs968027	17	43781250	**T**	C	0.2249	1.78E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762361	17	43781778	**G**	A	0.2249	9.70E-09	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689104	17	43782492	**G**	A	0.2249	5.29E-10	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689116	17	43782558	**C**	T	0.2249	2.88E-11	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689218	17	43785808	**C**	T	0.2249	1.57E-12	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762535	17	43787130	**C**	T	0.2249	8.58E-14	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563433	17	43800351	**C**	A	0.2249	4.54E-15	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17649019	17	43801593	**A**	G	0.2249	3.43E-16	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10514879	17	43802971	**T**	C	0.2249	0.001305988	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1358071	17	43803189	**C**	A	0.2737	0.05453782	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1880752	17	43806264	**T**	C	0.2249	0.000368109	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4617909	17	43806451	**T**	C	0.2249	0.000377418	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2902662	17	43806925	**A**	G	0.2249	0.000314181	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2864087	17	43807063	**T**	C	0.2249	0.000221995	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4471726	17	43807134	**C**	T	0.2249	0.000135032	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563599	17	43807955	**C**	A	0.2249	0.0000935	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17649138	17	43808067	**A**	G	0.2249	0.000127446	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4390635	17	43809016	**T**	C	0.2249	0.000238305	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17649162	17	43810371	**C**	G	0.2249	0.000399118	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563683	17	43811072	**G**	A	0.2249	0.000573351	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563718	17	43811673	**T**	C	0.2249	0.000721845	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1526125	17	43812177	**T**	C	0.2249	0.00081938	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1526126	17	43812218	**T**	C	0.2249	0.001060402	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12938476	17	43812897	**C**	T	0.4173	0.02195125	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563787	17	43813252	**G**	C	0.2249	0.000491339	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563800	17	43817459	**T**	C	0.2249	0.000706677	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563827	17	43818222	**A**	C	0.2249	0.000995748	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563861	17	43818906	**G**	A	0.2249	0.001069207	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563889	17	43818946	**T**	A	0.2249	0.001120845	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17563923	17	43819450	**A**	G	0.2249	0.001164721	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150683	17	43824848	**G**	A	0.2249	0.001205276	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17334797	17	43825912	**G**	A	0.2249	0.001247251	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150658	17	43826305	**A**	G	0.2249	0.001293839	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150672	17	43826637	**A**	G	0.2249	0.00134584	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs17334894	17	43827209	**A**	G	0.2249	0.00140193	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150451	17	43827431	**G**	A	0.2249	0.001555818	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150048	17	43827471	**C**	G	0.2249	0.001596748	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150455	17	43827508	**G**	A	0.2249	0.001217494	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150604	17	43828221	**A**	T	0.2249	0.001170824	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17334944	17	43828617	**A**	G	0.2249	0.001178644	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17426064	17	43828698	**T**	C	0.2249	0.001423638	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17426106	17	43828935	**C**	G	0.2249	0.001448245	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17426174	17	43830938	**C**	G	0.2249	0.001458227	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17426195	17	43832367	**A**	G	0.2249	0.001465288	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079717	17	43835351	**C**	T	0.2249	0.001483305	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079718	17	43839951	**T**	A	0.2249	0.001481492	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079721	17	43840107	**A**	C	0.2249	0.001475958	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079723	17	43841729	**C**	T	0.2263	0.06188248	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079724	17	43841912	**T**	C	0.2263	0.05915647	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4074462	17	43855228	**T**	G	0.2249	0.000571546	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689471	17	43892973	**C**	T	0.2249	0.000777365	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762769	17	43893403	**A**	G	0.2249	0.000696432	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs8072451	17	43893716	**T**	C	0.2249	0.000605836	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4277389	17	43895653	**G**	A	0.2249	0.000552607	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4566211	17	43895696	**A**	G	0.2249	0.000566408	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689653	17	43898963	**T**	A	0.2249	0.000648905	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17762954	17	43899786	**T**	C	0.2249	0.000779494	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1912151	17	43902944	**T**	C	0.2249	0.000931447	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1396862	17	43902997	**A**	G	0.2249	0.001082963	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689824	17	43904397	**T**	C	0.2249	0.001220648	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17763086	17	43905481	**G**	T	0.2249	0.001338577	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689882	17	43906828	**A**	G	0.2249	0.001435911	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1876831	17	43907745	**T**	C	0.2249	0.00151464	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs16940665	17	43907896	**C**	T	0.2249	0.001577925	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17689918	17	43910088	**A**	G	0.2249	0.001629086	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs16940674	17	43910507	**T**	C	0.2249	0.00167108	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1876829	17	43911443	**C**	T	0.2249	0.001706291	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs16940677	17	43911898	**T**	C	0.2249	0.001736511	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs878886	17	43912490	**G**	C	0.2249	0.001763007	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs878887	17	43912582	**T**	C	0.2249	0.001786619	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4640231	17	43912786	**C**	G	0.2249	0.001807856	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10445364	17	43916356	**A**	G	0.2249	0.001826988	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17763533	17	43918190	**C**	T	0.2249	0.001349707	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17690314	17	43919884	**G**	T	0.2249	0.001378231	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17690326	17	43920974	**C**	T	0.2249	0.001439556	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17763596	17	43921210	**T**	G	0.2249	0.001493893	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17763634	17	43921754	**C**	T	0.2249	0.001535602	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12185233	17	43923654	**C**	G	0.2249	0.00148742	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12185268	17	43923683	**G**	A	0.2249	0.001488475	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12185235	17	43923703	**T**	C	0.2249	0.001472108	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079725	17	43923934	**C**	T	0.2249	0.001463613	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12373123	17	43924073	**C**	T	0.2249	0.001454504	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12373139	17	43924130	**A**	G	0.2249	0.001444359	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12373142	17	43924200	**G**	C	0.2249	0.001407127	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12373124	17	43924219	**C**	T	0.2249	0.001393833	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12373168	17	43924337	**C**	A	0.2263	0.08811154	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17690661	17	43924521	**A**	G	0.2249	0.00212914	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17690679	17	43924803	**G**	A	0.2249	0.00221808	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17769490	17	43925605	**A**	G	0.2249	0.00217472	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs885639	17	43928614	**G**	T	0.2249	0.002128497	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2873269	17	43931122	**T**	C	0.2249	0.002103446	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs4627402	17	43932741	**T**	C	0.2209	0.04895312	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs10445335	17	43934896	**A**	T	0.2249	0.000301384	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs10445370	17	43935118	**A**	G	0.2249	0.000694561	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs12150516	17	43944519	**T**	C	0.2249	0.00064822	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs1078830	17	43946112	**C**	T	0.2249	0.000585512	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs34097347	17	43949448	**A**	C	0.2249	0.00056271	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2106784	17	43949892	**T**	C	0.2249	0.000621306	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2158072	17	43950195	**C**	T	0.2249	0.000762367	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs10491140	17	43950976	**T**	G	0.2249	0.00095478	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2055794	17	43951717	**A**	G	0.2249	0.001161961	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs916793	17	43954686	**A**	G	0.2249	0.001357828	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs4441322	17	43955030	**G**	A	0.2249	0.001529311	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691328	17	43955487	**T**	C	0.2249	0.001672715	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2019822	17	43959918	**A**	T	0.2249	0.00178947	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770108	17	43961292	**T**	G	0.2249	0.001883197	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770120	17	43963943	**A**	C	0.2249	0.001958102	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770150	17	43964163	**A**	G	0.2249	0.002018207	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770186	17	43964191	**A**	C	0.2249	0.002067035	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691449	17	43964283	**C**	G	0.2249	0.00210751	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691466	17	43968219	**G**	A	0.2249	0.002141977	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691508	17	43968463	**G**	C	0.2249	0.002172263	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770296	17	43969136	**T**	C	0.2249	0.002199774	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691556	17	43969168	**A**	T	0.2249	0.002225578	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770337	17	43969779	**T**	G	0.2249	0.002250482	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17770343	17	43970154	**C**	T	0.2249	0.000122707	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17691610	17	43970662	**T**	G	0.2249	6.69E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs1864325	17	43977827	**T**	C	0.2249	3.65E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs1560310	17	43978534	**A**	G	0.2249	1.99E-08	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2099151	17	43979822	**T**	A	0.2249	1.08E-09	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2082068	17	43979971	**T**	C	0.2249	5.91E-11	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs1984937	17	43980530	**C**	A	0.2249	3.22E-12	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17563965	17	43990919	**G**	A	0.2249	1.76E-13	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17563986	17	43991272	**G**	A	0.2249	9.69E-15	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649518	17	43994386	**A**	C	0.2249	4.43E-16	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649553	17	43994648	**T**	C	0.2249	4.43E-17	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649571	17	43994952	**G**	A	0.2249	4.43E-17	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649866	17	44000914	**C**	T	0.2249	0.000943615	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564493	17	44001379	**T**	C	0.2249	0.001418885	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649918	17	44001621	**G**	A	0.2249	0.001547886	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17649954	17	44001661	**G**	A	0.2249	0.001019227	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564619	17	44002138	**G**	A	0.2249	0.001021219	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17650063	17	44002555	**G**	A	0.2249	0.001060417	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564703	17	44002595	**T**	C	0.2249	0.000851451	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs16940742	***17***	***44004924***	***G***	***A***	***0.05962***	***-0.09094916***	***-0.0007***	***0.0125***	***0.9571***	***-0.0534***	***0.02698***	***0.04777***
rs17564780	17	44005413	**G**	A	0.2249	0.0008741	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564829	17	44006601	**C**	T	0.2249	0.000977098	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs7501759	17	44009921	**G**	A	0.2249	0.001373387	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2316782	17	44010040	**G**	A	0.2249	0.001443441	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs2316783	17	44010118	**C**	G	0.2249	0.001485974	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564871	17	44011018	**G**	A	0.2249	0.001521204	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564948	17	44011749	**G**	A	0.2249	0.001552284	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17564983	17	44011825	**C**	A	0.2236	0.0311736	Reaching GWAS significance in either BCAC or OCAC, See Table S7					
rs17650335	17	44012343	**A**	G	0.2249	0.001139983	Reaching GWAS significance in either BCAC or OCAC, See Table S7					

rs17565025	17	44012463	**C**	T	0.2249	0.001252378	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650381	17	44013024	**C**	T	0.2249	0.001186063	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650417	17	44013103	**T**	G	0.2249	0.001474458	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150111	17	44013938	**G**	A	0.2249	0.001487956	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150460	17	44014137	**T**	G	0.2249	0.001480576	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150195	17	44014263	**C**	T	0.2249	0.001473107	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150229	17	44015446	**G**	A	0.2249	0.001469105	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150230	17	44015464	**G**	A	0.2249	0.001469708	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150576	17	44015624	**A**	G	0.2249	0.001473632	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150235	17	44015745	**G**	A	0.2249	0.001487216	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150242	17	44015816	**G**	A	0.2249	0.00144392	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150104	17	44015929	**A**	G	0.2249	0.001432316	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2316784	17	44021699	**T**	G	0.2249	0.001422232	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4327091	17	44021717	**A**	G	0.2249	0.001411652	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650579	17	44030115	**T**	C	0.2249	0.001385346	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650597	17	44030195	**T**	A	0.2249	0.001372108	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650633	17	44030231	**C**	T	0.2249	0.001359425	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650651	17	44030311	**G**	T	0.2249	0.001346548	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17571718	17	44032768	**C**	T	0.2249	0.00133353	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17571739	17	44032915	**C**	T	0.2249	0.001320472	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17571781	17	44033802	**C**	T	0.2249	0.001307521	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17571809	17	44034859	**G**	A	0.2249	0.001294834	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650771	17	44035367	**G**	A	0.2249	0.001282538	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17571857	17	44035706	**G**	A	0.2249	0.001270719	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650818	17	44036787	**C**	T	0.2249	0.001259427	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650842	17	44037491	**G**	A	0.2249	0.001248691	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650860	17	44039008	**A**	G	0.2249	0.001238531	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650872	17	44039516	**T**	G	0.2249	0.001228963	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650901	17	44039691	**G**	A	0.2249	0.001220003	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650973	17	44044220	**T**	A	0.2249	0.001211669	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17650991	17	44044508	**C**	A	0.2249	0.001203976	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572147	17	44044985	**G**	A	0.2249	0.00119694	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572169	17	44045974	**T**	C	0.2249	0.001190576	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651093	17	44049550	**A**	G	0.2249	0.001184895	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572248	17	44049867	**G**	A	0.2249	0.001179905	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651134	17	44050340	**A**	G	0.2249	0.001175611	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1800547	17	44051846	**G**	A	0.2249	0.001172013	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651213	17	44051924	**A**	G	0.2249	0.00116911	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572361	17	44052009	**C**	T	0.2249	0.001166894	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651243	17	44052284	**A**	G	0.2249	0.001165356	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2217394	17	44053448	**G**	A	0.2249	0.00116448	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651285	17	44054237	**A**	G	0.2249	0.00116425	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572467	17	44054388	**C**	T	0.2249	0.001164641	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572495	17	44054596	**G**	T	0.2249	0.001165629	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs754512	17	44055647	**T**	A	0.2249	0.001167183	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2163129	17	44056433	**C**	T	0.2249	0.00116927	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1981997	17	44056767	**A**	G	0.2249	0.001171852	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1981998	17	44056833	**A**	G	0.2249	0.001174888	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572613	17	44058004	**G**	A	0.2249	0.001178334	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572627	17	44058629	**A**	T	0.2249	0.001182143	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651483	17	44058861	**A**	C	0.2249	0.001186265	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651549	17	44061278	**T**	C	0.2249	0.001190649	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1529534	17	44063140	**G**	A	0.2249	0.00119524	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572795	17	44063393	**A**	G	0.2249	0.001199985	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572823	17	44063563	**C**	T	0.2249	0.001204829	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs9901937	17	44063723	**C**	A	0.2249	0.001209716	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572851	17	44063766	**G**	A	0.2249	0.001214594	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17572893	17	44064208	**A**	G	0.2249	0.001219409	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1529535	17	44064759	**C**	A	0.2249	0.001224113	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10445371	17	44065410	**A**	G	0.2249	0.001228658	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs919461	17	44065669	**T**	A	0.2249	0.001233	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs919464	17	44065901	**T**	C	0.2249	0.001237099	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651700	17	44066634	**G**	C	0.2249	0.001240919	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10445337	17	44067400	**C**	T	0.2249	0.001244427	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17651754	17	44067546	**C**	T	0.2249	0.001247597	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10445338	17	44067682	**A**	G	0.2249	0.001250403	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1052551	17	44068924	**A**	G	0.2249	0.001252829	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17573175	17	44071089	**G**	C	0.2249	0.001254858	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1052553	17	44073889	**G**	A	0.2249	0.001256481	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652121	17	44073973	**C**	T	0.2249	0.001257691	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2004674	17	44075110	**T**	A	0.2249	0.001258485	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1078269	17	44075837	**C**	T	0.2249	0.001258864	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1078268	17	44075901	**G**	A	0.2249	0.001258831	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17573593	17	44082603	**C**	A	0.2249	0.001258393	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17573607	17	44083081	**A**	G	0.2249	0.001257559	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652337	17	44083323	**T**	C	0.2249	0.00125634	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1991556	17	44083402	**A**	G	0.2236	0.06153875	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652449	17	44088937	**C**	G	0.2249	0.000153022	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs733966	17	44089563	**T**	C	0.2249	0.000428497	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150506	17	44090536	**A**	G	0.2249	0.000384417	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150170	17	44090646	**G**	A	0.2249	0.000299351	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150515	17	44090685	**T**	G	0.2249	0.000204852	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17573858	17	44090796	**C**	T	0.2249	0.000139184	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652502	17	44094471	**A**	G	0.2249	0.000128627	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs9468	17	44101563	**C**	T	0.2249	0.000174054	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1052587	17	44102604	**C**	T	0.2249	0.000257659	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1052594	17	44102689	**C**	G	0.2249	0.000356471	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574040	17	44102865	**C**	A	0.2249	0.000452224	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs16940799	17	44102933	**C**	T	0.2249	0.000534696	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs7687	17	44103296	**C**	T	0.2249	0.000600552	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652748	17	44103616	**T**	C	0.2249	0.00065067	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2158257	17	44104343	**C**	A	0.2249	0.000687785	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574228	17	44104509	**C**	T	0.2249	0.000715011	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs7350928	17	44108100	**T**	C	0.2249	0.00073513	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574361	17	44108202	**G**	A	0.2249	0.000750345	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17652961	17	44108355	**A**	G	0.2249	0.000762282	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574425	17	44109188	**G**	C	0.2249	0.000772075	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1076222	17	44109769	**G**	C	0.2249	0.000780487	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574604	17	44111613	**G**	A	0.2249	0.000788015	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653162	17	44111827	**A**	C	0.2249	0.000794983	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653193	17	44112441	**A**	G	0.2249	0.0008016	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653211	17	44112638	**C**	T	0.2249	0.000807997	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653255	17	44112743	**A**	C	0.2249	0.000814248	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4608377	17	44113359	**C**	T	0.2249	0.000820383	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574796	17	44115074	**C**	T	0.2249	0.000826384	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17574824	17	44115107	**T**	C	0.2249	0.000832202	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12185243	17	44115351	**C**	T	0.2249	0.000837758	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs11079729	17	44115569	**A**	C	0.2249	0.000842969	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150542	17	44115730	**A**	G	0.2249	0.000847752	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150090	17	44115886	**T**	C	0.2249	0.00085205	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs41437445	17	44116238	**A**	G	0.2249	0.000855835	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10514897	17	44117397	**G**	A	0.2249	0.000859116	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs41382552	17	44118999	**G**	A	0.2249	0.000861935	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10514898	17	44119636	**C**	A	0.2249	0.000864364	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs41374248	17	44120442	**G**	A	0.2249	0.000866488	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs41399444	17	44121469	**T**	C	0.2249	0.000868399	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150570	17	44126218	**A**	G	0.2249	0.000870184	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150447	17	44128125	**C**	A	0.2249	0.000871912	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150064	17	44128407	**A**	C	0.2249	0.000873637	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653836	17	44128876	**A**	T	0.2249	0.000875387	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575423	17	44129253	**C**	T	0.2249	0.000877174	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575437	17	44133031	**A**	T	0.2249	0.000878996	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653889	17	44133070	**T**	A	0.2249	0.000880836	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653906	17	44133142	**A**	G	0.2249	0.000882677	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575507	17	44134095	**G**	A	0.2249	0.0008845	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs876944	17	44134391	**T**	G	0.2249	0.000886292	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1107820	17	44135359	**C**	T	0.2249	0.000888047	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575556	17	44135827	**A**	G	0.2249	0.000889768	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17653998	17	44135985	**G**	A	0.2249	0.00089147	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs41384744	17	44137070	**G**	A	0.2249	0.000893177	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17654016	17	44137925	**C**	T	0.2249	0.000894919	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2316951	17	44139083	**C**	G	0.2249	0.000896736	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575683	17	44139662	**T**	C	0.2249	0.000898669	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2838	17	44141347	**G**	A	0.2249	0.000900761	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575773	17	44142879	**T**	C	0.2249	0.000903055	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17575850	17	44144387	**A**	C	0.2249	0.000905589	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17659731	17	44144634	**A**	G	0.2249	0.000908398	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1117253	17	44149297	**C**	A	0.2249	0.000911507	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150625	17	44149448	**G**	C	0.2249	0.000914934	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150627	17	44149537	**G**	C	0.2249	0.000918688	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150628	17	44149581	**T**	C	0.2249	0.000922767	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150611	17	44149741	**A**	G	0.2249	0.000927157	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs974293	17	44150233	**A**	G	0.2249	0.000931837	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs974291	17	44150480	**T**	A	0.2249	0.000936773	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150551	17	44150920	**C**	T	0.2249	0.000941923	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150558	17	44151156	**C**	T	0.2249	0.000947238	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17659881	17	44157597	**G**	A	0.2249	0.000952662	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1476554	17	44159102	**T**	C	0.2249	0.000958135	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17659953	17	44159725	**T**	C	0.2249	0.000963594	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660017	17	44160674	**C**	G	0.2249	0.000968976	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660065	17	44162284	**C**	T	0.2249	0.000974216	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs3912061	17	44165098	**T**	C	0.2249	0.000979254	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660132	17	44165803	**C**	T	0.2249	0.000984033	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660167	17	44166311	**T**	C	0.2249	0.000988501	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660228	17	44166500	**A**	G	0.2249	0.000992613	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660251	17	44166646	**T**	C	0.2249	0.000996329	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660294	17	44167101	**C**	T	0.2249	0.000999617	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660337	17	44169605	**C**	T	0.2249	0.001002449	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576631	17	44170018	**C**	G	0.2249	0.001004808	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660398	17	44170612	**T**	C	0.2249	0.001006678	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576695	17	44172327	**A**	T	0.2249	0.001008053	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576709	17	44173356	**G**	C	0.2249	0.001008928	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660464	17	44177993	**A**	C	0.2249	0.001009303	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576779	17	44178272	**T**	C	0.2249	0.001009181	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660488	17	44178337	**C**	T	0.2249	0.001008565	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs17576842	17	44179992	**G**	A	0.2249	0.001007462	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576870	17	44180442	**G**	A	0.2249	0.001005877	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660595	17	44180954	**G**	A	0.2249	0.001003817	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576954	17	44181933	**C**	T	0.2249	0.001001286	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17576989	17	44183616	**A**	C	0.2249	0.00099829	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4510068	17	44184828	**T**	G	0.374	0.004630343	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577024	17	44186252	**A**	G	0.2249	0.000255957	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577052	17	44186301	**C**	T	0.2249	0.000607142	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577094	17	44187492	**G**	A	0.2249	0.000755794	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577159	17	44188477	**G**	T	0.2249	0.000863199	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660847	17	44189373	**T**	C	0.2249	0.000924965	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660865	17	44189408	**C**	T	0.2249	0.000951388	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660907	17	44191085	**A**	G	0.2249	0.000958126	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17660936	17	44191159	**T**	C	0.2249	0.000955976	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577313	17	44191835	**G**	A	0.2249	0.000950264	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4548919	17	44192395	**T**	G	0.2249	0.000943107	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4630591	17	44192568	**T**	C	0.2222	0.000212133	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4606752	17	44192618	**G**	A	0.2249	0.000166376	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577369	17	44192923	**G**	A	0.2249	0.000295619	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661015	17	44192957	**C**	T	0.2249	0.000256085	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661027	17	44193097	**A**	C	0.2249	0.000200995	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661045	17	44194152	**A**	T	0.2249	0.000137139	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577447	17	44194381	**A**	T	0.2249	0.0000805	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10514901	17	44194735	**T**	G	0.2249	0.0000411	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577496	17	44194835	**C**	T	0.2249	0.0000185	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661141	17	44196015	**G**	C	0.2249	7.52E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1468241	17	44196153	**G**	A	0.2249	2.78E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577650	17	44205500	**G**	A	0.2249	1.12E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs4471723	17	44205690	**T**	C	0.2249	0.0000126	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1122381	17	44205839	**G**	A	0.2249	0.0000546	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1122380	17	44206079	**T**	C	0.2249	0.000132218	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs10514903	17	44206646	**G**	C	0.2249	0.00023202	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661348	17	44207066	**G**	A	0.2249	0.000333448	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661385	17	44207778	**G**	A	0.2249	0.000421232	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17661428	17	44208144	**G**	C	0.2249	0.000489486	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577877	17	44208218	**G**	A	0.2249	0.000539108	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577954	17	44209628	**C**	T	0.2249	0.000573713	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17577975	17	44210442	**T**	C	0.2249	0.000596993	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150087	17	44210988	**G**	C	0.2249	0.000611769	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs12150320	17	44213204	**T**	C	0.2249	0.000619997	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532316	17	44213712	**A**	G	0.2249	0.000623057	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696604	17	44214094	**G**	A	0.2249	0.000034	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696600	17	44216226	**G**	A	0.2249	1.85E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532314	17	44217112	**T**	G	0.2249	1.01E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532313	17	44217293	**A**	G	0.2249	5.51E-09	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1918799	17	44218242	**T**	C	0.2249	3.00E-10	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1528075	17	44220454	**G**	T	0.2249	1.64E-11	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532307	17	44221350	**A**	G	0.2249	8.93E-13	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696590	17	44221602	**C**	G	0.2249	4.87E-14	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1406074	17	44222067	**G**	T	0.2249	2.62E-15	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1918798	17	44222335	**A**	G	0.2249	1.99E-16	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1918789	17	44240107	**C**	T	0.2249	0.000709485	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2141299	17	44240986	**A**	C	0.2249	0.000560221	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696567	17	44241304	**G**	C	0.2249	0.00037906	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532286	17	44241664	**C**	T	0.2249	0.00023119	Reaching GWAS significance in either BCAC or OCAC, See Table S7

rs4792843	17	44243179	**G**	A	0.2249	0.000127312	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17585608	17	44243979	**T**	C	0.2249	0.0000635	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696684	17	44244397	**A**	G	0.2249	0.0000288	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs17585644	17	44244581	**C**	T	0.2249	0.0000119	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696657	17	44244926	**G**	T	0.2249	4.53E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696660	17	44246211	**G**	A	0.2249	1.59E-06	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532278	17	44246405	**A**	C	0.2249	5.19E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532276	17	44246624	**A**	C	0.2249	1.59E-07	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532275	17	44246997	**A**	G	0.2249	4.56E-08	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532273	17	44247314	**T**	C	0.2249	1.24E-08	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532271	17	44248042	**A**	G	0.2249	3.18E-09	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1881193	17	44248769	**C**	T	0.2249	7.80E-10	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs1881194	17	44248814	**A**	G	0.2249	1.83E-10	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696662	17	44249621	**G**	A	0.2249	4.11E-11	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532270	17	44249800	**A**	G	0.2249	8.87E-12	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532267	17	44250616	**A**	G	0.2249	1.85E-12	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs956329	17	44251230	**C**	T	0.2249	1.01E-13	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696666	17	44251972	**A**	G	0.2249	5.47E-15	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532264	17	44252416	**C**	G	0.2249	3.32E-16	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2696557	17	44347218	**A**	C	0.2209	0.04326429	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2532329	17	44350090	**A**	G	0.2182	0.01570899	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2668617	17	44351285	**G**	A	0.2182	0.0165208	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2732706	17	44351686	**T**	C	0.2182	0.01729271	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2732705	17	44351929	**G**	T	0.2195	0.09992224	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2668624	17	44352872	**G**	A	0.2168	0.0444957	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2668628	17	44353885	**A**	G	0.2168	0.04416764	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs2261201	17	44354549	**G**	C	0.2182	0.01755723	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs199528	17	44843136	**T**	C	0.2127	0.02384363	Reaching GWAS significance in either BCAC or OCAC, See Table S7
rs199498	17	44865603	**C**	T	0.2127	0.03189908	Reaching GWAS significance in either BCAC or OCAC, See Table S7

a Online Supplementary Note